



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 114881**

**To: Terra Gibbs**  
**Location: rem/2d10/2c18**  
**Art Unit: 1635**  
**Wednesday, March 03, 2004**

**Case Serial Number: 10/029115**

**From: Beverly Shears**  
**Location: Remsen Bldg.**  
**RM 1A54**  
**Phone: 571-272-2528**

**beverly.shears@uspto.gov**

### **Search Notes**

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## SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

### Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

### STAFF USE ONLY

Date completed: <u>03-03-04</u>	Search Site	Vendors
Searcher: <u>Beverly C 2528</u>	<input type="checkbox"/> STIC	<input type="checkbox"/> IG
Terminal time: <u>20</u>	<input type="checkbox"/> CM-1	<input type="checkbox"/> STN
Elapsed time: _____	<input type="checkbox"/> Pre-S	<input type="checkbox"/> Dialog
CPU time: _____	Type of Search	<input type="checkbox"/> APS
Total time: <u>25</u>	<input type="checkbox"/> N.A. Sequence	<input type="checkbox"/> Geninfo
Number of Searches: _____	<input type="checkbox"/> A.A. Sequence	<input type="checkbox"/> SDC
Number of Databases: <u>1</u>	<input type="checkbox"/> Structure	<input type="checkbox"/> DARC/Questel
	<input type="checkbox"/> Bibliographic	<input checked="" type="checkbox"/> Other <u>CGN</u>

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STIC-Biotech/ChemLib

114881

From: Gibbs, Terra  
Sent: Sunday, February 22, 2004 1:51 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search request

Please do a regular search of SEQ ID NO:1 of USSN 10/029,115.

Also, include an oligomer search of SEQ ID NO:1 as I am looking for a nucleic acid capable of hybridizing to SEQ ID NO:1.

Terra Cotta Gibbs, Ph.D.  
Art Unit 1635  
Remsen Building 2D10  
571-272-0758

RECEIVED  
FEB 23 2004  
STIC

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
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Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
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Lexis/Nexis: \_\_\_\_\_  
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Other (specify): \_\_\_\_\_

AGE BLANK (USPTO)

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 09:55:00 ; Search time 8004 Seconds  
(without alignments)  
13368.860 Million cell updates/sec

Title: US-10-029-115-1  
Perfect score: 3951  
Sequence: 1 gccctatggggcagccaccgc.....tcatactggtgaagggc 3951

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 37577330 seqs, 17593059518 residues  
Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Gibbs T.  
10/029/115 Page 1  
Seq. ID 1 w/Interf

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4	3867	97.9	4989	1 PCT-US03-37730-26	Sequence 26, Appl
5	3838.6	97.2	5191	89 US-60-324-185-5555	Sequence 5555, Ap
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7	3772.8	95.5	4032	1 PCT-US02-33845-6	Sequence 6, Appli
8	3637.4	92.1	4631	107 US-60-500-337-1177	Sequence 1177, Ap
9	3637.4	92.1	4681	107 US-60-500-337-1176	Sequence 1176, Ap
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ALIGNMENTS

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GENERAL INFORMATION:  
APPLICANT: Luo, Ying  
APPLICANT: Fu, Alan C  
APPLICANT: Shen, Mary  
TITLE OF INVENTION: Novel Germinal Center Kinase Cell Cycle Proteins, Compositions and Methods of Use  
FILE REFERENCE: A-70229/RMS/DHR  
CURRENT APPLICATION NUMBER: US/10/029, 115  
CURRENT FILING DATE: 2001-10-19  
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SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 3951  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-029-115-1

Query Match 100.0%; Score 3951; DB 43; Length 3951;  
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Db 1561 TGGGCCCCGAGAGTGAAGAGAGAAACAAGATGAACAAGCAGCAGCAATCTCTCTGGCC 1620  
QY 1621 AAGAGCAAGCCAGGACAGCGGGGCTGAGCCGCCATCCGCCAGGCTCTCCCAAGGAGCC 1680  
Db 1621 AAGAGCAAGCCAGGACAGCGGGGCTGAGCCGCCATCCGCCAGGCTCTCCCAAGGAGCC 1680  
QY 1681 CCAAGACCCCTTTTCCAGACTCTCTTAAGAGAGCGGTGAGAGCCCAAGAGGAGACCG 1740  
Db 1681 CCAAGACCCCTTTTCCAGACTCTCTTAAGAGAGCGGTGAGAGCCCAAGAGGAGACCG 1740  
QY 1741 CACAAGTCCCTGACAGAGCAAGCCCAAGGAACTGGCTGCTTCCAGCCTCCCATGAC 1800  
Db 1741 CACAAGTCCCTGACAGAGCAAGCCCAAGGAACTGGCTGCTTCCAGCCTCCCATGAC 1800  
QY 1801 CCGACCCCTGACATCCCGGACCCCACTGACAGCCAGCCAGTGCAGAGAGCTGATCCGC 1860  
Db 1801 CCGACCCCTGACATCCCGGACCCCACTGACAGCCAGCCAGTGCAGAGAGCTGATCCGC 1860  
QY 1861 CAGAATTCAGACCCCACTCTGAAGAGACTGAGGCCCAAGCCCAAGCTCCGAGCTGGTCC 1920  
Db 1861 CAGAATTCAGACCCCACTCTGAAGAGACTGAGGCCCAAGCCCAAGCTCCGAGCTGGTCC 1920  
QY 1921 CGCCCAAGTAAAGAGGCCCAAGGAGTGCCTGAGAGAGCTCAATCTATGCGCCTGCGC 1980  
Db 1921 CGCCCAAGTAAAGAGGCCCAAGGAGTGCCTGAGAGAGCTCAATCTATGCGCCTGCGC 1980  
QY 1981 CTTAAACCAAGTGGGGCGGAGGGGTCCGGGCAAGCCAGGAGTCCGAGCAGAGCTGAGC 2040  
Db 1981 CTTAAACCAAGTGGGGCGGAGGGGTCCGGGCAAGCCAGGAGTCCGAGCAGAGCTGAGC 2040  
QY 2041 AGCAACTCCGCTGGCAAAATCTATCTGCAAAAGCGCGGAGAGCGGGGCAAGCCCAAGCT 2100  
Db 2041 AGCAACTCCGCTGGCAAAATCTATCTGCAAAAGCGGGGAGAGCGGGGCAAGCCCAAGCT 2100  
QY 2101 CCAAGGCCCCCTGCTCAGGCCCCCTGAGCCGCCCAAGCCTCTAATGAAACCCGAGCCTCAGG 2160

Db 2101 CCAAGGCCCCCTGCTCAGGCCCCCTGAGCCGCCCAAGCCTCTAATGAAACCCGAGCCTCAGG 2160  
QY 2161 AGAGCGACCCCTGCTGAGAAAGCTGAGACAGCTCTTCCAGCTCTCAGGCGACCTC 2220  
Db 2161 AGAGCGACCCCTGCTGAGAAAGCTGAGACAGCTCTTCCAGCTCTCAGGCGACCTC 2220  
QY 2221 CCGCAGGCTGGCTCACTGAGAGCGGAAACCGGTGGGAACTCTCCAACTGGAGAGCTCC 2280  
Db 2221 CCGCAGGCTGGCTCACTGAGAGCGGAAACCGGTGGGAACTCTCCAACTGGAGAGCTCC 2280  
QY 2281 CCTGTGCTCTCCCTGGGAAATAAGCAAGCCAGACCAAGCAGCTCAGCGCAGCGCG 2340  
Db 2281 CCTGTGCTCTCCCTGGGAAATAAGCAAGCCAGACCAAGCAGCTCAGCGCAGCGCG 2340  
QY 2341 CCGGCAAGCTTTGTGTTGCTGAAAGACCGAGCTTGAACAGAGCCCTCGGCTTCCAG 2400  
Db 2341 CCGGCAAGCTTTGTGTTGCTGAAAGACCGAGCTTGAACAGAGCCCTCGGCTTCCAG 2400  
QY 2401 AAGGCAATGACCTAATGCTGCTCAGAGAGAGAGTGAAGAGATGAGAGAGAGAG 2460  
Db 2401 AAGGCAATGACCTAATGCTGCTCAGAGAGAGAGTGAAGAGATGAGAGAGAGAG 2460  
QY 2461 GAAAGCGAAGCGCGGCGCAGAGAGGAGCAGAGATACCCCTGGGGGCGCAGGATGG 2520  
Db 2461 GAAAGCGAAGCGCGGCGCAGAGAGGAGCAGAGATACCCCTGGGGGCGCAGGATGG 2520  
QY 2521 GATACAGACAGCGTCAGACCAATGATGATCCAGAGCTGAGAGATCACCGGAGCCAG 2580  
Db 2521 GATACAGACAGCGTCAGACCAATGATGATCCAGAGCTGAGAGATCACCGGAGCCAG 2580  
QY 2581 CCCCCTAATCGGGGGGCGCAGATGATGATCCAGGCGACCCCTTGAAGAGAGAGAGAGCTG 2640  
Db 2581 CCCCCTAATCGGGGGGCGCAGATGATGATCCAGGCGACCCCTTGAAGAGAGAGAGAGCTG 2640  
QY 2641 CTGCAATGCTGACAGCAATGGGATACAAACCTGCTGAGCTGCTCAGGCGACGACCTCA 2700  
Db 2641 CTGCAATGCTGACAGCAATGGGATACAAACCTGCTGAGCTGCTCAGGCGACGACCTCA 2700  
QY 2701 CCAACCGAAGACAGCAAGGCGCAAGCCCACTTGAAGAGTGGAGTGTGACTACAG 2760  
Db 2701 CCAACCGAAGACAGCAAGGCGCAAGCCCACTTGAAGAGTGGAGTGTGACTACAG 2760  
QY 2761 TCTGTGGGCTGTGTAAGGCCCCCTGCAAGAGCTCTGTAAGAGTGTGTAATCTAGGG 2820  
Db 2761 TCTGTGGGCTGTGTAAGGCCCCCTGCAAGAGCTCTGTAAGAGTGTGTAATCTAGGG 2820  
QY 2821 ATCTACAGCCTGAGAGCAAGTGGGAGCAGCATCCCAATCAGAGCCCTAGTGGTGAAG 2880  
Db 2821 ATCTACAGCCTGAGAGCAAGTGGGAGCAGCATCCCAATCAGAGCCCTAGTGGTGAAG 2880  
QY 2881 GGCATCTGGCTGACAGCTGCACTGATGAGAGAGGTTTGTGTCAACGTGAAT 2940  
Db 2881 GGCATCTGGCTGACAGCTGCACTGATGAGAGAGGTTTGTGTCAACGTGAAT 2940  
QY 2941 CCAACCAACCCCGGGGCGCAGTGAACCCCTGAGATCCGGAAGTACAAAGCGATTC 3000  
Db 2941 CCAACCAACCCCGGGGCGCAGTGAACCCCTGAGATCCGGAAGTACAAAGCGATTC 3000  
QY 3001 AACCTCGAGATCCCTGATGAGCCCTTGGGGGGGTCAACCTGCTGTGGGCAAGAGAAC 3060  
Db 3001 AACCTCGAGATCCCTGATGAGCCCTTGGGGGGGTCAACCTGCTGTGGGCAAGAGAAC 3060  
QY 3061 GGGCTGATGTTGCTGAGACCAAGTGGCAAGGAGTGAATGAGCTCATTTGGCGGCGA 3120  
Db 3061 GGGCTGATGTTGCTGAGACCAAGTGGCAAGGAGTGAATGAGCTCATTTGGCGGCGA 3120  
QY 3121 CGCTTCAAGAGATGATGATGCTGAGAGGGGCTCAACTGCTCATCACTTCAGGGAAA 3180  
Db 3121 CGCTTCAAGAGATGATGATGCTGAGAGGGGCTCAACTGCTCATCACTTCAGGGAAA 3180  
QY 3181 AGGAACAACTGGGGGTATTAACCTGCTGCTGCGGAACAAGATTTCTGCAATGAC 3240

Db	3181	AGGAACAACTGCGGGTATTTACTGTCTGGCTCCGGAAACAGATTCTGCACAATGAC	3248
Qy	3241	CCAGAACTGAGAGAGAACAGGGCTGAGCAACCTGGGGGGAATGAGAGGGCTCGGGCAC	3300
Db	3241	CCAGAACTGAGAGAGAACAGGGCTGAGCAACCTGGGGGGAATGAGAGGGCTCGGGCAC	3300
Qy	3301	TACCGTGTGGAAATACGAGCGGATTAAATTCTGGTCAATCGCCCTAAGAGCTCCGTG	3360
Db	3301	TACCGTGTGGAAATACGAGCGGATTAAATTCTGGTCAATCGCCCTAAGAGCTCCGTG	3360
Qy	3361	GAGGTATATGCTGGGCCCCCAAAACCTACACAAATTATGAGCCCTTCAAGCTCTTGGCC	3420
Db	3361	GAGGTATATGCTGGGCCCCCAAAACCTACACAAATTATGAGCCCTTCAAGCTCTTGGCC	3420
Db	3421	GACCTCCCCCAACCGCCCTCTGTGTCGACCTGACAGTAGAGAGAGGGCAGCGGCTCAAG	3480
Qy	3421	GACCTCCCCCAACCGCCCTCTGTGTCGACCTGACAGTAGAGAGAGGGCAGCGGCTCAAG	3480
Db	3481	GTCAATCTATGGCTCCAGTGTGGCTTCCATGCTGTGGATTGTGCACTCGGGAAACAGCTAT	3540
Qy	3481	GTCAATCTATGGCTCCAGTGTGGCTTCCATGCTGTGGATTGTGCACTCGGGAAACAGCTAT	3540
Db	3541	GACATCTATATCCCTGGTGCATATCCAGAGCCAGATCAAGCCCCAATGCCATATCTCTC	3600
Qy	3541	GACATCTATATCCCTGGTGCATATCCAGAGCCAGATCAAGCCCCAATGCCATATCTCTC	3600
Db	3541	GACATCTATATCCCTGGTGCATATCCAGAGCCAGATCAAGCCCCAATGCCATATCTCTC	3600
Qy	3601	CCCAACACCGGACCGGATGAGATGTCTGTGCTACGAGGACGAGGGGTCTACGTCAC	3660
Db	3601	CCCAACACCGGACCGGATGAGATGTCTGTGCTACGAGGACGAGGGGTCTACGTCAC	3660
Qy	3661	ACGTACGGGGCGATCTTAAAGATGTGGTGTCTGCACTGGGGGAGATGCTTACTTGTG	3720
Db	3661	ACGTACGGGGCGATCTTAAAGATGTGGTGTCTGCACTGGGGGAGATGCTTACTTGTG	3720
Qy	3721	GCCATCACTCTCTCCAAACAGATATATGGGCTGGGTGAGAAAGCATTTGAATCCGCTCT	3780
Db	3721	GCCATCACTCTCTCCAAACAGATATATGGGCTGGGTGAGAAAGCATTTGAATCCGCTCT	3780
Qy	3781	GTGAGAGACGGGCACTTGAACGGGGTCTTATGACCAACAGAGCTCAGAGCTCAAGTTT	3840
Db	3781	GTGAGAGACGGGCACTTGAACGGGGTCTTATGACCAACAGAGCTCAGAGCTCAAGTTT	3840
Qy	3841	CTGTGTGAGCGGAATGACAAGGTGTTTTTTTGCTCAGTCCGCTCTGGGGGAGAGCCAA	3900
Db	3841	CTGTGTGAGCGGAATGACAAGGTGTTTTTTTGCTCAGTCCGCTCTGGGGGAGAGCCAA	3900
Qy	3901	GTTTACTTTCATGACTCTGAACCGTATCTGCATCATGAATCTGTGAAAAGGC	3951
Db	3901	GTTTACTTTCATGACTCTGAACCGTATCTGCATCATGAATCTGTGAAAAGGC	3951

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RESULT 2
PCT-US02-33845-2
Sequence 2, Application PC/TUS0233845
GENERAL INFORMATION:
APPLICANT: Rigel Pharmaceuticals, Inc.
APPLICANT: Leo, Cindy
APPLICANT: Luo, Ying
APPLICANT: Xu, Xiang
APPLICANT: Yu, Simon
TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE PROTEINS, COMPOSITIONS,
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: 021044-005600PC
CURRENT APPLICATION NUMBER: PCT/US02/33845
CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: US 10/029,115
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 3951
TYPE: DNA
ORGANISM: Homo sapiens

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; FEATURE:
; OTHER INFORMATION: mishapen/NIK-related kinase isoform 3a
PCT-US02-33845-2

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Query Match	98.5%	Score 3692	DB 1	Length 3951
Best Local Similarly	99.8%	Pred. No. 0		
Matches 3948	Conservative	0	Mismatches	6
			Indels	5
			Gaps	

[illegible]



[illegible]

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3178 AAAGGACAACTGGGGGTGTATACCTGCTCGGCTCCGGAAACAAGATTCTGACAATG 3237  
3239 ACCCGAAGTGAAGAAAGACGAGGCTGAGCCACCTGGGGGACATGAGGGCTCGGGC 3298  
3238 ACCCGAAGTGAAGAAAGACGAGGCTGAGCCACCTGGGGGACATGAGGGCTCGGGC 3297  
3299 ACTACCGTGTGTAAATACGAGCGGATTAAGTCTCTGCTCATTCGCCCTCAAGAGCTCG 3358  
3298 ACTACCGTGTGTAAATACGAGCGGATTAAGTCTCTGCTCATTCGCCCTCAAGAGCTCG 3357  
3359 TGGAGGTGATGCTGGGCCCCCAACCTTACCAAAATTCATGGCCTTCAAGTCTTTG 3418  
3358 TGGAGGTGATGCTGGGCCCCCAACCTTACCAAAATTCATGGCCTTCAAGTCTTTG 3417  
3419 CCGACCTCCCCCAGCGCCTCTGCTGTGCTGACCTGACAGTAGAGAGGGGACGGGCTCA 3478  
3418 CCGACCTCCCCCAGCGCCTCTGCTGTGCTGACCTGACAGTAGAGAGGGGACGGGCTCA 3477  
3479 AGGTATCTATGCTGCTCAAGTCTGCTTCCATGCTGTGATGTCGATTCGGGGAAACGCT 3538  
3478 AGGTATCTATGCTGCTCAAGTCTGCTTCCATGCTGTGATGTCGATTCGGGGAAACGCT 3537  
3539 ATGACATCTACATCCCTGTGACATTCAGAGCCAGATCAGGCCCATGCTCATCTTCC 3598  
3538 ATGACATCTACATCCCTGTGACATTCAGAGCCAGATCAGGCCCATGCTCATCTTCC 3597  
3599 TCCCCCAACCGGACGAGATGAGATGCTGCTGTGCTACGAGGACGAGGCTCTACGTC- 3657  
3598 TCCCCCAACCGGACGAGATGAGATGCTGCTGTGCTACGAGGACGAGGCTCTACGTC- 3657  
3658 AACAGTACGGGGGATCTTAAGATGCTGCTGACAGTGGGGGAGATGCTCTTCT 3717  
3658 AACAGTACGGGGGATCTTAAGATGCTGCTGACAGTGGGGGAGATGCTCTTCT 3717  
3718 GTGGCTACATCTGCTCCACAGATTAATGAGCTGGGGGTGAAGAACATTTGATCCG 3777  
3718 GTGGCTACATCTGCTCCACAGATTAATGAGCTGGGGGTGAAGAACATTTGATCCG 3777  
3778 TCTGTGAGACGGGCGACCTCGACGGGGTCTTCATGACAAACAGAGCTCAGAGCTCAG 3837  
3778 TCTGTGAGACGGGCGACCTCGACGGGGTCTTCATGACAAACAGAGCTCAGAGCTCAG 3837  
3838 TTCCGTGTGAGACGGGAAATGACAGAGTCTTTTCTCAGTCCGCTGCGGGGACAGAGC 3897  
3838 TTCCGTGTGAGACGGGAAATGACAGAGTCTTTTCTCAGTCCGCTGCGGGGACAGAGC 3897  
3898 CAAGTTACTTATGACTGTAACGTGTAACGTGTAACGTGTAACGTGTAACGTGTAACGT 3951  
3898 CAAGTTACTTATGACTGTAACGTGTAACGTGTAACGTGTAACGTGTAACGTGTAACGT

## RESULT 3

PCT-US03-37730-22  
Sequence 22, Application PC/TUS0337730

GENERAL INFORMATION:

APPLICANT: EXELIXIS, INC.

TITLE OF INVENTION: MARKS AS MODIFIERS OF THE RAC, AXIN, AND BETA-CATENIN PATHWAYS

TITLE OF INVENTION: AND METHODS OF USE

FILE REFERENCE: EX03-089C-PC

CURRENT APPLICATION NUMBER: PCT/US03/37730

CURRENT FILING DATE: 2003-11-24

PRIOR APPLICATION NUMBER: US 60/429,061

PRIOR FILING DATE: 2002-11-25

PRIOR APPLICATION NUMBER: US 60/437,163

PRIOR FILING DATE: 2002-12-30

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PatentIn version 3.2

SEQ ID NO 22

LENGTH: 5014

TYPE: DNA

ORGANISM: Homo sapiens  
PCT-US03-37730-22

Query Match 98.0%; Score 3870.2; DB 1; Length 5014;  
Best Local Similarity 98.4%; Pred. No. 0;  
Matches 3942; Conservative 0; Mismatches 3; Indels 60; Gaps 1;

7 ATGGGCGACCCAGCCCGCCGAGCTGGACGACATCGACTGTCCGCTCGGGAC 66  
197 ATGGGCGACCCAGCCCGCCGAGCTGGACGACATCGACTGTCCGCTCGGGAC 256  
67 CTTGCTGGGATCTTTGAGCTTGTGAGGTGTGGGAAATGGAACCTACGACAGGTGAC 126  
257 CTTGCTGGGATCTTTGAGCTTGTGAGGTGTGGGAAATGGAACCTACGACAGGTGAC 316  
127 AAGGCTGGGATGTCAGACGGGGACGCTGCTGCTCATCAAGTCTATGATGACGAG 186  
317 AAGGCTGGGATGTCAGACGGGGACGCTGCTGCTCATCAAGTCTATGATGACGAG 376  
187 GACGAGGAGAAAGATCAACAGAGATCAACATGCTGAAAAGTACTTACACCGC 246  
377 GACGAGGAGAAAGATCAACAGAGATCAACATGCTGAAAAGTACTTACACCGC 436  
247 AACATCGCCACTTACTAGAGCTTCTCATCAAGAAAGCCCCCGGGAAGATGACAG 306  
437 AACATCGCCACTTACTAGAGCTTCTCATCAAGAAAGCCCCCGGGAAGATGACAG 496  
307 CTTGCTGGGATGATGAGATGCTGTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 366  
497 CTTGCTGGGATGATGAGATGCTGTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 556  
367 AAAGGCGACCGCTGAAAGAGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 426  
557 AAAGGCGACCGCTGAAAGAGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 616  
427 CTGGGCCATCTTCATGCCCCAAGAGTATCCATGAGACATCAAGGGGCAAAATGCTG 486  
617 CTGGGCCATCTTCATGCCCCAAGAGTATCCATGAGACATCAAGGGGCAAAATGCTG 676  
487 CTGACAGAGATGCTGAGGTCAAGTATGATGATTTTGGGGTGAAGTCTCACTGAGCCG 546  
677 CTGACAGAGATGCTGAGGTCAAGTATGATGATTTTGGGGTGAAGTCTCACTGAGCCG 736  
547 ACCGTGGGACAGCGAACACTTTCATTTGGAATCTTCATGAGTCTCAGAGTCTC 606  
727 ACCGTGGGACAGCGAACACTTTCATTTGGAATCTTCATGAGTCTCAGAGTCTC 796  
607 GCTGTGATGAGAACCTTGATGCCACTTATGATTAACAGAGTGAATTTGCTCTAGGA 666  
797 GCTGTGATGAGAACCTTGATGCCACTTATGATTAACAGAGTGAATTTGCTCTAGGA 856  
667 ATCAAGGCGATGAGATGAGAGGAGAGCCCGCTGTGTGACATGACCCCATGCGA 726  
857 ATCAAGGCGATGAGATGAGAGGAGAGCCCGCTGTGTGACATGACCCCATGCGA 916  
727 GCCCTCTTCTCATTCCTCGAAACCTTCGCGGACGCTCAAGTCCAAAGAGTGTAA 786  
917 GCCCTCTTCTCATTCCTCGAAACCTTCGCGGACGCTCAAGTCCAAAGAGTGTAA 976  
787 AAGTTCATGACTTATGACATGATGCTCATCAAGATTTACAGAGGCGCCACCGCAG 846  
977 AAGTTCATGACTTATGACATGATGCTCATCAAGATTTACAGAGGCGCCACCGCAG 1036  
847 GAGGAGCTACTGAAGTTCCCTCATCCGGGACGAGCCACGAGCGGACAGTCCGATC 906  
1037 GAGGAGCTACTGAAGTTCCCTCATCCGGGACGAGCCACGAGCGGACAGTCCGATC 1096  
907 CAGCTTAAAGACCAATGACGATCCGGAAGAAAGCGGGGTGAGAAAGAGAGACAGAA 966  
1097 CAGCTTAAAGACCAATGACGATCCGGAAGAAAGCGGGGTGAGAAAGAGAGACAGAA 1156  
967 TATGAGTACAGGGGACGAGAGAGAGATGACAGCTGAGAGAGAGAGAGAGAGAGAGAG 1026

Db	1157	TATGATGATCAAGCGGCGAGGAGGAGAAATGACACCATGAGAGAGAAAGAGAGCCAAAGC	1216
Oy	1027	TCCATCATGAAAGTGCCTTGAGAGATGACTCTTAAGCGCGAGATTCTCCGCTCCAGAG	1086
Db	1217	TCCATCATGAAAGTGCCTTGAGAGATGACTCTTAAGCGCGAGATTCTCCGCTCCAGAG	1276
Oy	1087	GAATAAAGAGCACTCAGAGGCTTTAAACAGCAGCAGCAGCTGACAGCAGCAGCAG	1146
Db	1277	GAATAAAGAGCACTCAGAGGCTTTAAACAGCAGCAGCAGCTGACAGCAGCAGCAG	1336
Oy	1147	CGAGCCCCGAGGCAACATCAAAACGCTGCAACGCGCAGCGCGCATAGAGAG	1206
Db	1337	CGAGCCCCGAGGCAACATCAAAACGCTGCAACGCGCAGCGCGCATAGAGAG	1396
Oy	1207	CAGAGAGAGAGCGCGCGCTGAGAGAGCAACAGCGCGGAGCGGAGAGCGGAG	1266
Db	1397	CAGAGAGAGAGCGCGCGCTGAGAGAGCAACAGCGCGGAGCGGAGAGCGGAG	1456
Oy	1267	CTGCAGAGAGAGAGCAGCAGCGCGCTGAGAGCAATGCAAGCTCTGCGCGGAGAG	1326
Db	1457	CTGCAGAGAGAGAGCAGCAGCGCGCTGAGAGCAATGCAAGCTCTGCGCGGAGAG	1516
Oy	1327	GAGCGCGCGGAGCGCGGCTGAGAGAGAAATCAAGCGGAGCAGCTGAGAGAGAGG	1386
Db	1517	GAGCGCGCGGAGCGCGGCTGAGAGAGAAATCAAGCGGAGCAGCTGAGAGAGAGG	1576
Oy	1387	CAGTCAGAACGTCTTCAGAGGAGCTGAGAGAGAGCAATGCTCAAGCTCTGAG	1446
Db	1577	CAGTCAGAACGTCTTCAGAGGAGCTGAGAGAGAGCAATGCTCAAGCTCTGAG	1636
Oy	1447	CAGCAGCAACAGCAGCAGCAGCTTCAAAACAGCAGCAGCAGCAGCTCTGCGGAG	1506
Db	1637	CAGCAGCAACAGCAGCAGCAGCTTCAAAACAGCAGCAGCAGCAGCTCTGCGGAG	1696
Oy	1507	AGGAAGCCCCCTGTAACATTAATGCTGCGGAGATGAATCCCGCTGAACAAACAGCCCTG	1566
Db	1697	AGGAAGCCCCCTGTAACATTAATGCTGCGGAGATGAATCCCGCTGAACAAACAGCCCTG	1756
Oy	1567	CGAGAGGTAGAAGAGAGAAACAAAGATGAAACAAAGCAGAACTCTCCCTTGCCAAAGC	1626
Db	1757	CGAGAGGTAGAAGAGAGAAACAAAGATGAAACAAAGCAGAACTCTCCCTTGCCAAAGC	1816
Oy	1627	AAGCCAGGCGACGCGGCGCTGAGCGCCCCCATCCCCAGGCTCTCCAGGCGCCCAAGA	1686
Db	1817	AAGCCAGGCGACGCGGCGCTGAGCGCCCCCATCCCCAGGCTCTCCAGGCGCCCAAGA	1876
Oy	1687	CCCCCTTCCCAAGCTCTCTCTTAATGAGAGGCGGTGAGAGCCCAAGAGAGACCGACA--	1744
Db	1877	CCCCCTTCCCAAGCTCTCTCTTAATGAGAGGCGGTGAGAGCCCAAGAGAGACCGACAAG	1936
Oy	1745	-----AG 1746	
Db	1937	AGCTGATGAGCAACCGGCTCCCATGAAAGCCATATGACAGCACTGTACCCCGATCCAG	1996
Oy	1747	TCCCTGAGAGACAGAGCCCAACCGAAACTGTGCTGCTTCCAGCTCCCATGACCCGAG	1806
Db	1997	TCCCTGAGAGACAGAGCCCAACCGAAACTGTGCTGCTTCCAGCTCCCATGACCCGAG	2056
Oy	1807	CCTGCGATCTCCCGACCACTGCGCAGCGCCAGTGCCTGAGAGAGCTGTCACTCCGCAAAAT	1866
Db	2057	CCTGCGATCTCCCGACCACTGCGCAGCGCCAGTGCCTGAGAGAGCTGTCACTCCGCAAAAT	2116
Oy	1867	TCAGACCCCACTCTGAAGAGACTGTGCGCCAGCGCCGAATCCCGCAGCTGAGTCCGACCA	1926
Db	2117	TCAGACCCCACTCTGAAGAGACTGTGCGCCAGCGCCGAATCCCGCAGCTGAGTCCGACCA	2176
Oy	1927	GATTAAGAGGCGCCCAACCAAGGTGCTCAGAGACCTCATCTATGCGCACTGCGCTTAAC	1986
Db	2177	GATTAAGAGGCGCCCAACCAAGGTGCTCAGAGACCTCATCTATGCGCACTGCGCTTAAC	2236
Oy	1987	ACAGGTGGGCGGAGGGTCCCGGCGACGCCAGCGAGTTCCTGCGCAACTTCCGAGCAAC	2046
Db	2237	ACAGGTGGGCGGAGGGTCCCGGCGACGCCAGCGAGTTCCTGCGCAACTTCCGAGCAAC	2296

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QY 3127 CAGCAGATGATGTCGTGAGGGGCTCAACCTGCTCATCAACCTCTCAGGGAAAGAAC 3186
DB 3377 CAGCAGATGATGTCGTGAGGGGCTCAACCTGCTCATCAACCTCTCAGGGAAAGAAC 3436
QY 3187 AAACCTGCGGTGATTAACCTGTCGTGCTCCGAAACAAGATTCTGCAATGACCAAGA 3246
DB 3437 AAACCTGCGGTGATTAACCTGTCGTGCTCCGAAACAAGATTCTGCAATGACCAAGA 3496
QY 3247 GTGGAGAAAGACAGGGCTGAGCAACCGTGGGGGACATGAGAGGGCTGGGGACCTACCGT 3306
DB 3497 GTGGAGAAAGACAGGGCTGAGCAACCGTGGGGGACATGAGAGGGCTGGGGACCTACCGT 3556
QY 3307 GTTGTGAATAAGACAGCGATTAAAGTCTGTGATCGCCCTCAAGAGCTCCGTGAGGTG 3366
DB 3557 GTTGTGAATAAGACAGCGATTAAAGTCTGTGATCGCCCTCAAGAGCTCCGTGAGGTG 3616
QY 3367 TATGCTGGGCCCCCAACCCCTACCAAAATTCAATGACCTTCAAGTCTTTGCCGACTC 3426
DB 3617 TATGCTGGGCCCCCAACCCCTACCAAAATTCAATGACCTTCAAGTCTTTGCCGACTC 3676
QY 3427 CCCCACCCCTCTGCTGTGTCGACCTGACAGTAAAGAGGGGCGAGGCTCAAGGTCATC 3486
DB 3677 CCCCACCCCTCTGCTGTGTCGACCTGACAGTAAAGAGGGGCGAGGCTCAAGGTCATC 3736
QY 3487 TATGCTCAGTGTGCTTCCATGCTGTGATGTGATCTCGGGAAACAGTATGACATC 3546
DB 3737 TATGCTCAGTGTGCTTCCATGCTGTGATGTGATCTCGGGAAACAGTATGACATC 3796
QY 3547 TACATCTCTGTGACATTCAGAGCCAGATCACGCCCATGCAATCTTCTCCCAAC 3606
DB 3797 TACATCTCTGTGACATTCAGAGCCAGATCACGCCCATGCAATCTTCTCCCAAC 3856
QY 3607 ACCGACGGATGAGATGCTGTGCTGCTACAGAGAGAGGGGTCTACGCTCAACAGTAC 3666
DB 3857 ACCGACGGATGAGATGCTGTGCTGCTACAGAGAGAGGGGTCTACGCTCAACAGTAC 3916
QY 3667 GGGCCCATCATTAAGATGTGTGCTGACAGTGGGGAGATGCTTCTGTGGCTTAC 3726
DB 3917 GGGCCCATCATTAAGATGTGTGCTGACAGTGGGGAGATGCTTCTGTGGCTTAC 3976
QY 3727 ATCTGCTCAACCAAGTAATGAGGCTGTGAGAAAGCCATTGAGATCCGCTGTGTGAG 3786
DB 3977 ATCTGCTCAACCAAGTAATGAGGCTGTGAGAAAGCCATTGAGATCCGCTGTGTGAG 4036
QY 3787 AGGGCCCATCTGAGAGGGGTCTTCAATGACAAACGAGCTCAGAGGTCAAGTTCGTGT 3846
DB 4037 AGGGCCCATCTGAGAGGGGTCTTCAATGACAAACGAGCTCAGAGGTCAAGTTCGTGT 4096
QY 3847 GAGCGAATGACAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3906
DB 4097 GAGCGAATGACAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4156
QY 3907 TTGATGACTTGAACCGTACTGATGATGAAGTGTGAAGGGC 3951
DB 4157 TTGATGACTTGAACCGTACTGATGATGAAGTGTGAAGGGC 4201

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; SEQ ID NO 26
; LENGTH: 4989
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-37730-26

Query Match      97.9%; Score 3867; DB 1; Length 4989;
Best Local Similarity 98.4%; Pred.No. 0;
Matches 3940; Conservative 0; Mismatches 5; Indels 60; Gaps 1;

QY 7 ATGGGCGACCCAGCCCCCGCCGAGCCTGAGACCAATGACCTGTCCGCCCTGGGGAC 66
DB 197 ATGGGCGACCCAGCCCCCGCCGAGCCTGAGACCAATGACCTGTCCGCCCTGGGGAC 256
QY 67 CTTGCTGGGATCTTTGACCTTGTGAGAGGTGTGCGCAATGAACTACAGGAGTATC 126
DB 257 CTTGCTGGGATCTTTGACCTTGTGAGAGGTGTGCGCAATGAACTACAGGAGTATC 316
QY 127 AAGGCTCGCATGTGACAGAGCGGGGCAAGTGTGCTGCAATCAAGTATGATGTCAAGAG 186
DB 317 AAGGCTCGCATGTGACAGAGCGGGGCAAGTGTGCTGCAATCAAGTATGATGTCAAGAG 376
QY 187 GACGAGAGAGAAAGATCAAAACAGAGATCAAACTGTGAAAAGTACTCTACCAAGCCG 246
DB 377 GACGAGAGAGAAAGATCAAAACAGAGATCAAACTGTGAAAAGTACTCTACCAAGCCG 436
QY 247 AACATGCGACCTACTACGAGACCTTTCATCAAGAGAGCCGCCGGGAAAGATGACGAG 306
DB 437 AACATGCGACCTACTACGAGACCTTTCATCAAGAGAGCCGCCGGGAAAGATGACGAG 496
QY 307 CTCTGGCTGTGATGAGATTCTGTGTGCTGTGTGCTGTGTGCTGTGTGCTGTGTGCTGTGT 366
DB 497 CTCTGGCTGTGATGAGATTCTGTGTGCTGTGTGCTGTGTGCTGTGTGCTGTGTGCTGTGT 556
QY 367 AAAGGCAACGCCCTTAAAGAGAGATGATCGCTTATCTTCAAGGAGAAATCTCGAGGGGT 426
DB 557 AAAGGCAACGCCCTTAAAGAGAGATGATCGCTTATCTTCAAGGAGAAATCTCGAGGGGT 616
QY 427 CTGGCCCATCTTCATGAGCCCAAGAGTGAATCAATGAGACATCAAGAGGAGATGTGCTG 486
DB 617 CTGGCCCATCTTCATGAGCCCAAGAGTGAATCAATGAGACATCAAGAGGAGATGTGCTG 676
QY 487 CTGACAGAAATGCTGAGGTCAAGCTAGTGAATTTTGGGGTGAATGCTCAAGTCAAGCCG 546
DB 677 CTGACAGAAATGCTGAGGTCAAGCTAGTGAATTTTGGGGTGAATGCTCAAGTCAAGCCG 736
QY 547 ACCGTGGGCAACGGAACAATTTTCAATTTGAGATCTGATGAGTGGCTCCAGAGGTCAATC 606
DB 737 ACCGTGGGCAACGGAACAATTTTCAATTTGAGATCTGATGAGTGGCTCCAGAGGTCAATC 796
QY 607 GCTGTGATGAGAAACCTGATGACCTATGATTAACAGAGTGAATTTTGTCTCTAGGA 666
DB 797 GCTGTGATGAGAAACCTGATGACCTATGATTAACAGAGTGAATTTTGTCTCTAGGA 856
QY 797 GCTGTGATGAGAAACCTGATGACCTATGATTAACAGAGTGAATTTTGTCTCTAGGA 856
DB 857 ATCACAGCCATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 916
QY 727 GCTCTCTCTCTATCTCTGAGAAACCTTCCGAGAGCTCAAGTCCAAAGAGTGTCTAG 786
DB 917 GCTCTCTCTCTATCTCTGAGAAACCTTCCGAGAGCTCAAGTCCAAAGAGTGTCTAG 976
QY 787 AAGTTCATTGACTTATGACATGATGTCTCATCAAGACTTACCTGAGCCGCCCAACGAG 846
DB 977 AAGTTCATTGACTTATGACATGATGTCTCATCAAGACTTACCTGAGCCGCCCAACGAG 1036
QY 847 GAGCAGCTACTGAAATTTCTTCAATCCGAGACAGCCGAGAGAGAGAGAGAGAGAGAGAG 906
DB 1037 GAGCAGCTACTGAAATTTCTTCAATCCGAGACAGCCGAGAGAGAGAGAGAGAGAGAGAG 1096
QY 907 CAGCTTAAAGACCAATGACAGATCCGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 966
DB 1097 CAGCTTAAAGACCAATGACAGATCCGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1156

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RESULT 4
PCT-US03-37730-26
; Sequence 26, Application PC/TUS0337730
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: MARKS AS MODIFIERS OF THE RAC, AXIN, AND BETA-CATENIN PATHWAYS
; FILE REFERENCE: EX03-089C-PC
; CURRENT APPLICATION NUMBER: PCT/US03/37730
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 60/429,061
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 60/437,163
; PRIOR FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.2

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OY	967	TATGAGTTCAGCGGCGAGGAGGAGAAATGACAGCTTGGAGAGAAAGAGAGCTCAAGC	10286
Db	1157	TATGAGTTCAGCGGCGAGGAGGAGAAATGACAGCTTGGAGAGAAAGAGAGCTCAAGC	1216
OY	1057	TCGATCAGAAAGTGCCTGGAGAGTGCATCAAGCGGGAGTTTCTCCGGCTCAGAG	1086
Db	1217	TCGATCAGAAAGTGCCTGGAGAGTGCATCAAGCGGGAGTTTCTCCGGCTCAGAG	1276
OY	1087	GAAATTAAGCACTCAGAGGCTTTAAACAGCAGCAGCAGCTGCAGCAGCAGCAG	1146
Db	1277	GAAATTAAGCACTCAGAGGCTTTAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG	1336
OY	1147	CGAGACCCCGAGGCAACATCAACACTTGTCTGCACAGCGGAGCGGCGCATAGAGAG	1206
Db	1337	CGAGACCCCGAGGCAACATCAACACTTGTCTGCACAGCGGAGCGGCGCATAGAGAG	1396
OY	1207	CAGAAAGAGAGCGCGCGCGCTGGAGAGCAACAGCGCGGAGCGGAGCAACCGAGAG	1266
Db	1397	CAGAAAGAGAGCGCGCGCGCTGGAGAGCAACAGCGCGGAGCGGAGCAACCGAGAG	1456
OY	1267	CTGCAGAGAAAGAGCAGCAGCGGCGCTGGAGAGCATGCAGGCTCTCCGCGGAGAGAG	1326
Db	1457	CTGCAGAGAAAGAGCAGCAGCGGCGCTGGAGAGCATGCAGGCTCTCCGCGGAGAGAG	1516
OY	1327	GAGCGGCGGAGCGCGGCGCTGGAGAGCAACAGCGGAGCGGAGCTGGAGAGCAGCGG	1386
Db	1517	GAGCGGCGGAGCGCGGCGCTGGAGAGCAACAGCGGAGCGGAGCTGGAGAGCAGCGG	1576
OY	1387	CAGTCAGAAAGCTTTCAGAGGCACTGCAGCAGAGAGCATGCCCTCAAGTCCCTGAG	1446
Db	1577	CAGTCAGAAAGCTTTCAGAGGCACTGCAGCAGAGAGCATGCCCTCAAGTCCCTGAG	1636
OY	1447	CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCTGCGGAGC	1506
Db	1637	CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCTGCGGAGC	1696
OY	1507	AGGAAGCCCTGTACCATTAATGTCGCGGCAATGATCCCGCTGACAAACAGCCTGGGC	1566
Db	1697	AGGAAGCCCTGTACCATTAATGTCGCGGCAATGATCCCGCTGACAAACAGCCTGGGC	1756
OY	1567	CGAGAGGTAGAAAGAGAAACAAGATGAAACAAGCAGCAAACTCTCTTGGCCAGAGC	1626
Db	1757	CGAGAGGTAGAAAGAGAAACAAGATGAAACAAGCAGCAAACTCTCTTGGCCAGAGC	1816
OY	1627	AAGCCAGGCAACAGCGGGGCTGAGCGGCGCCCATTCGCCAGGCGCTCCCAAGGGCGCCCA	1686
Db	1817	AAGCCAGGCAACAGCGGGGCTGAGCGGCGCCCATTCGCCAGGCGCTCCCAAGGGCGCCCA	1876
OY	1687	CCCGCTTTCAGAGCTCTCTATGAGAGGCGGAGGAGCCCAAGAGAGAGCCGACAAG	1744
Db	1877	CCCGCTTTCAGAGCTCTCTATGAGAGGCGGAGGAGCCCAAGAGAGAGCCGACAAG	1936
OY	1745	-----AG 1746	
Db	1937	AGCGTGTGGACACCGGGTCCCACTGAAGCAATATGACAGCACTGTACCCGATCCAG	1996
OY	1747	TCCCTGCAGAGACAGCGCCCACTCGGAAACTGTGCTGCTTCCAGAGCTCCCATGAGCCGAGC	1806
Db	1997	TCCCTGCAGAGACAGCGCCCACTCGGAAACTGTGCTGCTTCCAGAGCTCCCATGAGCCGAGC	2056
OY	1807	CCTGCGATCCCGGCAACAGCTGCCAGCGGCGGAGTGCAGAGAGCTGATCATCCGCGAGAT	1866
Db	2057	CCTGCGATCCCGGCAACAGCTGCCAGCGGCGGAGTGCAGAGAGCTGATCATCCGCGAGAT	2116
OY	1867	TCAGACCCCACTTGAAGAGACTTGGCCCAAGCGGAATCCCCAGCCTGGGCTCGCCCA	1926
Db	2117	TCAGACCCCACTTGAAGAGACTTGGCCCAAGCGGAATCCCCAGCCTGGGCTCGCCCA	2176
OY	1927	GATTAACAGAGGCCCACTCAAGGTGCTCAGAGAGACTTATATGCGCATCTGAGCCCTTAAC	1986
Db	2177	GATTAACAGAGGCCCACTCAAGGTGCTCAGAGAGACTTATATGCGCATCTGAGCCCTTAAC	2236

QY	1987	ACCAATGGGGCCGGAGGGATCCCCGACAGCCCAAGGCAATGTCCTGGCCAGAACCTTCGACGAAC	2048
Db	2237	ACCAATGGGGCCGGAGGGATCCCCGACAGCCCAAGGCAATGTCCTGGCCAGAACCTTCGACGAAC	2296
QY	2047	TCGGCTGGCAAAATCTATCTGCAAAAGGCGGGCAGAGCGGGCACCCTCCAAAGCTCTCAAGG	2106
Db	2297	TCGGCTGGCAAAATCTATCTGCAAAAGGCGGGCAGAGCGGGCACCCTCCAAAGCTCTCAAGG	2356
QY	2107	CCCCCTGGTCAAGCCCTCTGGCCGCGCCCAAGCTCTAGTAACTCCGAACTTCAGAGAGAGC	2166
Db	2357	CCCCCTGGTCAAGCCCTCTGGCCGCGCCCAAGCTCTAGTAACTCCGAACTTCAGAGAGAGC	2418
QY	2167	GAACCTGGCTGGAAACGCTCGGACAAGCTCTTTCAGATCTTCAAGGGCACCCTCCAG	2228
Db	2417	GAACCTGGCTGGAAACGCTCGGACAAGCTCTTTCAGATCTTCAAGGGCACCCTCCAG	2478
QY	2227	GCTGGCTCACTGGAGCGGAAACCGGGTGGGAAACCTCTCAAACTGGACAGCTCCCTCTGTG	2286
Db	2477	GCTGGCTCACTGGAGCGGAAACCGGGTGGGAAATCTCTCTCAAACTGGAGAGCTCCCTCTGTG	2538
QY	2287	CTCTCCCTGGGAAATTAAGCCAAAGCCCAACACACACGCTCAAGGACGAGCCGAGCCGCA	2348
Db	2537	CTCTCCCTGGGAAATTAAGCCAAAGCCCAACACACGCTCAAGGACGAGCCGAGCCGAGCCGCA	2598
QY	2347	GACTTTGTGTGTCTGAAAAGACGGACCTCTGAGCAAGGCCCCCTCGACCTCCCAAGAGGCC	2406
Db	2597	GACTTTGTGTGTCTGAAAAGACGGACCTCTGAGCAAGGCCCCCTCGACCTCCCAAGAGGCC	2658
QY	2407	ATGGAATTAATCTGTGCTCCAGGCAAGAGGTGGAAAGCACTGAGAGCAACGAAAGAAAGGC	2466
Db	2657	ATGGAATTAATCTGTGCTCCAGGCAAGAGGTGGAAAGCACTGAGAGCAACGAAAGAAAGGC	2718
QY	2467	GAAAGCGGGCCAGCAGAGGGGAGAGAGATACCCCTGGGGGCCGACAGCAATGGGGATACA	2528
Db	2717	GAAAGCGGGCCAGCAGAGGGGAGAGAGATACCCCTGGGGGCCGACAGCAATGGGGATACA	2778
QY	2527	GACAGCGTCAAGCACCATTGTGTGTCAAGACGTGAGAGATACCGGAGCCAGCCGCCCA	2586
Db	2777	GACAGCGTCAAGCACCATTGTGTGTCAAGACGTGAGAGATACCGGAGCCAGCCGCCCA	2838
QY	2587	TACGGGGCGGCAACATGTGTGTTCACACGCAACCCCTAAGAGAGCGGAACTGTCTGAT	2646
Db	2837	TACGGGGCGGCAACATGTGTGTTCACACGCAACCCCTAAGAGAGCGGAACTGTCTGAT	2896
QY	2647	GCTGACAGCAATGGGTATACAACAACCTGCGCTACGTTGCTCCAGGCCAGCCACTCACCAAC	2706
Db	2897	GCTGACAGCAATGGGTATACAACAACCTGCGCTACGTTGCTCCAGGCCAGCCACTCACCAAC	2956
QY	2707	GAGAACAGCAAAAGGCCAAAGCCCACTCGAAGATGGGAGTGTGATCACTACAGTCTTGT	2766
Db	2957	GAGAACAGCAAAAGGCCAAAGCCCACTCGAAGATGGGAGTGTGATCACTACAGTCTTGT	3016
QY	2767	GGGCTGTGTAAGGCCCTCTGGCAAGCTCGTTCAAGATTTTGTGATCTTAGGGATCTAC	2828
Db	3017	GGGCTGTGTAAGGCCCTCTGGCAAGCTCGTTCAAGATTTTGTGATCTTAGGGATCTAC	3078
QY	2827	CAGCTTGAAGGCAATGGGGAGAGATCCCATCAAGCGCTAAGTGGGGCGAGAGGGCACT	2886
Db	3077	CAGCTTGAAGGCAATGGGGAGAGATCCCATCAAGCGCTAAGTGGGGCGAGAGGGCACT	3138
QY	2887	CGGCTGCAACAGCTGACGTACGATGAGAGAGGGTTCTGTGTCTCAAGTGAATCCCAAC	2946
Db	3137	CGGCTGCAACAGCTGACGTACGATGAGAGAGGGTTCTGTGTCTCAAGTGAATCCCAAC	3196
QY	2947	AAACAACCGGGCCCAAGTGAAGACCTCTGAGATCCGAAAGTACAAAGACGATTTCACTCC	3006
Db	3197	AAACAACCGGGCCCAAGTGAAGACCTCTGAGATCCGAAAGTACAAAGACGATTTCACTCC	3256
QY	3007	GAGATTCCTCTGTGAAGCCCTTTGGGGGGGTCAACCTGCTGGTGGGCAAGGAAAGCGGGCTG	3066
Db	3257	GAGATTCCTCTGTGAAGCCCTTTGGGGGGGTCAACCTGCTGGTGGGCAAGGAAAGCGGGCTG	3316
QY	3067	ATGTTGTCTGAACCGAAGTGGCAGGGCAAGGATGTATGACCTATTTGGCGGGCAGCGCTTC	3126





1243 GAGCAGCTACTGAAATTTCCCTTCATCCGGGACCGACGAGCGGACGAGTCCGCAATC 1302  
QY  
907 CAGCTTAAAGACCACTTGAACCGATCCCGGAAAGAAAGCGGGGTGAGAAAGAGAGACAGAA 966  
Db  
1303 CAGCTTAAAGACCACTTGAACCGATCCCGGAAAGAAAGCGGGGTGAGAAAGAGAGACAGAA 1362  
QY  
967 TATGATGACAGCGGACGAGGAGAGAGATGACAGCCATGAGAGAGAGAGAGAGAGAGAGAG 1026  
Db  
1363 TATGATGACAGCGGACGAGGAGAGAGATGACAGCCATGAGAGAGAGAGAGAGAGAGAGAG 1422  
QY  
1027 TCCATCATGAACTGCTGAGAGAGTGAATCTAGCGCCGGAGATTCTCCGGCTCCAGAG 1086  
Db  
1423 TCCATCATGAACTGCTGAGAGAGTGAATCTAGCGCCGGAGATTCTCCGGCTCCAGAG 1482  
QY  
1087 GAAAAATAAGAGCACTCAGAGGCTTTAAACAGCAGCAGCAGCTGACAGCAGCAGCAGCAG 1146  
Db  
1483 GAAAAATAAGAGCACTCAGAGGCTTTAAACAGCAGCAGCAGCTGACAGCAGCAGCAGCAG 1542  
QY  
1147 CGAAGACCCCGAGGACACATGAAACACCTGCTGACAGCGGACAGCGGCGGATAGAGAG 1206  
Db  
1543 CGAAGACCCCGAGGACACATGAAACACCTGCTGACAGCGGACAGCGGCGGATAGAGAG 1602  
QY  
1207 CAGAAAGAGAGAGCGGCGCGCTGAGAGAGCAACGCGCGGAGCGGAGCAGCGAGAG 1266  
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1603 CAGAAAGAGAGAGCGGCGCGCTGAGAGAGCAACGCGCGGAGCGGAGCAGCGAGAG 1662  
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1267 CTGCAAG 1326  
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1327 GAGCGGCGGAG 1386  
Db  
1723 GAGCGGCGGAG 1782  
QY  
1387 CAGTCAGAACCTCTCTCAGAGGAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1446  
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1783 CAGTCAGAACCTCTCTCAGAGGAGAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1842  
QY  
1447 CAGCAGCAACAGCAGCAGCAGCAGCTTCAGAAA-----CAGCAGCAGCAGCAGCTTCGCTGG 1502  
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1843 CAGCAGCAACAGCAGCAGCAGCAGCTTCAGAAAACCGCAGCAGCAGCAGCTTCGCTGG 1902  
QY  
1503 GGAAG 1562  
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1903 GGAAG 1962  
QY  
1563 GGCAG 1622  
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1963 GGCAG 2022  
QY  
1623 GAGCAG 1682  
Db  
2023 GAGCAG 2082  
QY  
1683 AG 1742  
Db  
2083 AG 2142  
QY  
1743 CA----- 1744  
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2143 CAAG 2202  
QY  
1745 --AGTCCCTGAG 1802  
Db  
2203 CAGTCCCTGAG 2262  
QY  
1803 CAG 1862  
Db  
2263 CAG 2322  
QY  
1863 GAATTCAG 1922  
Db  
2323 GAATTCAG 2382

QY  
1923 CCCGATTAAG 1982  
Db  
2283 CCCGATTAAG 2442  
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1983 TAAACAG 2042  
Db  
2443 TAAACAG 2502  
QY  
2043 CAATCCGCTGAG 2102  
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2503 CAATCCGCTGAG 2562  
QY  
2103 AG 2162  
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2563 AG 2622  
QY  
2163 GAGCAG 2222  
Db  
2623 GAGCAG 2682  
QY  
2223 CAG 2282  
Db  
2683 CAG 2742  
QY  
2283 TGTGCTCTCCCTGGAG 2342  
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2743 TGTGCTCTCCCTGGAG 2802  
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2343 CGCAG 2402  
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2803 CGCAG 2862  
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2403 GGCATGAG 2462  
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2863 GGCATGAG 2922  
QY  
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2923 AGGAG 2982  
QY  
2523 TACAG 2582  
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2983 TACAG 3042  
QY  
2583 CCCATGAG 2642  
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3043 CCCATGAG 3102  
QY  
2643 GCATGAG 2702  
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3103 GCATGAG 3162  
QY  
2703 CACCGAG 2762  
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3163 CACCGAG 3222  
QY  
2763 TCGTGGCTGTAAAG 2822  
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3223 TCGTGGCTGTAAAG 3282  
QY  
2823 CTACAG 2882  
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3283 CTACAG 3342  
QY  
2883 CACTGGCTGAG 2942  
Db  
3343 CACTGGCTGAG 3402  
QY  
2943 CACCAAG 3002  
Db  
3403 CACCAAG 3462

QY	3003	CTCCGAGATCCTCTGTGACGCCCTTTGGGGGGTCAACCTGTGGTGGGACAGGANAAGG	3062
Db	3463	CTCCGAGATCCTCTGTGACGCCCTTTGGGGGGTCAACCTGTGGTGGGACAGGANAAGG	3522
QY	3063	GCTGATGTTGCTGGAACGAAGTGGGACAGGACAAAGTGTATGACTCATTTGGGCGGCGACG	3122
Db	3523	GCTGATGTTGCTGGAACGAAGTGGGACAGGACAAAGTGTATGACTCATTTGGGCGGCGACG	3582
QY	3123	CTTCAGCAGATGATGTGTGAGGGGGCTCAACCTGTCTATCAACATCTCAGGAAAAG	3182
Db	3583	CTTCAGCAGATGATGTGTGAGGGGGCTCAACCTGTCTATCAACATCTCAGGAAAAG	3642
QY	3183	GAACAAACGCGGGGTGATTAACCTGTCTGGCTCGGAAACAAGATTCTGCACAATGACCC	3242
Db	3643	GAACAAACGCGGGGTGATTAACCTGTCTGGCTCGGAAACAAGATTCTGCACAATGACCC	3702
QY	3243	AGAAGTGAGAAAGAACAGAGGCTGGAACACGCTGGGGGACATGAGGGCTGGGACACTA	3302
Db	3703	AGAAGTGAGAAAGAACAGAGGCTGGAACACGCTGGGGGACATGAGGGCTGGGACACTA	3762
QY	3303	CCGTGTTGTGAATTAACGAGCGGATTAAGTTCTGTGATCGCCCTCANAAGCTCCGTGA	3362
Db	3763	CCGTGTTGTGAATTAACGAGCGGATTAAGTTCTGTGATCGCCCTCANAAGCTCCGTGA	3822
QY	3363	GGTGTATGCTGTGGGCCCCCAACCCCTACCAAAATTCATGAGCCTTCAAGTCTTTGGCGA	3422
Db	3823	GGTGTATGCTGTGGGCCCCCAACCCCTACCAAAATTCATGAGCCTTCAAGTCTTTGGCGA	3882
QY	3423	CCGCCCCCAACCGGCTGTGCTGTGCGACCTGACAGTAGAGAGGGGACAGGCTCAAGT	3482
Db	3883	CCGCCCCCAACCGGCTGTGCTGTGCGACCTGACAGTAGAGAGGGGACAGGCTCAAGT	3942
QY	3483	CATCTATGCTCAAGTCTGAGCTTCCATGCTGTGAGATGCACTCGGGAAACAGCTATGA	3542
Db	3943	CATCTATGCTCAAGTCTGAGCTTCCATGCTGTGAGATGCACTCGGGAAACAGCTATGA	4002
QY	3543	CATCTATCCTCCGTGTGACATCCAGACCCATACAGGCCCATGTCATCATTTCTCTCC	3602
Db	4003	CATCTATCCTCCGTGTGACATCCAGACCCATACAGGCCCATGTCATCATTTCTCTCC	4062
QY	3603	CACACCGACGAGATGAGATGCTGTGCTGTACGAGACGAGGTGTCTTACGTCAACAC	3662
Db	4063	CACACCGACGAGATGAGATGCTGTGCTGTACGAGACGAGGTGTCTTACGTCAACAC	4122
QY	3663	GTAACGGGCGCATTTAAGATGTGTGCTGCAAGTGGGGGAGATGCTTCTGTGGC	3722
Db	4123	GTAACGGGCGCATTTAAGATGTGTGCTGCAAGTGGGGGAGATGCTTCTGTGGC	4182
QY	3723	CTACATCTGTCCAAACGATTAATGGGCTGGGGGTGAGAAAGCATTTGAGATCCGGCTGT	3782
Db	4183	CTACATCTGTCCAAACGATTAATGGGCTGGGGGTGAGAAAGCATTTGAGATCCGGCTGT	4242
QY	3783	GGAGACGGGCGACCTCGACGGGGCTTTCATGACAAACGAGCTCAGAGGCTCAAGTTCT	3842
Db	4243	GGAGACGGGCGACCTCGACGGGGCTTTCATGACAAACGAGCTCAGAGGCTCAAGTTCT	4302
QY	3843	GTTGTGACGGGAATGACAAAGGTTTTTTTGGCTCAAGTCCGCTCTGGGGGACAGCCAGT	3902
Db	4303	GTTGTGACGGGAATGACAAAGGTTTTTTTGGCTCAAGTCCGCTCTGGGGGACAGCCAGT	4362
QY	3903	TTAACCTCAGTACTGTGAACCGTAACTGCATATGAACTGTGGAAGGCG 3951	
Db	4363	TTAACCTCAGTACTGTGAACCGTAACTGCATATGAACTGTGGAAGGCG 4411	

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RESULT 6
US-10-029-115-5
; Sequence 5, Application US/10029115
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Pu, Alan C
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: Novel Germinal Center Kinase Cell Cycle Proteins, Compositions and Methods of Use

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; TITLE OF INVENTION: Method of Use
; FILE REFERENCE: A-70229/RMS/DHR
; CURRENT APPLICATION NUMBER: US/10/029,115
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 4033
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-029-115-5

Query Match          96.0%  Score 3792.8;  DB 43;  Length 4033;
Best Local Similarity 98.4%  Pred. No. 0;
Matches 3877;  Conservative 0;  Mismatches 2;  Indels 63;  Gaps 2

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QY	64	GACCTGCTGGAGATCTTTGACTTGTGGAGGTGGCCAAATGGAACTTACGACAGGTG	123
Db	95	GACCTGCTGGAGATCTTTGACTTGTGGAGGTGGCCAAATGGAACTTACGACAGGTG	154
QY	124	TACAAAGGTGCGGACATGTCAGACGGGGCAGCTGGCTGCCATCAGAGTATGATGTCACG	183
Db	155	TACAAAGGTGCGGACATGTCAGACGGGGCAGCTGGCTGCCATCAGAGTATGATGTCACG	214
QY	184	GAGACGAGGAGGAGAGATCAATCAAGGAGATCAATGCTGAAGAAATATACCTTCACAC	243
Db	215	GAGACGAGGAGGAGAGATCAATCAAGGAGATCAATGCTGAAGAAATATACCTTCACAC	274
QY	244	CGCAACATCGCCACTTACTACGAGCCCTTCATCAAGAAAGCCCCCGGGAAAAGATGAC	303
Db	275	CGCAACATCGCCACTTACTACGAGCCCTTCATCAAGAAAGCCCCCGGGAAAAGATGAC	334
QY	304	CAGCTCTGGCTGGTGTATGGAAGTTCTGTGTGTCTGGTTAGTACATGACCTGGTAAAGAC	363
Db	335	CAGCTCTGGCTGGTGTATGGAAGTTCTGTGTGTCTGGTTAGTACATGACCTGGTAAAGAC	394
QY	364	ACAAAGGCAACGCCCTGAGAGAGACTGTATCGCCTATATCTGCAGGAGATCTCTCAGG	423
Db	395	ACAAAGGCAACGCCCTGAGAGAGACTGTATCGCCTATATCTGCAGGAGATCTCTCAGG	454
QY	424	GGTCTGAGCCATCTTCATATGCCACAGAGTATCCATCGAGACATTAAGGGGCAAAATGTG	483
Db	455	GGTCTGAGCCATCTTCATATGCCACAGAGTATCCATCGAGACATTAAGGGGCAAAATGTG	514
QY	484	CTGCTGACAGAGATGCTGAGGTCAAGGTAGTGGATTTTGGGGTGAAGTCTCAGCTGAC	543
Db	515	CTGCTGACAGAGATGCTGAGGTCAAGGTAGTGGATTTTGGGGTGAAGTCTCAGCTGAC	574
QY	544	CGCACCGTGGGCAAGCGGAACACTTTCATTGGGACTCTCTCATCTGATGAGCTTCAGAGTTC	603
Db	575	CGCACCGTGGGCAAGCGGAACACTTTCATTGGGACTCTCTCATCTGATGAGCTTCAGAGTTC	634
QY	604	ATCGGCTGTGATGAGAACCTCGATGCCACATATGATTAAGGAGGATATTTGGTCTCTA	663
Db	635	ATCGGCTGTGATGAGAACCTCGATGCCACATATGATTAAGGAGGATATTTGGTCTCTA	694
QY	664	GGAATCAAGCAATGAGATGGCAGAGGAGAGCCCCCTCTGTGTGACATGCAACCCCATG	723
Db	695	GGAATCAAGCAATGAGATGGCAGAGGAGAGCCCCCTCTGTGTGACATGCAACCCCATG	754
QY	724	CGAGCCCTTCTCTCATTTCTTGGAACCTTCGCGCCAGGCTCAAGTCCAAAGAAATGTGTT	783
Db	755	CGAGCCCTTCTCTCATTTCTTGGAACCTTCGCGCCAGGCTCAAGTCCAAAGAAATGTGTT	814
QY	784	AAGAAGTTCATTGACTTCAATGACATATGTCATCAAGAACTTACCTGAGCCGCCACCC	843
Db	815	AAGAAGTTCATTGACTTCAATGACATATGTCATCAAGAACTTACCTGAGCCGCCACCC	874
QY	844	ACGAGCAGACTACTGAAAGTTTCCCTTCAATCCGGGACAGAGCCACGAGCGGAGGTCTGC	903
Db	875	ACGAGCAGACTACTGAAAGTTTCCCTTCAATCCGGGACAGAGCCACGAGCGGAGGTCTGC	934
QY	904	ATCCAGCTTAAAGAACCAATTTGACCGATCTCCGGAAAGAGCGGGGTGAGAAAGAGAGACA	963



Db 935 ATCCAGCTTAAAGACACATTGACCGATCCCGGAAGAACCGGGGTGAGAAAAGAGAGCA 994  
Qy 964 GAATATAGTACAGCGGAGCGAGAGAGAGATGACAGCCATGAGAGAGAGAGCCCA 1023  
Db 995 GAATATAGTACAGCGGAGCGAGAGAGATGACAGCCATGAGAGAGAGAGCCCA 1054  
Qy 1024 AGCTCCATCATGAACTGTCCCTGAGAGATGACTCTACGCCCGGAGTTTCTCCGGTCCAG 1083  
Db 1055 AGCTCCATCATGAACTGTCCCTGAGAGATGACTCTACGCCCGGAGTTTCTCCGGTCCAG 1114  
Qy 1084 CAGAAAAATAAGAGCACTCAGAGGCTTTAAACACAGCAGCAGCTCAGCAGAGCAG 1143  
Db 1115 CAGAAAAATAAGAGCACTCAGAGGCTTTAAACACAGCAGCAGCTCAGCAGAGCAG 1174  
Qy 1144 CAGGAGACCCCGAGGACACATCAACACCTGTGACACAGCGGACGGCGCATAGAG 1203  
Db 1175 CAGGAGACCCCGAGGACACATCAACACCTGTGACACAGCGGACGGCGCATAGAG 1234  
Qy 1204 GAGCAAGAGAGAGAGCGGCGCGCTGAGAGAGACACAGCGGCGGAGAGCGAGCGG 1263  
Db 1235 GAGCAAGAGAGAGAGCGGCGCGCTGAGAGAGACACAGCGGCGGAGAGCGAGCGG 1294  
Qy 1264 AAGCTGACAGAGAGAGAGAGAGCGGCGGCTGAGAGACATGACAGGCTCTGCGGCGGAG 1323  
Db 1295 AAGCTGACAGAGAGAGAGAGAGCGGCGGCTGAGAGACATGACAGGCTCTGCGGCGGAG 1354  
Qy 1324 GAGGAGCGGCGGACAGCGCGGAGCTGAGAGAGATACAAAGCGGAGCAGCTGAGAGAGCAG 1383  
Db 1355 GAGGAGCGGCGGACAGCGCGGAGCTGAGAGAGATACAAAGCGGAGCAGCTGAGAGAGCAG 1414  
Qy 1384 CGGCACTGACAACTCTTCAAGAGCAGCTGACAGAGAGCATGCTTACTCAATGCTCCCTG 1443  
Db 1415 CGGCACTGACAACTCTTCAAGAGCAGCTGACAGAGAGCATGCTTACTCAATGCTCCCTG 1474  
Qy 1444 CAGGAGCAGCAACAGCAGCAGCTTCAAGAAACAGCAGCAGCAGCAGCTCTGCTGAGG 1503  
Db 1475 CAGGAGCAGCAACAGCAGCAGCTTCAAGAAACAGCAGCAGCAGCAGCTCTGCTGAGG 1534  
Qy 1504 GACAGAAAGCCCTGTACCATTTATGTTGAGGAGATGAATCCCGTGAACAAACAGACCTGAG 1563  
Db 1535 GACAGAAAGCCCTGTACCATTTATGTTGAGGAGATGAATCCCGTGAACAAACAGACCTGAG 1594  
Qy 1564 GCCCGAGAGTGAAGAGAGAAACAGATGAACAGCAGCAGAACTCTTCCCTGAGCAG 1623  
Db 1595 GCCCGAGAGTGAAGAGAGAAACAGATGAACAGCAGCAGAACTCTTCCCTGAGCAG 1654  
Qy 1624 AGCAAGCAGGACAGACGCGGAGCTGAGGCCCCCAATCCCCCAGGCTCCCGAGGAGCCCCCA 1683  
Db 1655 AGCAAGCAGGACAGACGCGGAGCTGAGGCCCCCAATCCCCCAGGCTCCCGAGGAGCCCCCA 1714  
Qy 1684 GGAACCCCTTCCCAAGCTCTTATGCAAGAGCGCGTGAAGCCCAAGAGAGAGCCGAGC 1743  
Db 1715 GGAACCCCTTCCCAAGCTCTTATGCAAGAGCGCGTGAAGCCCAAGAGAGAGCCGAGC 1774  
Qy 1744 A----- 1744  
Db 1775 AAGAGCCTGATGAGACACCGGAGTCCCACTGAAGCCATATGAGAGACCTGTACCCCGATCC 1834  
Qy 1745 -AGTCCCTGAGAGACAGGCCCAACCGGAAACCTGGTGTGCTTCCCAAGCTCCCATGAAGCCC 1803  
Db 1835 CAGTCCCTGAGAGACAGGCCCAACCGGAAACCTGGTGTGCTTCCCAAGCTCCCATGAAGCCC 1894  
Qy 1804 GACCTGACATCCCGCAGCAGCAGCTGACAGCCAGATGCGGAGAGAGCTGATCCGAGCAG 1863  
Db 1895 GACCTGACATCCCGCAGCAGCAGCTGACAGCCAGATGCGGAGAGAGCTGATCCGAGCAG 1954  
Qy 1864 AATTCAAGCCCACTCTGAAGAGACTGAGCCCAAGCCGAAATCCCCAGCCTGGGTCCGC 1923  
Db 1955 AATTCAAGCCCACTCTGAAGAGACTGAGCCCAAGCCGAAATCCCCAGCCTGGGTCCGC 2014  
Qy 1924 CCAATTAACGAGGCGCCCAACCAAGGTGCTGAGAGAGCTCATCTATGCGACCTGCGCTT 1983

Db 2015 CCAATTAACGAGGCGCCCAACCAAGGTGCTGAGAGAGCTCATCTATGCGACCTGCGCTT 2074  
Qy 1984 AACACCACTGAGGAGCGGAGAGGTCCTCGGACAGGCCAGAGCTCCGTGCAAGCTTCGAGC 2043  
Db 2075 AACACCACTGAGGAGCGGAGAGGTCCTCGGACAGGCCAGAGCACTGTGCTCAAGCTTCGAGC 2134  
Qy 2044 AACTCGGCTGAGCAATCTATCTGCAAAAGCGGAGCAGAGCGGAGCAGCCCAAGCTTCA 2103  
Db 2135 AACTCGGCTGAGCAATCTATCTGCAAAAGCGGAGCAGAGCGGAGCAGCCCAAGCTTCA 2194  
Qy 2104 GGGCCCCCTGTCAAGCCCCCTGAGCCGAGCCCAAGCTTCTAGTAAACCTCGACCTCAGAGG 2163  
Db 2195 GGGCCCCCTGTCAAGCCCCCTGAGCCGAGCCCAAGCTTCTAGTAAACCTCGACGAGG 2254  
Qy 2164 AGCGACCTGTGCTGAGAAAGCTCGGACAGAGCTCTTCAAGCTTCAAGGGCAGCTCCCG 2223  
Db 2255 AGCGACCTGTGCTGAGAAAGCTCGGACAGAGCTCTTCAAGCTTCAAGGGCAGCTCCCG 2314  
Qy 2224 CAGGCTGACTCACTGAGCGGAAACCGGTGGAGCCTCTTCAAACTGAGACAGCTCCCT 2283  
Db 2215 CAGGCTGACTCACTGAGCGGAAACCGGTGGAGCCTCTTCAAACTGAGACAGCTCCCT 2374  
Qy 2284 GTGCTCTCCCTGAGAAATAAGCCAAAGCCGACAGCAAGCTTCAAGGCGAGGCC 2343  
Db 2375 GTGCTCTCCCTGAGAAATAAGCCAAAGCCGACAGCAAGCTTCAAGGCGAGGCC 2434  
Qy 2344 GCAGACTTTGTGTGCTGAAAGAGCGGACTTGTGAGACAGAGCCCTCGGCTTCCCAAGAG 2403  
Db 2435 GCAGACTTTGTGTGCTGAAAGAGCGGACTTGTGAGACAGAGCCCTCGGCTTCCCAAGAG 2494  
Qy 2404 GCCATGACATCTGTGTGTCAGCGAGAGAGGTGAGAAAGCATGAGAGAGAGAGAGAA 2463  
Db 2495 GCCATGACATCTGTGTGTCAGCGAGAGAGGTGAGAAAGCATGAGAGAGAGAGAGAA 2554  
Qy 2464 GGCAGAGGCGGCGCAGAGAGAGGAGAGAGATACCCCTGAGGAGCGCAGAGATGAGGAT 2523  
Db 2555 GGCAGAGGCGGCGCAGAGAGAGGAGAGAGATACCCCTGAGGAGCGCAGAGATGAGGAT 2611  
Qy 2524 ACAGACAGCGTCAGACACATGATGTGTCAAGAGCTCGAGAGAGATACAGCGGAGCCAGC 2583  
Db 2612 ACAGACAGCGTCAGACACATGATGTGTCAAGAGCTCGAGAGAGATACAGCGGAGCCAGC 2671  
Qy 2584 CCATACGAGGAGCGGACCATGATGTGTCAAGGACCCCTGAGAGAGAGCGGAGCCTGCTG 2643  
Db 2672 CCATACGAGGAGCGGACCATGATGTGTCAAGGACCCCTGAGAGAGAGCGGAGCCTGCTG 2731  
Qy 2644 CATGCTGACAGCAATGAGTACAAACCTGCTGACGTGTGTCAGCCAGCAGCTCAACC 2703  
Db 2732 CATGCTGACAGCAATGAGTACAAACCTGCTGACGTGTGTCAGCCAGCAGCTCAACC 2791  
Qy 2704 ACCGAGAAACAGCAAAAGCCCAAGCCCACTCGAAGATGAGAGTGTGATACAGTCT 2763  
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Qy 2764 CGTGGGCTGTAAGAGGCCCCCTGAGAGAGCTCGTTCAGATGTTTGTGATCTAGGGATC 2823  
Db 2852 CGTGGGCTGTAAGAGGCCCCCTGAGAGAGCTCGTTCAGATGTTTGTGATCTAGGGATC 2911  
Qy 2824 TACAGCCTGAGAGCAGATGAGGAGACAGATCCCATCAAGCCCTAGTGTGAGAGAGGCG 2883  
Db 2912 TACAGCCTGAGAGCAGATGAGGAGACAGATCCCATCAAGCCCTAGTGTGAGAGAGGCG 2971  
Qy 2884 ACTGAGCTGACAGAGCTGACATGACAGCTGAGAGAGGATCTGTGTCAACGTGAATCCC 2943  
Db 2972 ACTGAGCTGACAGAGCTGACATGACAGCTGAGAGAGGATCTGTGTCAACGTGAATCCC 3031  
Qy 2944 ACCGAAACCCGAGCCCAACATGAGAGCCCTGAGATCCGGAAGTCAAGAGAGGATTAAC 3003  
Db 3032 ACCGAAACCCGAGCCCAACATGAGAGCCCTGAGATCCGGAAGTCAAGAGAGGATTAAC 3091  
Qy 3004 TCCGAGATCTCTGTGAGAGCCCTTGTGAGGAGTCAACCTGTGATGTGAGCAGAGAGAGCGG 3063  
Db 3092 TCCGAGATCTCTGTGAGAGCCCTTGTGAGGAGTCAACCTGTGATGTGAGCAGAGAGAGCGG 3151

QY	3064	CTGATGTTGCTGCAACCGAAGTGGGCAAGGCTGTATGCACTCATTTGGGCGCGACGC	3123
Db	3152	CTGATGTTGCTGGACCGAAGTGGGCAAGGCTGTATGCACTCATTTGGGCGCGACGC	3211
QY	3124	TTCCAGCAGATGSAATGTCGTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGAAAAAG	3183
Db	3212	TTCCAGCAGATGSAATGTCGTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGAAAAAG	3271
QY	3184	AACAAACTGCGGGGTGTATTACTGTCTTGCTCCGGAAACAAGATTTCGACATATGACCA	3243
Db	3272	AACAAACTGCGGGGTGTATTACTGTCTTGCTCCGGAAACAAGATTTCGACATATGACCA	3331
QY	3244	GAAGTGGAGAAAGAACAGAGGCTGGACCAACGTTGGGGGACATGGAGGCTGGCGGGCATAC	3303
Db	3332	GAAGTGGAGAAAGAACAGAGGCTGGACCAACGTTGGGGGACATGGAGGCTGGCGGGCATAC	3391
QY	3304	CGTGTGTGAAATAAGACGGATTAAGTTCTTGCTCATCGCCCTTCMAAGCTCCGTGGAG	3363
Db	3392	CGTGTGTGAAATAAGACGGATTAAGTTCTTGCTCATCGCCCTTCMAAGCTCCGTGGAG	3451
QY	3384	GTTATGCTTGCGGGCCCCCAACCTTACCAAAATTATGAGCTTCAATCTTTTGGCGAC	3423
Db	3452	GTTATGCTTGCGGGCCCCCAACCTTACCAAAATTATGAGCTTCAATCTTTTGGCGAC	3511
QY	3424	CTCCCCCAACGGCCCTCTGTGGTGCACCTGACAGTAAAGAGAGGGGCAACGGCTCAAGGTC	3483
Db	3512	CTCCCCCAACGGCCCTCTGTGGTGCACCTGACAGTAAAGAGAGGGGCAACGGCTCAAGGTC	3571
QY	3484	ATCTATGAGCTCCAGTGCCTGCTTCATGCTGTGATGTGCATCTGGGGAACAGCTATGAC	3543
Db	3572	ATCTATGAGCTCCAGTGCCTGCTTCATGCTGTGATGTGCATCTGGGGAACAGCTATGAC	3631
QY	3544	ATCTATGATCCCTGTGCAATCCAGAGCCAGATACGCCCATTCGCATATCTTCCTCCCC	3603
Db	3632	ATCTATGATCCCTGTGCAATCCAGAGCCAGATACGCCCATTCGCATATCTTCCTCCCC	3691
QY	3604	AACACCGACGGCATGAGATGCTGCTGTGCTACAGAGACGAGGGGTCTTACGTCAACACG	3663
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QY	3664	TACGGGCGCATCTTAAGGATGTGTGCTGCACTGGGGGAGAGTCCCTACTTCTGTGGCC	3733
Db	3752	TACGGGCGCATCTTAAGGATGTGTGCTGCACTGGGGGAGAGTCCCTACTTCTGTGGCC	3811
QY	3724	TACATCTGCTCCAAACAGATATAATGGGCTGGGTTGGAAGCATTTGAAATCCGCTCTGTG	3783
Db	3812	TACATCTGCTCCAAACAGATATAATGGGCTGGGTTGGAAGCATTTGAAATCCGCTCTGTG	3871
QY	3784	GAGACGGGCGCATCTGACGGGGTCTTCAATGCACAACAGAGCTCAGAGGCTCAAGTTCTCTG	3843
Db	3872	GAGACGGGCGCATCTGACGGGGTCTTCAATGCACAACAGAGCTCAGAGGCTCAAGTTCTCTG	3931
QY	3844	TGTGACGGGAATGACAAGTGTTTTTTGTGCTCAGTCCGCTCTGGGGGACAGGCCAAGTT	3903
Db	3932	TGTGACGGGAATGACAAGTGTTTTTTGTGCTCAGTCCGCTCTGGGGGACAGGCCAAGTT	3991
QY	3904	TACTTCATGACCTGGAACCGTAACTGCATCAATGAATCTGTGTA	3945
Db	3992	TACTTCATGACCTGGAACCGTAACTGCATCAATGAATCTGTGTA	4033
RESULT 7			
PCT-US02-33845-6			
Sequence 6, Application PC/TUS0233845			
GENERAL INFORMATION:			
APPLICANT: Rigel Pharmaceuticals, Inc.			
APPLICANT: Leo, Cindy			
APPLICANT: Luo, Ying			
APPLICANT: Xu, Xiang			
APPLICANT: Yu, Simon			
TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE PROTEINS, COMPOSITIONS,			
TITLE OF INVENTION: AND METHODS OF THEIR USE			

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; FILE REFERENCE: 021044-005600PC
; CURRENT APPLICATION NUMBER: PCT/US02/33845
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 10/029,115
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 6
; LENGTH: 4032
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: mishapen/NIK-related Kinase isoform c
PCT-US02-33845-6

Query Match      95.5%; Score 3772.8; DB 1; Length 4032;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 3871; Conservative 0; Mismatches 7; Indels 64; Gaps 3

QY      64  GACCCGTGGGATTCCTTTGAGCTGTGGAGGGGTGGCAATGGAACCTAGGACAGAGG 123
DB      95  GACCCGTGGGATTTTGTAGCTTGTGGAGGGGTGGCAATGGAACCTAGGACAGAGG 154
QY      124 TACAAGGGTGGCATGTCAAGCGGGGAGCTGCTGCATCAAGATCATGATGTCAAG 183
DB      155 TACAAGGGTGGCATGTCAAGCGGGGAGCTGCTGCATCAAGATCATGATGTCAAG 214
QY      184 GAGGACGAGAGGAAGAGATCAACAGAGATCAACATGCTGTAAGAAAGTACTTCAAC 243
DB      215 GAGGACGAGAGGAAGAGATCAACAGAGATCAACATGCTGTAAGAAAGTACTTCAAC 274
QY      244 CGCAACATCGCACCTACTAGGAGCCCTTCATCAAGAAAGCCCCCGGAAACGATGAC 303
DB      275 CGCAACATCGCACCTACTAGGAGCCCTTCATCAAGAAAGCCCCCGGAAACGATGAC 334
QY      304 CAGCTCTGGCTGATGAGATTCTGTGTGCTGTGTCAAGTCACTGACCTGTGTAAGAAC 363
DB      335 CAGCTCTGGCTGATGAGATTCTGTGTGCTGTGTCAAGTCACTGACCTGTGTAAGAAC 394
QY      364 ACAAAGGCAACGCCCTGAAGGAGAGCTGTATCGCTATATCTGACAGAGAGATCTCAGG 423
DB      395 ACAAAGGCAACGCCCTGAAGGAGAGCTGTATCGCTATATCTGACAGAGAGATCTCAGG 454
QY      424 GGTCTGGCCCATCTTCATAGTCCCAAGGTATCCATCGAGACATCAAGGGGCAAGATG 483
DB      455 GGTCTGGCCCATCTTCATAGTCCCAAGGTATCCATCGAGACATCAAGGGGCAAGATG 514
QY      484 CTGCTGACAGAGATGCTGAGGTCAAGGTAGTGAATTTTGGGGGTGAGTCTCAGCTGAC 543
DB      515 CTGCTGACAGAGATGCTGAGGTCAAGGTAGTGAATTTTGGGGGTGAGTCTCAGCTGAC 574
QY      544 CGCACCGTGGGACAGCGAACACTTTCAATGGGACTCCCTACATGATGGCTTCAAGAGTC 603
DB      575 CGCACCGTGGGACAGCGAACACTTTCAATGGGACTCCCTACATGATGGCTTCAAGAGTC 634
QY      604 ATCGCTGTGATGAGAACCTTGATGCCACTATGATTAACAGAGTGAATTTTGGTCTCTA 663
DB      635 ATCGCTGTGATGAGAACCTTGATGCCACTATGATTAACAGAGTGAATTTTGGTCTCTA 694
QY      664 GGAATCAACAGCATGAGATGGGCAAGGAGAGCCCCCTCTGTGTGACATGACCCCATG 723
DB      695 GGAATCAACAGCATGAGATGGGCAAGGAGAGCCCCCTCTGTGTGACATGACCCCATG 754
QY      724 CGAGCCCTCTTCTCATTTCTCGAAGCCCTCGCCACAGGCTCAAGTCCAAAGATGGTCT 783
DB      755 CGAGCCCTCTTCTCATTTCTCGAAGCCCTCGCCACAGGCTCAAGTCCAAAGATGGTCT 814
QY      784 AAGAAATTCAATTGACTTCATATGACATATGTTCTCATCAAGACTTACCTGAGCCGCCACCC 843
DB      815 AAGAAATTCAATTGACTTCATATGACATATGTTCTCATCAAGACTTACCTGAGCCGCCACCC 874
QY      844 ACGAGCAGCTACGAAAGTTTCCCTTCAATCCGGGACAGGCCACGGAAGGGGAGGTCCGC 903

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Dh 875 ACGGAGCAGCTACGAACTTCCCTTCATCCGGGACAGCCCAAGGAGCGGAGGTCCGC 934  
Qy 904 ATCCAGCTTAAAGACACATTGACCGATCCCGAAGAAAGCGGGTGAAGAAAGAGAGCA 963  
Db 935 ATCCAGCTTAAAGACACATTGACCGATCCCGAAGAAAGCGGGTGAAGAAAGAGAGCA 994  
Qy 964 GAATATAGATACACCGGAGGAGAGAGATGACAGCCATGAGAGAGAGAGAGCA 1023  
Db 995 GAATATAGATACACCGGAGGAGAGAGATGACAGCCATGAGAGAGAGAGAGCA 1054  
Qy 1024 AGCTCATCATGAAAGTGCCTGAGAGATCGACTACCGCGAGATTCTCCGGCTCCAG 1083  
Db 1055 AGCTCATCATGAAAGTGCCTGAGAGATCGACTACCGCGAGATTCTCCGGCTCCAG 1114  
Qy 1084 CAGGAAATTAAGCACTCAGAGGCTTTAAACAGCAGCAGCAGCTGACAGCAGCAG 1143  
Db 1115 CAGGAAATTAAGCACTCAGAGGCTTTAAACAGCAGCAGCAGCTGACAGCAGCAG 1174  
Qy 1144 CAGGAGACCCCGAGGAGCAGATGAAACACTGCTGACAGCGGAGCGGAGCGGATAGAG 1203  
Db 1175 CAGGAGACCCCGAGGAGCAGATGAAACACTGCTGACAGCGGAGCGGAGCGGATAGAG 1234  
Qy 1204 GAGCAGAAAGAGAGAGCGGCGCGCTGAGAGAGCAAGCGGAGGAGCGGAGAGCGG 1263  
Db 1235 GAGCAGAAAGAGAGAGCGGCGCGCTGAGAGAGCAAGCGGAGGAGCGGAGAGCGG 1294  
Qy 1264 AAGCTGAGAGAGAGAGAGAGCAGCGGCGGCTGAGAGATGCAAGGCTTCCGCGGAG 1333  
Db 1295 AAGCTGAGAGAGAGAGAGAGCAGCGGCGGCTGAGAGATGCAAGGCTTCCGCGGAG 1354  
Qy 1324 GAGGAGCGGCGGAGCGGCGGAGAGAGATGCAAGCGGAGGAGCGGAGAGAGAGAG 1383  
Db 1355 GAGGAGCGGCGGAGCGGCGGAGAGAGATGCAAGCGGAGGAGCGGAGAGAGAGAG 1414  
Qy 1384 CGGAGCTCAGAAAGCTCTCAGAGGAGCTGAGAGAGAGATGCTACCTAAGTCCCTG 1443  
Db 1415 CGGAGCTCAGAAAGCTCTCAGAGGAGCTGAGAGAGAGATGCTACCTAAGTCCCTG 1474  
Qy 1444 CAGCAGAGCAACAGCAGCAGCAGCTTCAAGAACAGCAGCAGCAGCTCTGCGTGG 1503  
Db 1475 CAGCAGAGCAACAGCAGCAGCAGCTTCAAGAACAGCAGCAGCAGCTCTGCGTGG 1534  
Qy 1504 GACAGAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1563  
Db 1535 GACAGAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1594  
Qy 1564 GCGGAG 1623  
Db 1595 GCGGAG 1654  
Qy 1624 AGCAG 1683  
Db 1655 AGCAG 1714  
Qy 1684 GAG 1743  
Db 1715 GAG 1774  
Qy 1744 A----- 1744  
Db 1775 AAG 1834  
Qy 1745 -AGTCCCTGAG 1803  
Db 1835 CAGTCCCTGAG 1894  
Qy 1804 GAG 1863  
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Qy 1864 AATTGAG 1923  
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Qy 1924 CAGAGATTAAG 1983  
Db 2015 CAGAGATTAAG 2074  
Qy 1984 AACACAG 2043  
Db 2075 AACACAG 2134  
Qy 2044 AACTCGGCTGAG 2103  
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Qy 2104 GAG 2163  
Db 2195 GAG 2254  
Qy 2164 AGCAG 2223  
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Qy 2224 CAGGCTGCTCAG 2283  
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Qy 2284 GTGCTTCCCTGAG 2343  
Db 2375 GTGCTTCCCTGAG 2434  
Qy 2344 GAG 2403  
Db 2435 GAG 2494  
Qy 2404 GCGATGAGATTAAG 2463  
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Qy 2464 GCGAG 2523  
Db 2555 GCGAG 2611  
Qy 2524 ACAG 2583  
Db 2612 ACAG 2671  
Qy 2584 CCAATACGAG 2643  
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Qy 2644 CATGCTGACAG 2703  
Db 2732 CATGCTGACAG 2791  
Qy 2704 ACCGAG 2763  
Db 2792 ACCGAG 2851  
Qy 2764 CGTGGCTGTAAG 2823  
Db 2852 CGTGGCTGTAAG 2911  
Qy 2824 TACAG 2883  
Db 2912 TACAG 2971  
Qy 2884 ACTGAGCTGACAG 2943  
Db 2972 ACTGAGCTGACAG 3031  
Qy 2944 ACCAG 3003  
Db 3032 ACCAG 3091

OY	3004	CCGAGATACCTCTGTGAGGCCCTTTGGGGGGGTCAACCTGCTGGTGGGACAGGAAACGGG	3063
Db	3092	TCGAGATTCCTCTGTGAGGCCCTTTGGGGGGGTCAACCTGCTGGTGGGACAGGAAACGGG	3151
OY	3064	CTGATGTTGTGTGACCGAGATGGGACAGGGCAAGGTGATGGAATCTAATTGGGGCGGCGACGC	3123
Db	3152	CTGATGTTGTGTGACCGAGATGGGACAGGGCAAGGTGATGGAATCTAATTGGGGCGGCGACGC	3211
OY	3124	TTCCAGCAGATGATGTGTCTGAGAGGGGCTCAACTGTCTATCAACCATCTTCAGGAAAAAGG	3183
Db	3212	TTTCAGCAGATGATGTGTCTGAGAGGGGCTCAACTGTCTATCAACCATCTTCAGGAAAAAGG	3271
OY	3184	AACAAACTGGGGGGGTATTAACCTGTCTCGGGAACAAGATTCTGCACATGACCA	3243
Db	3272	AACAAACTGGGGGGGTATTAACCTGTCTCGGGAACAAGATTCTGCACATGACCA	3331
OY	3244	GAAGTGAGAAAGAACGAGGCTGGAACCAACGGTGGGGACATGAGAGGGCTCGGGGACATAC	3303
Db	3332	GAAGTGAGAAAGAACGAGGCTGGAACCAACGGTGGGGACATGAGAGGGCTCGGGGACATAC	3391
OY	3304	CGTGTGTGAATTCGAGCGGATTTAAGTTCCTGTGTCATGCGCTTCAAGAGCTCCGTGGAG	3363
Db	3392	CGTGTGTGAATTCGAGCGGATTTAAGTTCCTGTGTCATGCGCTTCAAGAGCTCCGTGGAG	3451
OY	3364	GTCATATGCTGGGGGCCCCCAACCCCTACCAAAATTCATGAGCCCTTCAAGCTCTTGGCCAGC	3423
Db	3452	GTCATATGCTGGGGGCCCCCAACCCCTACCAAAATTCATGAGCCCTTCAAGCTCTTGGCCAGC	3511
OY	3424	CTCCCCACCGCCCTCTGTCTGTGTGACCTTGACAGTAAAGAGGGGCGAGCGGCTCAAGGTC	3483
Db	3512	CTCCCCACCGCCCTCTGTGTGTGACCTTGACAGTAAAGAGGGGCGAGCGGCTCAAGGTC	3571
OY	3484	ATCTATGGCTTCAAGTCTGGCTTCATAGCTGTGATGTGACTTCGGGGAAACAGCTATGAC	3543
Db	3572	ATCTATGGCTTCAAGTCTGGCTTCATAGCTGTGATGTGACTTCGGGGAAACAGCTATGAC	3631
OY	3544	ATCTAATATCCCTGTGACATCTCAAGAGCAGATACAGCGCCCAATGCATCAATCTTCCMCCCC	3603
Db	3632	ATCTAATATCCCTGTGACATCTCAAGAGCAGATACAGCGCCCAATGCATCAATCTTCCMCCCC	3691
OY	3604	AACACCGACGCGATGAGATGCTGCTGTGCTACAGAGACGAGGGTGTCTTACGTCAACAG	3663
Db	3692	AACACCGACGCGATGAGATGCTGCTGTGCTACAGAGACGAGGGTGTCTTACGTCAACAG	3751
OY	3664	TACGGGGGCATCATTTAAGATGTGTGCTGCAAGTGGGGGAGATGCTTACTTGTGTGCC	3723
Db	3752	TACGGGGGCATCATTTAAGATGTGTGCTGCAAGTGGGGGAGATGCTTACTTGTGTGCC	3811
OY	3724	TACATCTGCTCCACACAGATTAATGGGCTGGGGGTGAAAGACCTTAGATATCCGCTGTGG	3783
Db	3812	TACATCTGCTCCACACAGATTAATGGGCTGGGGGTGAAAGACCTTAGATATCCGCTGTGG	3871
OY	3784	GAGACGGGCGACCTCGACGGGGGCTTTCATATGCAAAAAGACTCAGAGGCTCAAGTTCCTGG	3843
Db	3872	GAGACGGGCGACCTCGACGGGGGCTTTCATATGCAAAAAGACTCAGAGGCTCAAGTTCCTGG	3931
OY	3844	TGTGAGCGGAATGACAAGTGTGTTTTTGGCTCAAGTCGCTCTGGGGGACAGACCCAAGTT	3903
Db	3932	TGTGAGCGGAATGACAAGTGTGTTTTTGGCTCAAGTCGCTCTGGGGGACAGACCCAAGTT	3991
OY	3904	TACTTCATGATCTGAAACCGTAATCGATATGATATGATCAATGCTGGA	3945
Db	3992	TA-TTCATGATCTGAAACCGTAATGATATGATATGATCAATGCTGGA	4032

RESULT 8  
US-60-500-337-1177  
; Sequence 1177, Application US/60500337  
; GENERAL INFORMATION:  
; APPLICANT: CARCILL, Michele  
; TITLE OF INVENTION: POLYMERISMS IN NUCLEIC ACID MOLECULES  
; TITLE OF INVENTION: ENCODING HUMAN KINASE PROTEINS, METHODS OF DETECTION AND  
; TITLE OF INVENTION: USES THEREOF

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: FILE REFERENCE: CLD001483
: CURRENT APPLICATION NUMBER: US/60/500,337
: CURRENT FILING DATE: 2003-09-05
: NUMBER OF SEQ ID NOS: 123188
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1177
: LENGTH: 4631
: TYPE: DNA
: ORGANISM: Homo sapiens
US-60-500-337-1177

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Query Match	92.1%;	Score 3637.4;	DB 107;	Length 4631;
Best Local Similarity	95.5%;	Pred. No. 0;		
Matches 3826;	Conservative	6;	Mismatches 2;	Indels 171;
			Gaps	2;

OY	7	TTGGGCGACACCCAGGCCCCCGGACCGGAGCTGGAGACACATCGACTGTCCGCGCTTGCGGGAC	66
Db	196	ATGGGCGACACCGCCCCCGGAGCGACTGGACGACATCGACTGTCCGCGCTTGCGGGAC	255
OY	67	CCTGCTGGGATCTTTGAGCTTGTGGAGTGGTCG3CAATGGACCTTACG3A CAGGTGAC	126
Db	256	CCTGCTGGGATCTTTGAGCTTGTGGAGTGGTCG3CAATGGACCTTACG3A CAGGTGAC	315
OY	127	AAAGGTGGGCATGTTCMAAGACGGGGCAGCTGGCTCCATCAAGGTTCATGGATGTCA CCGGAG	186
Db	316	AAAGGTGGGCATGTTCMAAGACGGGGCAGCTGGCTCCATCAAGGTTCATGGATGTCA CCGGAG	375
OY	187	GACGAGGAGGAAGAGATCAACACAGAGATCAACA TGTCTGA AAAAGTACTTCACCA CCGC	246
Db	376	GACGAGGAGGAAGAGATCAACACAGAGATCAACA TGTCTGA AAAAGTACTTCACCA CCGC	435
OY	247	AACATCGGCACCTTACTACGAGCCTTCAATCAAGAA GAGCCCCCGGGGAA CGATGACAG	306
Db	436	AACATCGGCACCTTACTACGAGCCTTCAATCAAGAA GAGCCCCCGGGGAA CGATGACAG	495
OY	307	CTCTGGCTGTGTGAATGGAGTTCTGTGTGTGTGGTTCAGTAC TGA CTTGTGTAAGAACAC	366
Db	496	CTCTGGCTGTGTGAATGGAGTTCTGTGTGTGTGGTTCAGTAC TGA CTTGTGTAAGAACAC	555
OY	367	AAAGGCAACGCCCTGAAAGAGAGACTGTATCGCTATATCTGCAGGAGATCCTCAGGGGT	426
Db	556	AAAGGCAACGCCCTGAAAGAGAGACTGTATCGCTATATCTGCAGGAGATCCTCAGGGGT	615
OY	427	CTGGCCCATCTCCATGCCCCAAGGTGATCCATGAGACATCAAGGGCAGATGTGCTG	486
Db	616	CTGGCCCATCTCCATGCCCCAAGGTGATCCATGAGACATCAAGGGCAGATGTGCTG	675
OY	487	CTGCACAGGATGTCTGAGGTCAAGCTGATGGATTTTGGGGTGAAGTGT CAGCTG3A CCGG	546
Db	676	CTGCACAGGATGTCTGAGGTCAAGCTGATGGATTTTGGGGTGAAGTGT CAGCTG3A CCGG	735
OY	547	ACCGTGGGACACGGAA CACTTTGATTTGGGACTCCCTA CTG3AATG3CTCCAGAGGTCA TC	606
Db	736	ACCGTGGGACACGGAA CACTTTGATTTGGGACTCCCTA CTG3AATG3CTCCAGAGGTCA TC	795
OY	607	GCTGTGTATGAGAACCTTGATGCCACTATGATTA CAGAGTGA TATTTGGTCTCTAGGA	666
Db	796	GCTGTGTATGAGAACCTTGATGCCACTATGATTA CAGAGTGA TATTTGGTCTCTAGGA	855
OY	667	ATCA CAGGCATTCGAGATGGGACAGAGAGCCCCCTCTGTGTGATGACATGCA CCCCATGGGA	726
Db	856	ATCA CAGGCATTCGAGATGGGACAGAGAGCCCCCTCTGTGTGATGACATGCA CCCCATGGGA	915
OY	727	GCCCTCTTCCATCTCCCTCGAGAACCCCTCGGCCACG3CTCAAGTCCMAAGTGTCTAAG	786
Db	916	GCCCTCTTCCATCTCCCTCGAGAACCCCTCGGCCACG3CTCAAGTCCMAAGTGTCTAAG	975
OY	787	AAAGTTCATGTA CTTCAATTGACACATGTCTCATCAAGACTTA CTTAGCCGCCACCCACG	846
Db	976	AAAGTTCATGTA CTTCAATTGACACATGTCTCATCAAGACTTA CTTAGCCGCCACCCACG	1033
OY	847	GAGCAGCTACTGAAGTTTCCCTTCA TCCGGGACCAAGCCCA GAGCGGACAGGTCCGCA TC	906

Db	1036	GAGCAGCTACTGAACTTTCCTTCATTCGGGACCAAGCCACGAGCGGAGGTCCGCATC	1095
OY	907	CAGCTTAAGAACCACTATTGCCGATCCGGAGAAAGCGGAGTGAAGAAAGAGAGACAGA	966
Db	1096	CAGCTTAAAGAACCACTATTGCCGATTCGGAGAAAGCGGAGTGAAGAAAGAGAGACAGA	1155
OY	967	TATGAGTACAGCGGACCGAGGAGAAAGATGACAGCCATGAGAGAAAGAGAGCCAAAGC	1028
Db	1156	TATGAGTACAGCGGACCGAGGAGAAAGATGACAGCCATGAGAGAAAGAGAGCCAAAGC	1215
OY	1027	TCGCATCATGAAGTGCCTGTGAGAAAGTGCATCTTAAGCCGGAGTTTCTCCGCTCCAGAG	1088
Db	1216	TCGCATCATGAAGTGCCTGTGAGAAAGTGCATCTTAAGCCGGAGTTTCTCCGCTCCAGAG	1275
OY	1087	GAAATTAAGAGCACTCAGAGGCTTTAAACACGACGACAGACTGCACAGCAGCAGAG	1146
Db	1276	GAAATTAAGAGCACTCAGAGGCTTTAAACACGACGACAGACTGCACAGCAGCAGAG	1335
OY	1147	CGAGACCCCGAGGACACATCAACACCTGTGCACAGCGGACGCGCATAGAGAG	1206
Db	1336	CGAGACCCCGAGGACACATCAACACCTGTGCACAGCGGACGCGCATAGAGAG	1395
OY	1207	CAGAAAGAGAGAGCGGCGCCGCTGTGAGAGCAACGCGCGGAGACGGAGAGAG	1266
Db	1396	CAGAAAGAGAGAGCGGCGCCGCTGTGAGAGCAACGCGCGGAGACGGAGAGAG	1455
OY	1267	CTGCAGAGAAAGAGCAGAGCGGCGGCTGTGAGAGCATTCAGAGGCTCTCGCGGGAGAG	1328
Db	1456	CTGCAGAGAAAGAGCAGAGCGGCGGCTGTGAGAGCATTCAGAGGCTCTCGCGGGAGAG	1515
OY	1327	GAGCGCGGACAGCGCGGAGCTGTAGCAGGAAATACAGCGGAAACAGCTGAGAGCAGCGG	1388
Db	1516	GAGCGCGGACAGCGCGGAGCTGTAGCAGGAAATACAGCGGAAACAGCTGAGAGCAGCGG	1575
OY	1387	CAGTCAAGAACTTCTTCAGAGGAGCTGCACAGAGCATGCTTAAGTCTCTGAG	1448
Db	1576	CAGTCAAGAACTTCTTCAGAGGAGCTGCACAGAGCATGCTTAAGTCTCTGAG	1639
OY	1447	CAGCAGCAACAGCAGCAGAGCTTCAGAAACAGCAGCAGCAGCACTCTGCTGGGAG	1506
Db	1636	CAGCAGCAACAGCAGCAGAGCTTCAGAAACAGCAGCAGCAGCACTCTGCTGGGAG	1695
OY	1507	AGGAAGCCCTGTACCATTAATGTCGAGGACATGAATCCCGCTGACAAACAGCCTGGCC	1566
Db	1696	AGGAAGCCCTGTACCATTAATGTCGAGGACATGAATCCCGCTGACAAACAGCCTGGCC	1755
OY	1567	CGAGAGGTAAAGAGAGAAACAAAGATGAACAAAGCAGCAGAACTTCTCTGGCCAAAGC	1628
Db	1756	CGAGAGGTAAAGAGAGAAACAAAGATGAACAAAGCAGCAGAACTTCTCTGGCCAAAGC	1815
OY	1627	AAGCCAGGACAGACGGGGCTGAGGCCCTCCATCCCGAGGCTCCCGAGGGCCCCAGGA	1686
Db	1816	AAGCCAGGACAGACGGGGCTGAGGCCCTCCATCCCGAGGCTCCCGAGGGCCCCAGGA	1875
OY	1687	CCCTTTTCCAGACTCTCTTAATGAGAGGCGAGTGAAGCCCAAGAGAGGACCGCAC--	1744
Db	1876	CCCTTTTCCAGACTCTCTCTTAATGAGAGGCGAGTGAAGCCCAAGAGAGGACCGCACAG	1935
OY	1745	-----AG	1746
Db	1936	AGCCTGTAGGACACCGGGTCCCACTGAAGCCATATGACAGACTGTACCCCGATCCAG	1995
OY	1747	TCCCTGAGAGACAGGCCACCCGAAACCTGGCTGCTTCCAGCCTCCATGACCCGAC	1806
Db	1996	TCCCTGAGAGACAGGCCACCCGAAACCTGGCTGCTTCCAGCCTCCATGACCCGAC	2055
OY	1807	CCTGCGATCCCGACACCACTGCACAGCCCAAGTGCAGAGAGAGTGTATCCGACAGAT	1866
Db	2056	CCTGCGATCCCGACACCACTGCACAGCCCAAGTGCAGAGAGAGTGTATCCGACAGAT	2115
OY	1867	TCAAGACCCCACTCTGAAGAGACTTGAGCCCTCCAGCCGAATCCCCACCTGGAGTCCGCCA	1926
Db	2116	TCAAGACCCCACTCTGAAGAGACTTGAGCCCTCCAGCCGAATCCCCACCTGGAGTCCGCCA	2175

OY	1957	GATTAACGAGGCCCAACCCAGGTGCTTCAGAGCACTCATCTATTCGCACTGCCCTTAAC	1986
DB	2176	GATTAACGAGGCCCAACCCAGGTGCTTCAGAGCACTCATCTATTCGCACTGCCCTTAAC	2235
OY	1987	ACCAATGGGGCCGAGGGTCCCCGCAAGCCAGGCACTTCGTGCACAGCTTCGAGCAAC	2046
DB	2236	ACCAATGGGGCCGAGGGTCCCCGCAAGCCAGGCAAGTCCCTGTC-----	2280
OY	2047	TCGGCTGCAATCTATCTGCAAAAGGCGGCAAGCGGGCAACCCCAAGCTCAAGG	2106
DB	2281	-----	2280
OY	2107	CCCCCTGCTCAGCCCCCTGCGCCGCAACGCTCTAATAACCCCGAAGCTTCAGAGAGC	2166
DB	2281	-----AGTAACCCCGAAGCTTCAGAGAGC	2304
OY	2167	GAACCTGGCTGGAAACGCTCGGACAGGTCCTTCAAGCTTTCACGGGCACTTCCCCAG	2228
DB	2305	GAACCTGGCTGGAAACGCTCGGACAGGTCCTTCAAGCTTTCACGGGCACTTCCCCAG	2364
OY	2227	GCTGGCTACATGGAGCGGGAACGGGTGGGAAGCTCTCAAAAGGCAAGCTCCCTGTG	2286
DB	2365	GCTGGCTACATGGAGCGGGAACGGGTGGGAAGCTCTCTCAAAAGGCAAGCTCCCTGTG	2424
OY	2287	CTCTCCCTGGGAATAAAGCCAAAGCCGACAGCAACGCTTCACGGGCAAGCGGCGCA	2346
DB	2425	CTCTCCCTGGGAATAAAGCCAAAGCCGACAGCAACGCTTCACGGGCAAGCGGCGCA	2484
OY	2347	GACTTTGTGTCTGAAGAGCGGACCTCTYGACAGAGCCCTCGAGCTTCCCAAGAGCC	2406
DB	2485	GACTTTGTGTCTGAAGAGCGGACCTCTYGACAGAGCCCTCGAGCTTCCCAAGAGCC	2544
OY	2407	ATGCACTATCTGTGTCCAGCGGAAGGTGGAAGAGCTGAGAGCAAGAGAGAAAGGC	2466
DB	2545	ATGCACTATCTGTGTCCAGCGGAAGGTGGAAGAGCTGAGAGCAAGAGAGAAAGGC	2604
OY	2467	GAAGCGGGCCAGAGAGAGGGAGAGATACCCCTGGGGGCCCAAGCGATGGGGATACA	2526
DB	2605	GAAGCGGGCCAGAGAGAGGGAGAGATACCCCTGGGGGCCCAAGCGATGGGGATACA	2664
OY	2527	GACAGCGTCAGCACATGTTGTTCCAGACGTTCAGAGATCACCGGAGCCAGCCCCCA	2586
DB	2665	GACAGCGTCAGCACATGTTGTTCCAGACGTTCAGAGATCACCGGAGCCAGCCCCCA	2724
OY	2587	TACGGGGGGGACCAATGTGTGTTCAACGCAACCCCTGAAGAGAGCGGAACCTGCTCAT	2646
DB	2725	TACGGGGGGGACCAATGTGTGTTCAACGCAACCCCTGAAGAGAGCGGAACCTGCTCAT	2784
OY	2647	GCTGACAGCAATGGGTTACAACAACTGTCGTGAGGTGTCAGGCCAGCACTCAACCAAC	2706
DB	2785	GCTGACAGCAATGGGTTACAACAACTGTCGTGAGGTGTCAGGCCAGCACTCAACCAAC	2844
OY	2707	GAGAACAGCAAAAGGCCAAAGCCCAACCTTCGAAGATGGAGTGTGACTACAGTCTGT	2766
DB	2845	GAGAACAGCAAAAGGCCAAAGCCCAACCTTCGAAGATGGAGTGTGACTACAGTCTGT	2904
OY	2767	GGGCTGGTAAAGGCCCTCGGCAAGAGCTCGTTCAAGATGTTTGTGACTTAAGGATCTAC	2826
DB	2905	GGGCTGGTAAAGGCCCTCGGCAAGAGCTCGTTCAAGATGTTTGTGACTTAAGGATCTAC	2964
OY	2827	CAGCTTGAAGGCAATGGGGACAGATCCCATCAACCCCTAAGTGGGTGAGAGAGGCACT	2886
DB	2965	CAGCTTGAAGGCAATGGGGACAGATCCCATCAACCCCTAAGTGGGTGAGAGAGGCACT	3024
OY	2887	CGGCTCGACACAGCTGACGTACGAGTGAAGAGGGTTCGTGTGTCAACTGAATCCCAAC	2946
DB	3025	CGGCTCGACACAGCTGACGTACGAGTGAAGAGGGTTCGTGTGTCAACTGAATCCCAAC	3084
OY	2947	AAACACCCGGGCGCAACGTAGAGACCTCTGAGATTCGGAATGCAAGAACGATTCATCTCC	3006
DB	3085	AAACACCCGGGCGCAACGTAGAGACCTCTGAGATTCGGAAGATGCAAGAACGATTCATCTCC	3144



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QY 3007 GAGATCTCTGTGAGCCCTTTGGGGGGCTCAACTGTGTGGGAGACGGAGAACGGGCTG 3066
DB 3145 GAGATCTCTGTGAGCCCTTTGGGGGGCTCAACTGTGTGGGAGACGGAGAACGGGCTG 3204
QY 3067 ATGTGCTGAGACCGAAGTGGGCGAAGGTGTATGACTCATTTGGGGGAGAGCTTC 3126
DB 3205 ATGTGCTGAGACCGAAGTGGGCGAAGGTGTATGACTCATTTGGGGGAGAGCTTC 3264
QY 3127 CAGCAGATGATGTCTGGAGGGGGCTCAACTGTGTATGACTCATTTGGGGGAGAGAAC 3186
DB 3265 CAGCAGATGATGTCTGGAGGGGGCTCAACTGTGTATGACTCATTTGGGGGAGAGAAC 3324
QY 3187 AAACCTGGGTGTATTAATCTGTCTGTGCTCCGGAACAAGATTCTGCATATGACCCAGAA 3246
DB 3325 AAACCTGGGTGTATTAATCTGTCTGTGCTCCGGAACAAGATTCTGCATATGACCCAGAA 3384
QY 3247 GTGAGAAAGACGAGGCTGAGACCACTGTGGGGGACATGAGGGCTCGGGGACTTACCT 3306
DB 3385 GTGAGAAAGACGAGGCTGAGACCACTGTGGGGGACATGAGGGCTCGGGGACTTACCT 3444
QY 3307 GTTGTGAATATAGAGCGGATTAAGTTCTGTGATCATGAGCTCAAGAGCTCGGTGAGGTG 3366
DB 3445 GTTGTGAATATAGAGCGGATTAAGTTCTGTGATCATGAGCTCAAGAGCTCGGTGAGGTG 3504
QY 3367 TATGCTGGGCCCCCAAACTTACCAAAATTATATGACCTTCAAGTCTTTGCCGACTC 3426
DB 3505 TATGCTGGGCCCCCAAACTTACCAAAATTATATGACCTTCAAGTCTTTGCCGACTC 3564
QY 3427 CCCCACCCCTCTGTGTGTGCTGACCTGACAGTAAAGAGGGGACGGGCTCAAGTCTATC 3486
DB 3565 CCCCACCCCTCTGTGTGTGCTGACCTGACAGTAAAGAGGGGACGGGCTCAAGTCTATC 3624
QY 3487 TATGCTCAGTGTGGCTTCCATGCTGTGATGTGATCTCGGGGAAACAGTATGATC 3546
DB 3625 TATGCTCAGTGTGGCTTCCATGCTGTGATGTGATCTCGGGGAAACAGTATGATC 3684
QY 3547 TACATCTCTGTGACATCCAGAGCCAGATCACGCCCATGACATCTTCTCCCAAC 3606
DB 3685 TACATCTCTGTGACATCCAGAGCCAGATCACGCCCATGACATCTTCTCCCAAC 3744
QY 3607 ACCGACGGGATGAGATGCTGTGTGCTGACAGAGAGAGGGGTCTAAGTCAACAGTAC 3666
DB 3745 ACCGACGGGATGAGATGCTGTGTGCTGACAGAGAGAGGGGTCTAAGTCAACAGTAC 3804
QY 3667 GGGCGCATATTAAAGATGTGGGCTGAGTGGGGGAGATGCTTCTGTGGCTTAC 3726
DB 3805 GGGCGCATATTAAAGATGTGGGCTGAGTGGGGGAGATGCTTCTGTGGCTTAC 3864
QY 3727 ATCTGCTCCAAACAGATTAATGGGCTGGGGTGAAGAAACCATTTGATTCGCTGTGAG 3786
DB 3865 ATCTGCTCCAAACAGATTAATGGGCTGGGGTGAAGAAACCATTTGATTCGCTGTGAG 3924
QY 3787 ACGGCGCACTTGAAGGGGTCTTATGCAAAACGAGCTCAGAGGTCTCAAGTCTGTGT 3846
DB 3925 ACGGCGCACTTGAAGGGGTCTTATGCAAAACGAGCTCAGAGGTCTCAAGTCTGTGT 3984
QY 3847 GAGCGGAATGACAAGGTGTTTTTGGCTCAGTCCGCTCGGGGGGACGCAAGTTTAC 3906
DB 3985 GAGCGGAATGACAAGGTGTTTTTGGCTCAGTCCGCTCGGGGGGACGCAAGTTTAC 4044
QY 3907 TTCACTACTTGAACCGTAATGATCATGAATGCTGTGAAGGGC 3951
DB 4045 TTCACTACTTGAACCGTAATGATCATGAATGCTGTGAAGGGC 4089

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RESULT 9  
US-60-500-337-1176  
Sequence 1176, Application US/60500337

GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele  
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES  
TITLE OF INVENTION: ENCODING HUMAN KINASE PROTEINS, METHODS OF DETECTION AND  
TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CL001483  
CURRENT APPLICATION NUMBER: US/60/500.337  
CURRENT FILING DATE: 2003-09-05  
NUMBER OF SEQ ID NOS: 123188  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1176  
LENGTH: 4881  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-500-337-1176

Query Match 92.1%; Score 3637.4; DB 107; Length 4881;  
Best Local Similarity 95.5%; Pred. No. 0;  
Matches 3826; Conservative 6; Mismatches 2; Indels 171; Gaps 2;

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QY 7 ATGGGCGACCCAGCCCGCCGAGCTGTGACGACATGACCTGTCCGCTGGGGAGC 66
DB 196 ATGGGCGACCCAGCCCGCCGAGCTGTGACGACATGACCTGTCCGCTGGGGAGC 255
QY 67 CTTGTGGGATCTTTGAGCTTGTGAGGTGTGGCAATGAACTTACGACAGGTATC 126
DB 256 CTTGTGGGATCTTTGAGCTTGTGAGGTGTGGCAATGAACTTACGACAGGTATC 315
QY 127 AAGGTCGGCATGTCAACACGGGCGAGCTGGCTGCATCAAGTCAATGATGTACCGAG 186
DB 316 AAGGTCGGCATGTCAACACGGGCGAGCTGGCTGCATCAAGTCAATGATGTACCGAG 375
QY 187 GACGAGGAGGAGAGATCAACAGGATCAACATGTGAAAAGTCTTCAACACCGC 246
DB 376 GACGAGGAGGAGAGATCAACAGGATCAACATGTGAAAAGTCTTCAACACCGC 435
QY 247 AACATGCGCACCTTACTAGAGCTTCAACAAAGAGCCCGGGGAAACGATGACAG 306
DB 436 AACATGCGCACCTTACTAGAGCTTCAACAAAGAGCCCGGGGAAACGATGACAG 495
QY 307 CTCTGGCTGTGTATGAGATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 366
DB 496 CTCTGGCTGTGTATGAGATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 555
QY 367 AAAGGCAACGCGCTGAAGAGAGCTGTATCGCTTATCTGCAAGGAGATCTCAGGGGT 426
DB 556 AAAGGCAACGCGCTGAAGAGAGCTGTATCGCTTATCTGCAAGGAGATCTCAGGGGT 615
QY 427 CTGGCCCATCTTCAAGCCCAAGAGTGTATCATGAGACATCAAGGGGACAGATGTCTG 486
DB 616 CTGGCCCATCTTCAAGCCCAAGAGTGTATCATGAGACATCAAGGGGACAGATGTCTG 675
QY 487 CTGACAGAGATGCTGAGAGTCAAGTATGATTTTGGGGTGAAGTCTCAGTGGACGC 546
DB 676 CTGACAGAGATGCTGAGAGTCAAGTATGATTTTGGGGTGAAGTCTCAGTGGACGC 735
QY 547 ACCGTTGGGACGAGACATCTTCAATTTGGAAGTCCCTACTGGATGGCTCCAGAGGTATC 606
DB 736 ACCGTTGGGACGAGACATCTTCAATTTGGAAGTCCCTACTGGATGGCTCCAGAGGTATC 795
QY 607 GCTGTGTATGAGAACCTGTATGCCACTATGATTTACAGAGTGAATTTGGTCTCTAGGA 666
DB 796 GCTGTGTATGAGAACCTGTATGCCACTATGATTTACAGAGTGAATTTGGTCTCTAGGA 855
QY 796 GCTGTGTATGAGAACCTGTATGCCACTATGATTTACAGAGTGAATTTGGTCTCTAGGA 855
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QY 667 ATCAACGCGCATGAGATGGCAGAGGAGACCCCTCTGTGTGATGATCAACCCCATGGA 726
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DB 976 AAGTCAATGACTTATGACATGATGTCTCAATCAAGACTTACCTGAGCCGCCACCAACG 1035
QY 847 GAGCAGCTACTGAAGTTTCCCTTATCTGGGACGAGCCCAAGGACGGAGGTCCGCAATC 906

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1036 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACGAGCCCAAGGAGCGGAGTCCGCATC 1095  
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1096 CAGCTTAAAGACACATTTGACCGATCCGGAAAGAGCGGGTGAAGAAAGAGACAGAA 1155  
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1456 CTGCAAG 1515  
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1387 CAGTCAAG 1446  
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QY  
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Db  
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QY  
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Db  
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QY  
1687 CCCCCTTTCCAGAGCTCTCTCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1744  
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1876 CCCCCTTTCCAGAGCTCTCTCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1935  
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1745 -----AG 1746  
Db  
1936 AGCCTGAG 1995  
QY  
1747 TCCCTGAG 1806  
Db  
1996 TCCCTGAG 2055  
QY  
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2056 CCGTCAATCCCGGAG 2115  
QY  
1867 TCAAG 1926  
Db  
2116 TCAAG 2175

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Db  
2176 GATTAAG 2235  
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2305 GACCTGGCTGGAG 2364  
QY  
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2365 GCTGGCTCACTGAG 2424  
QY  
2287 CTCTCCCTGGAG 2346  
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2425 CTCTCCCTGGAG 2484  
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2485 GACTTTGTGTGCTGAAG 2544  
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2407 ATGAGTACTGTGCTGACAG 2466  
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2545 ATGAGTACTGTGCTGACAG 2604  
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2467 GAAGGCGGAG 2526  
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2605 GAAGGCGGAG 2664  
QY  
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2665 GACAGGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2724  
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2725 TACGGGGGCGGAG 2784  
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QY  
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Db  
2905 GGGCTGTAAAGGCGCTGAG 2964  
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Db  
3085 AACAGCCGGGCGCAG 3144

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3127 GAGCAGATGATGTGTGTGGAGGGGCTCAACTGTGTATGAGTCAATCATCTCAGGAAAAAGAAC 3186  
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3847 GAGCGGAATGAGCAAGGTGTTTTTGGCTGAGTCCGCTGTGGGGGAGAGCCAAAGTTAC 3906  
3985 GAGCGGAATGAGCAAGGTGTTTTTGGCTGAGTCCGCTGTGGGGGAGAGCCAAAGTTAC 4044  
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4045 TTTCATGACTCTGAACCGTAACTGATCATGAATCTGTGAAAGGCGC 4089

RESULT 10  
US-60-500-337-1175

; Sequence 1175, Application US/60500337  
; GENERAL INFORMATION:  
; APPLICANT: CARBIL, Michele  
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES  
; TITLE OF INVENTION: ENCODING HUMAN KINASE PROTEINS, METHODS OF DETECTION AND  
; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: CL001483  
; CURRENT APPLICATION NUMBER: US/60/500.337  
; CURRENT FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 123188  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 1175  
; LENGTH: 4982  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-500-337-1175

Query Match 92.1%; Score 3637.4; DB 107; Length 4982;  
Best Local Similarity 95.5%; Pred. No. 0;  
Matches 3826; Conservative 6; Mismatches 2; Indels 171; Gaps 2;

7 ATGGCGACCCAGCCCGCCGAGCTGTGACGATCTGTCCGCTGGGAGC 66  
196 ATGGCGACCCAGCCCGCCGAGCTGTGACGATCTGTCCGCTGGGAGC 255  
67 CCTGTGGGATCTTGAAGCTGTGGAGGTGTGGCAATGAACTTACGGA 126  
256 CCTGTGGGATCTTGAAGCTGTGGAGGTGTGGCAATGAACTTACGGA 315  
127 AAGGTCGACATGTCAAGACGGGCGAGCTGTGCTCATGAAGTCAATG 186  
316 AAGGTCGACATGTCAAGACGGGCGAGCTGTGCTCATGAAGTCAATG 375  
187 GACGAGAGGAGAAAGATCAACAGGAGATCAACATGCTGAAAGTACT 246  
376 GACGAGAGGAGAAAGATCAACAGGAGATCAACATGCTGAAAGTACT 435  
247 AACATGCGCACCTACTTACGAGCTTCTCATCAAGAGACCCCGGAA 306  
436 AACATGCGCACCTACTTACGAGCTTCTCATCAAGAGACCCCGGAA 495  
307 CTGTGGCTGTGATGAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 366  
496 CTGTGGCTGTGATGAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 555  
367 AAAGGCAAGCGCCGTAAGAGAGAGCTGTATGCTTATCTGCAAGG 426  
556 AAAGGCAAGCGCCGTAAGAGAGAGCTGTATGCTTATCTGCAAGG 615  
427 CTGGCCATCTTCATGAGCCCAAGGTGATCATGAGACATCAAGGG 486  
616 CTGGCCATCTTCATGAGCCCAAGGTGATCATGAGACATCAAGGG 675  
487 CTGACAGAGATGCTGAGGTCAAGTATGATTTTGGGGTGTGAGTCT 546  
676 CTGACAGAGATGCTGAGGTCAAGTATGATTTTGGGGTGTGAGTCT 735  
547 ACCGTTGGGAGAGGAGACATTTCAATGGGACTCCCTCTGAGTGG 606  
736 ACCGTTGGGAGAGGAGACATTTCAATGGGACTCCCTCTGAGTGG 795  
607 GCTGTGATGAGAACTTGAATGCACTTATGATTTTGAAGTATTTGG 666  
796 GCTGTGATGAGAACTTGAATGCACTTATGATTTTGAAGTATTTGG 855  
667 ATGACAGCATGAGATGAGCAGAGGAGCCCGCTCTGTGTGATGAT 726  
856 ATGACAGCATGAGATGAGCAGAGGAGCCCGCTCTGTGTGATGAT 915  
727 GCGCTCTTCCATCTCTGAGAACCTTCGCGGAGGCTCAAGTCCAA 786  
916 GCGCTCTTCCATCTCTGAGAACCTTCGCGGAGGCTCAAGTCCAA 975  
787 AAGTTCATTTGATTTGATGACATGATCTCATCAAGTCTTACGAG 846  
976 AAGTTCATTTGATTTGATGACATGATCTCATCAAGTCTTACGAG 1035  
847 GAGGACTACTGAAATTTCCCTTATCCGGGAGCAAGCCGAGCGAG 906



Dh	1036	GAGCAGCCTACTGAAAGTTCCCTTACTCCGGGACCAAGGCCACGGACGGCAGGTCCGATC	10939
Qy	907	CAGCTTAAGACA CATTGACCGATCCCGAAGAACGGGCGTGAGAAAGAGAGACAGAA	966
Dh	1096	CAGCTTAAGACA CATTGACCGATCCCGAAGAACGGGCGTGAGAAAGAGAGACAGAA	11555
Qy	967	TATGAGTACACGGGACGGAGAGGAATGACAGCTTGGAGAGAAAGAGAGCCAAAGC	10286
Dh	1156	TATGAGTACACGGGACGGAGAGGAATGACAGCTTGGAGAGAAAGAGAGCCAAAGC	12151
Qy	1027	TTCCATCATGAAGCGTGCCTGGAGAGTGCATCTCAAGCGGGAGATTCTCCGGCTCCAGAG	10866
Dh	1216	TTCCATCATGAAGCGTGCCTGGAGAGTGCATCTCAAGCGGGAGATTCTCCGGCTCCAGAG	12757
Qy	1087	GAATAATAGACCACTCAGAGGCTTTAAACAGCAGCAGCAGCTTGCAGCAGCAGCAG	11466
Dh	1276	GAATAATAGACCACTCAGAGGCTTTAAACAGCAGCAGCAGCTTGCAGCAGCAGCAG	13359
Qy	1147	CGAGACCCCGAGGCACATCAACACCTGTCACACGGCGAGCGGCGATTAGAGAG	12066
Dh	1336	CGAGACCCCGAGGCACATCAACACCTGTCACACGGCGAGCGGCGATTAGAGAG	13959
Qy	1207	CAGAAAGAGAGCGCGCGCGGTGGAGAGCAACAGCGCGGGAGCGGAGACAGCGAG	12666
Dh	1396	CAGAAAGAGAGCGCGCGCGGTGGAGAGCAACAGCGCGGGAGCGGAGACAGCGAG	14555
Qy	1267	CTGCAGAGAGAGAGCAGCAGCAGCGCGGTGGAGAGCATGCAGAGCTTGCAGCGAGAG	13366
Dh	1456	CTGCAGAGAGAGAGCAGCAGCAGCGCGGTGGAGAGCATGCAGAGCTTGCAGCGAGAG	15151
Qy	1327	GAGCGGCGGCAGCGCGGACGTGAGCAGGAATTCAGCGGAAAGCAGCTGGAGAGCAGCG	13866
Dh	1516	GAGCGGCGGCAGCGCGGACGTGAGCAGGAATTCAGCGGAAAGCAGCTGGAGAGCAGCG	15757
Qy	1387	CAGTCAGAACCTTCTCCAGAGGCAGCTGAGCAGAGCAATGCTCACTCAATCTCCCTGAG	14466
Dh	1576	CAGTCAGAACCTTCTCCAGAGGCAGCTGAGCAGAGCAATGCTCACTCAATCTCCCTGAG	16359
Qy	1447	CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCTGCGGGAC	15066
Dh	1636	CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCTGCGGGAC	16959
Qy	1507	AGGAAGCCCTGTACATTAATGTCGGGGCATGAATCCCGCTGACAAACAGCCTGGGCG	15666
Dh	1696	AGGAAGCCCTGTACATTAATGTCGGGGCATGAATCCCGCTGACAAACAGCCTGGGCG	17555
Qy	1567	CGAAGAGTAAAGAGAGAAACAAGATGAACAAGCAGCAGAACTCTCTTGGCCAAAGAC	16266
Dh	1756	CGAAGAGTAAAGAGAGAAACAAGATGAACAAGCAGCAGAACTCTCTTGGCCAAAGAC	18151
Qy	1627	AAGCAGAGCAGACAGGGGCTGAGCGCCCAATCCCGAGGCTCCCGCAGGGGCCCAAGAA	16866
Dh	1816	AAGCAGAGCAGACAGGGGCTGAGCGCCCAATCCCGAGGCTCCCGCAGGGGCCCAAGAA	18757
Qy	1687	CCCCCTTCCAGACTCTCTTATGCGAGAGCGCGGTGAGAGCCCAAGAGAGACCGACA -	17444
Dh	1876	CCCCCTTCCAGACTCTCTTATGCGAGAGCGCGGTGAGAGCCCAAGAGAGACCGACAAG	19355
Qy	1745	-----AG 1746	
Dh	1936	AGCCTGTGTGACACACCGGGTCCCACTGAAGCATATGACAGACCTGTACCCCGATCCGAG	19959
Qy	1747	TTCCCTGACAGACAGGCCCAACCGAAACCTGTGCTGCTTCCAGAGCTCCCATAGACCGGAC	18066
Dh	1996	TTCCCTGACAGACAGGCCCAACCGAAACCTGTGCTGCTTCCAGAGCTCCCATAGACCGGAC	20555
Qy	1807	CCTGCAATCCCGGACACCACTGCGCACGCGCCAGTGCCTCAGAGAGCTGTCAATCCGCAGAAAT	18666
Dh	2056	CCTGCAATCCCGGACACCACTGCGCACGCGCCAGTGCCTCAGAGAGCTGTCAATCCGCAGAAAT	21151
Qy	1867	TCAGACCCCACTGTGAAGACCTTGAGCCCAAGCCCAATTCGCCAGCTGGAGTCCGCCCA	19266
Dh	2116	TCAGACCCCACTGTGAAGACCTTGAGCCCAAGCCCAATTCGCCAGCTGGAGTCCGCCCA	21757

OY	1987	GATTAACGAGGCCCAACCCTCAAGTGCCTTCACAAGACCTCATTAACTGACACTGGCCCTTAAC	1988
Db	2176	GATTAACGAGGCCCAACCCTCAAGTGCCTTCACAAGACCTCATTAACTGACACTGGCCCTTAAC	2239
OY	1987	ACCATGTGGGGCGGAGGGTCCCGGCGAAGCCAGGACAGTCCGTGCAGAACCTCGAGCANAC	2046
Db	2236	ACCATGTGGGGCGGAGGGTCCCGGCGAAGCCAGGACAGTCCGTGC-----	2280
OY	2047	TCCGCTTGGAATCTATCTGCAAAAGCGGCGAGAGCGGGCACCCCAAAGCTTCAGGG	2106
Db	2281	-----	2280
OY	2107	CCCCCTGTCAAGCCCCCTGGCCCGGCCCAAGSCTCTTAGTAAACCCGGAACCTTAGAGGAGC	2166
Db	2281	-----AGTAACCCCAGACTTCAGAGAGAC	2304
OY	2167	GACCCGTGGTGGGAACGCTCGGACAGGCTCCTTCAGCCTTCACAGGAGCACTTCCCGAG	2226
Db	2305	GACCCGTGGTGGGAACGCTCGGACAGGCTCCTTCAGCCTTCACAGGAGCACTTCCCGAG	2364
OY	2227	GCTGGCTCATCTGGAGCGGAAACCGGTTGGAGGCTCTCTCCAATCTGGACAGCTCCCTGTG	2286
Db	2365	GCTGGCTCATCTGGAGCGGAAACCGGTTGGAGGCTCTCTCCAATCTGGACAGCTCTCCCTGTG	2424
OY	2287	CTTCCCTCGGGAATTAAGCCAAACCCGAGCAGACACGCTCACCGGCGAGGCGGCGCGCA	2346
Db	2425	CTTCCCTCGGGAATTAAGCCAAACCCGAGCAGACACGCTCACCGGCGAGGCGGCGCGCA	2484
OY	2347	GACTTTGTGTCTGAAAGAAGCGGAGCTCTGGACGAGGCCCTCTGGCTTCCAGAGAGCC	2406
Db	2485	GACTTTGTGTCTGAAAGAAGCGGAGCTCTGGACGAGGCCCTCTGGCTTCCCAAGAGCC	2544
OY	2407	ATGGACTAATCTGTGTCTCAAGCGAAGAGTGGAAAGCACTGAGAGCAGCAGAGAGAAAGGC	2466
Db	2545	ATGGACTAATCTGTGTCTCAAGCGAAGAGTGGAAAGCACTGAGAGCAGCAGAGAGAAAGGC	2604
OY	2467	GAAGCGGGCGCAGAGAGGGGAGCAGAGATACCCCTGGGGCGCGACAGATGGGGATACA	2526
Db	2605	GAAGCGGGCGCAGAGAGGGGAGCAGAGATACCCCTGGGGCGCGACAGATGGGGATACA	2664
OY	2527	GACAGCCTCAGACACATGTGTGTCTACAAGAGTGGAGAGATACACCGGAGCCCAACCCCCA	2586
Db	2665	GACAGCCTCAGACACATGTGTGTCTACAAGAGTGGAGAGATACACCGGAGCCCAACCCCCA	2724
OY	2587	TACGGGGGCGGACCAATGTGTGTCTCAGCGCACCCCTGAAGAGAGCGGAACCTGTCTCAT	2646
Db	2725	TACGGGGGCGGACCAATGTGTGTCTCAGCGCACCCCTGAAGAGAGCGGAACCTGTCTCAT	2784
OY	2647	GCTGACAGCAATGGGTACACAAACCTGTCTGACGTGTTCAGGCCAGCCACTCACCCAC	2706
Db	2785	GCTGACAGCAATGGGTACACAAACCTGTCTGACGTGTTCAGGCCAGCCACTCACCCAC	2844
OY	2707	GAGAAACAGCAAAAGGCCAAAAGCCCACTTCAGAGGATGGGATGTGACTACCACTCTCGT	2766
Db	2845	GAGAAACAGCAAAAGGCCAAAAGCCCACTTCAGAGGATGGGATGTGACTACCACTCTCGT	2904
OY	2767	GGGCTGGTAAAGGCCCTTGGCAAGCTCGTTCCAGATGTTTTGTGATCTTAGGATCTAC	2826
Db	2905	GGGCTGGTAAAGGCCCTTGGCAAGAGCTCGTTCCAGATGTTTTGTGATCTTAGGATCTAC	2964
OY	2827	CAGCTTGAAGGCAATGGGGGACAGATATCCCATCACACCTTAAGTGGGTGGAGAGGGCACT	2886
Db	2965	CAGCTTGAAGGCAATGGGGGACAGATATCCCATCACACCTTAAGTGGGTGGAGAGGGCACT	3024
OY	2887	CGGCTCAGACAGCTGCAGTACGACGTTGAGAGAGGGTCTGTGTCAACGTGAATCCCAAC	2946
Db	3025	CGGCTCAGACAGCTGCAGTACGACGTTGAGAGAGGGTCTGTGTCAACGTGAATCCCAAC	3084
OY	2947	AACACCCGGGCGCCAGTGAAGACCCCTGAGATCCGGAAGTACAAAGAACGATTTCACTCC	3006
Db	3085	AACACCCGGGCGCCAGTGAAGACCCCTGAGATCCGGAAGTACAAAGAACGATTTCACTCC	3144

3007 GAGATCCTCTGTGACGACCCCTTTGGGGGGGCAACTGTGTGGGACCGAGAACGGGGCTG 3066  
3145 GAGATCCTCTGTGACGACCCCTTTGGGGGGGCAACTGTGTGGGACCGAGAACGGGGCTG 3204  
3067 ATGTGCTGTGACCGAAGGTGGGCAAGGTGTATGACTCATTTGGGGGGGCGAGCGCTTC 3126  
3205 ATGTGCTGTGACCGAAGGTGGGCAAGGTGTATGACTCATTTGGGGGGGCGAGCGCTTC 3264  
3127 CAGCAGATGTGTGTGTGAGGGGGGCTCAACCTGTGTATGACTCATTTGGGGGGGAAAGAAC 3186  
3265 CAGCAGATGTGTGTGTGAGGGGGGCTCAACCTGTGTATGACTCATTTGGGGGGGAAAGAAC 3324  
3187 AAAGTGGGGGTATTAAGT 3246  
3325 AAAGTGGGGGTATTAAGT 3384  
3247 GTGAGAAAGACGAGGGCTGTGACCAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3306  
3385 GTGAGAAAGACGAGGGCTGTGACCAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3444  
3307 GTTGTGAAATAGAGAGGGATTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3366  
3445 GTTGTGAAATAGAGAGGGATTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3504  
3367 TATGCTGTGGGCCCCCAACCTTAACCAAAATTCATGTGCTTCAAGTCTTTGCCAGCTTC 3426  
3505 TATGCTGTGGGCCCCCAACCTTAACCAAAATTCATGTGCTTCAAGTCTTTGCCAGCTTC 3564  
3427 CCCCACCGGCTCTGT 3486  
3565 CCCCACCGGCTCTGT 3624  
3487 TATGCTGTGGGCTGT 3546  
3625 TATGCTGTGGGCTGT 3684  
3547 TATCATCCTGT 3606  
3685 TATCATCCTGT 3744  
3607 ACCGAGCGGATGAGATGT 3666  
3745 ACCGAGCGGATGAGATGT 3804  
3667 GGGCGGATGATTAAGATGT 3726  
3805 GGGCGGATGATTAAGATGT 3864  
3727 ATCTGCTCAACAGATTAATGGGCTGTGGGTGAGAAAGCCATTGAGATCCGCTCTGTGTGT 3786  
3865 ATCTGCTCAACAGATTAATGGGCTGTGGGTGAGAAAGCCATTGAGATCCGCTCTGTGTGT 3924  
3787 ACGGCGCATCTGTGACGGGGCTTTTCAATGACAAACGAGCTCAAGGCTCAAGTCTGTGTGT 3846  
3925 ACGGCGCATCTGTGACGGGGCTTTTCAATGACAAACGAGCTCAAGGCTCAAGTCTGTGTGT 3984  
3847 GAGCGGAAAGACAGAGGT 3906  
3985 GAGCGGAAAGACAGAGGT 4044  
3907 TTTATGATCTGTGAACCGTAACTGATCATGAATGTTGTAAGAGGC 3951  
4045 TTTATGATCTGTGAACCGTAACTGATCATGAATGTTGTAAGAGGC 4089

RESULT 11  
US-10-725-121-11

; Sequence 11, Application US/10725121  
; GENERAL INFORMATION:  
; APPLICANT: PLOMBAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHYTE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES

; FILE REFERENCE: 038602/0328  
; CURRENT APPLICATION NUMBER: US/10/725,121  
; CURRENT FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: US/09/688,188B  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 09/291,417  
; PRIOR FILING DATE: 1999-04-14  
; PRIOR APPLICATION NUMBER: 60/081,784  
; PRIOR FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 4133  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-725-121-11

Query Match 92.0%; Score 3635; DB 54; Length 4133;  
Best Local Similarity 95.9%; Pred. No. 0;  
Matches 3824; Conservative 0; Mismatches 15; Indels 150; Gaps 3;

110 CCTACGGACAGGTGTACAAAGGGGTGGGATGTCAAGAGGGGAGCTGGCTGCATCAAGG 169  
2 CATTTGGGAGGTGTATGAGGGGTGGCATGTACAGCGGGCAGCTGGCTGCATCAAGG 61  
170 TCATGATGTCAAGAGGACGAGAGGAGAGATCAACAGAGATCAACATGTGAAAA 229  
62 TCATGATGTCAAGAGGACGAGAGGAGAGATCAACAGAGATCAACATGTGAAAA 121  
220 AGTACTTCACCAACCGCAATTCGCACTTACTAGAGAGCTTTCATCAAGAAAGAGCCCC 289  
122 AGTACTTCACCAACCGCAATTCGCACTTACTAGAGAGCTTTCATCAAGAAAGAGCCCC 181  
220 CCGGAAAGATGACAGGCTGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 349  
182 CCGGAAAGATGACAGGCTGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 241  
350 ACTGTGAAAGAACCAAAAGGCAACGCTGTGAGAGAGAGCTGTATCGCTATATCTGCA 409  
242 ACTGTGAAAGAACCAAAAGGCAACGCTGTGAGAGAGAGCTGTATCGCTATATCTGCA 301  
410 GGGAGATCTCAAGGGGTGTGGCCATCTTCATGCTCCCAAGAGTATCCATGAGACATCA 469  
302 GGGAGATCTCAAGGGGTGTGGCCATCTTCATGCTCCCAAGAGTATCCATGAGACATCA 361  
410 AGGGCAGATGT 529  
362 AGGGCAGATGT 421  
530 GTGCTCAGCTGACCGCAACCGTGGGACAGCGAAACATTTGATTTGGAATCTCCCTAATGGA 589  
422 GTGCTCAGCTGACCGCAACCGTGGGACAGCGAAACATTTGATTTGGAATCTCCCTAATGGA 481  
590 TGGCTCAGAGGTATCGCTGT 649  
482 TGGCTCAGAGGTATCGCTGT 541  
650 AATATTGTCTTACGAATTCACGACATCGAGATGGGAGAGGAGGAGGAGGAGGAGGAGGAGG 709  
542 AATATTGTCTTACGAATTCACGACATCGAGATGGGAGAGGAGGAGGAGGAGGAGGAGGAGG 601  
710 ACATGACCCCAATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 769  
602 ACATGACCCCAATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 661  
770 CCAAGAGGTGTCTAAGAAATTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 829  
662 CCAAGAGGTGTCTAAGAAATTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 721  
830 TGAAGCGGCAACCGCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 889  
722 TGAAGCGGCAACCGCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 781

QY	890	AGCGGCAAGTCCGCATCCAGCTTAAAGACACATTTGACCGATCCCGGAAGAAAGCGGGTG	943
Db	782	AGCGGCAAGTCCGCATCCAGCTTAAAGACACATTTGACCGATCCCGGAAGAAAGCGGGTG	841
QY	950	AGAAAGAGAGACAGATATATAGTAGTACACCGGACGAGAGAGAAAGATGACAGCCATGGAG	1009
Db	842	AGAAAGAGAGACAGATATATAGTAGTACACCGGACGAGAGAGAAAGATGACAGCCATGGAG	901
QY	1010	AGGAAGAGAGACCAAGCTTCATCATGAAAGTGCCCTGAGAGATCGACTTACGCCGGAGT	1069
Db	902	AGGAAGAGAGACCAAGCTTCATCATGAAAGTGCCCTGAGAGATCGACTTACGCCGGAGT	961
QY	1070	TTCTCCGGCTCCAGCAGAGAAAATTAAGACACTCAGAGGCTTTTAAACACGACGACGACG	1129
Db	962	TTCTCCGGCTCCAGCAGAGAAAATTAAGACACTCAGAGGCTTTTAAACACGACGACGACG	1021
QY	1130	TGCAGCACAGCAGCAGGAGAGCCCCGAGGACACATGAAACACTGCTGCACGACGAGC	1189
Db	1022	TGCAGCACAGCAGCAGGAGAGCCCCGAGGACACATGAAACACTGCTGCACGAGGAGC	1081
QY	1190	AGCGCGCATAGAGAGACGAAAGAGAGCGCGCGCGCTGAGAGAGCAGCGCGCGG	1249
Db	1082	AGCGCGCATAGAGAGACGAAAGAGAGCGCGCGCGCTGAGAGAGCAGCGCGCGG	1141
QY	1250	AGCGGAGCAGCGGGAAGCTGCAGAGAGAGACAGCAGCGCGCTGAGAGCATGCAGG	1309
Db	1142	AGCGGAGCAGCGGGAAGCTGCAGAGAGAGACAGCAGCGCGCTGAGAGCATGCAGG	1201
QY	1310	CTCTCGCGCGGAGAGAGAGCGCGCGGCGGAGCGTGAACA-----	1352
Db	1202	CTCTCGCGCGGAGAGAGAGCGCGCGGCGGAGCGGAGCGTGAAGATATATTGTCACA	1261
QY	1353	-----	1352
Db	1262	GGCTTAGAGAGAGAGCAGCGACAGCTCGAGATCTTCACACAAACAGCTGCTCCAGGAACAG	1321
QY	1353	-----GGAATACAGCGGAAAGCACTGAGAGAGCAGCGGACGTCAAGAGTCTCC	1402
Db	1332	CCCTGCTCTGGAATACAGCGGAAAGCACTGAGAGACAGCAGGACGTCAAGAGTCTCTCC	1381
QY	1403	AGAGGCACTCAGCAGAGAGCATGCTCTCAAGTCCCTCAGCAGAGAGAAACAGCAGC	1462
Db	1382	AGAGGCACTCAGCAGAGAGCATGCTCTCAAGTCCCTCAGCAGAGAGAAACAGCAGC	1441
QY	1463	AGCAGCTTCAGAAAACAGCAGCAGCAGCCTCTGCTGCGGAGACAGAAAGCCCTGTATCC	1522
Db	1442	AGCAGCTTCAGAAAACAGCAGCAGCAGCCTCTGCTGCGGAGACAGAAAGCCCTGTATCC	1501
QY	1523	ATTATGATCGGGGACATGAATCCCGCTGCAAAACAGCAAGCTTGAGCCCGAGAGGTAGAAGA	1582
Db	1502	ATTATGATCGGGGACATGAATCCCGCTGCAAAACAGCAAGCTTGAGCCCGAGAGGTAGAAGA	1561
QY	1583	GAAACAGGATGAAACAGCAGCAGAACTCTCCCTTGCCCAAGAGCAGCAGCAGCAGG	1642
Db	1562	GAAACAGGATGAAACAGCAGCAGAACTCTCCCTTGCCCAAGAGCAGCAGCAGCAGG	1621
QY	1643	GGCCTGAGCCCCCATCCGCCAGGCGTCCCGCAGGGCCCCCAGAGACCCCTTCCAGACTC	1702
Db	1622	GGCCTGAGCCCCCATCCGCCAGGCGTCCCGCAGGGCCCCCAGAGACCCCTTCCAGACTC	1681
QY	1703	CTCTTATGACAGAGCCGGTGAAGCCCCCAGAGGAGCCGACACA-----	1744
Db	1682	CTCTTATGACAGAGCCGGTGAAGCCCCCAGAGGAGCCGACACAAGAGCTGTGTGGACAACC	1741
QY	1745	-----AGTCCCTGACGACCCAGC	1762
Db	1742	GGGTCCCACTGAAGCATATGAGACACTGTATACCCCAATCCCAAGTCCCTGAGAGACAGC	1801
QY	1763	CAACCCGAAACTGGCTGCTCTTCCAGGCTCCCATGACCCCGAACCCTGCAATCCCGCAC	1822
Db	1802	CAACCCGAAACTGGCTGCTCTTCCAGGCTCCCATGACCCCGAACCCTGCAATCCCGCAC	1861
QY	1823	CACTGCAAGCCCAAGTCCCGAGAGCTGTATCCCGCAGAAATTGACACCCACCTCTG	1882

Db	1862	CAACTGCCACGCGCCAGTGCCTCCGAGAGCTGTCAATCCCGCAGAAATTCAGACCCCACTCTG	1921
QY	1883	AAGGACTTGCCCGCAGCCGGAATCCCCAGCTGAGTCCGCCAGATPACAGAGCCCCAC	1942
Db	1922	AAGGACTTGCCCGCAGCCGGAATCCCCAGCTGAGTCCGCCAGATPACAGAGCCCCAC	1981
QY	1943	CCAAAGTGTCTCAGAGGACCTTCATCTATTCGCCATCTGCCCTTTAAACAAGATGTTGGCCCGGAG	2002
Db	1982	CCAAAGTGTCTCAGAGGACCTTCATCTATTCGCCACTGCGCTTTAAACAAGATGTTGGCCCGGAG	2041
QY	2003	GGTCCCGGCGCAGGCCAGGCAAGTCCGTGCGACAACCTCGCAGGACATCCGCGCTGGCAAAATCT	2062
Db	2042	GGTCCCGGCGCAGGCCAGGCAAGTCCGTGCGACAACCTCGCAGGACATCCGCGCTGGCAAAATCT	2101
QY	2063	ATCTGCAAAAGCGGGCAGAGCGGGGCAACCCCAAGCCTCCAGGGCCCCCTGCTCAGCCCC	2122
Db	2102	ATCTGCAAAAGCGGGCAGAGCGGGGCAACCCCAAGCCTCCAGGGCCCCCTGCTCAGCCCC	2161
QY	2123	CTGCGCCGCCCAAGCGCTCTTATGTATACCCCGACCTCAGAGAGAGGAGACCTCTGCTGGGAAAC	2182
Db	2162	CTGCGCCGCCCAAGCGCTCTTATGTATACCCCGACCTCAGAGAGAGGAGACCTCTGCTGGGAAAC	2221
QY	2183	GCTGGGACAGGGTCCCTTCAGCCTCTCAGCGGAGACCTCCCGCAGGCTGGCTCAGCTGAGAC	2242
Db	2222	GCTGGGACAGGGTCCCTTCAGCCTCTCAGCGGAGACCTCCCGCAGGCTGGCTCAGCTGAGAC	2281
QY	2243	GGAACCGGCTGGAGCCTCTCCAAATGTGACAGCTCCCTGTGCTCTCCCTGGGAAATA	2302
Db	2282	GGAACCGGCTGGAGTCTCTCCAAACCGGACACTCCCTGTGCTCTCCCTGGGAAATA	2341
QY	2303	AAGCCAAAGCCCGACGACCAACCGCTCAGCGGACCGGCCCCGACGACTTGTGTTGCTGA	2362
Db	2342	AAGCCAAAGCCCGACGACCAACCGCTCAGCGGACCGGCCCCGACGACTTGTGTTGCTGA	2401
QY	2363	AAGAGCGGACCTGTGAGCGAGGCCCCCTGGGCTCCCAAGAAAGGCATGACCTACCTGCTGCT	2422
Db	2402	AAGAGCGGACCTGTGAGCGAGGCCCCCTGGGCTCCCAAGAAAGGCATGACCTACCTGCTGCT	2461
QY	2423	CCAGCGAGGAGGTGGAAAGCAGTAGAGGACGACGAGAGGAGGAGGCGAAAGGCGGCGCAGAG	2482
Db	2462	CCAGCGAGGAGGTGGAAAGCAGTAGAGGACGACGAGAGGAGGAGGCGGCGCAGAG	2521
QY	2483	AGGGGAGCAGAGATACCCCTGAGGGGCGGACGCAATGGGATATCAGACAGCTCAGCACCA	2542
Db	2522	AGGGGAGCAGAGATACCCCTGAGGGGCGGACGCAATGGGATATCAGACAGCTCAGCACCA	2578
QY	2543	TGTGTGTCTCAGAGAGTGCAGAGGATCAACCCGGGACCCCAAGCCCCCATTAAGGGGGCGGACCA	2602
Db	2579	TGTGTGTCTCAGAGAGTGCAGAGGATCAACCCGGGACCCCAAGCCCCCATTAAGGGGGCGGACCA	2638
QY	2603	TGTGTGTCTCAGAGAGCACCCTGTAAGAGGAGCGGAACCTGTCTGACAGCTGACAGCATGTGGGT	2662
Db	2639	TGTGTGTCTCAGAGAGCACCCTGTAAGAGGAGCGGAACCTGTCTGACAGCTGACAGCATGTGGGT	2698
QY	2663	ACAACAAACTTGCCTGACGTGTCCAGGCCAGCACACTCAACCCACCGAGAAACGACAAAGGCC	2722
Db	2699	ACAACAAACTTGCCTGACGTGTCCAGGCCAGCACACTCAACCCACCGAGAAACGACAAAGGCC	2758
QY	2723	AAAGCCCACTCTCAGAGGATGGGAGTGGTGTCTACAGTCTCTGTGGGCTTGTAAAGGCC	2782
Db	2759	AAAGCCCACTCTCAGAGGATGGGAGTGGTGTCTACAGTCTCTGTGGGCTTGTAAAGGCC	2818
QY	2783	CTGGCAAGAGCTCGTTTGCATGATGTTTGAGATCTTAGGGATCTTACAGCTGAGAGGCAAGTGT	2842
Db	2819	CTGGCAAGAGCTCGTTTGCATGATGTTTGAGATCTTAGGGATCTTACAGCTGAGAGGCAAGTGT	2878
QY	2843	GGAACAGCATCCCATCAACGCTTGTGTGTGAGATCTTCCACCAACACCCGGGCCCCACA	2902
Db	2879	GGAACAGCATCCCATCAACGCTTGTGTGTGAGATCTTCCACCAACACCCGGGCCCCACA	2938
QY	2903	AGTACAGCTGAGGAGGATCTGTGTGTGAGATCTTCCACCAACACCCGGGCCCCACA	2962

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Db 2939 AGTACAGCGTGAAGAGGGTTCTGTGTCTCAACGTGAATCCCAACACCCGCGCCCA 2998
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Db 2999 GTGAGACCCCTGTAGATCCGGAGATCAAGAGCGATTCGACTCCGAGATCTCTGTGCG 3058
Qy 3023 CCCTTTGGGGGGGTCAACCTGCTGTGTGGGCGAGAGACGGGCTGATGTTGTCTGAG 3082
Db 3059 CCCTTTGGGGGGGTCAACCTGCTGTGTGGGCGAGAGACGGGCTGATGTTGTCTGAG 3118
Qy 3083 GTGGGAGGGGCAAGGTGTATGAGATCTATGGGCGGCGAGCTTCCAGCAGATGATGTC 3142
Db 3119 GTGGGAGGGGCAAGGTGTATGAGATCTATGGGCGGCGAGCTTCCAGCAGATGATGTC 3178
Qy 3143 TGGAGGGGGTCAACCTGCTCATCAGCATCTGAGGGGAAAGAAACAACCTGGGGGTAT 3202
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Qy 3203 ACCTGCTCTGCTCCGGAACAAGATTTGCAATGACCCAGAGTGAAGAGACAG 3262
Db 3239 ACTTCTCTGCTCCGGAACAAGATTTGCAATGACCCAGAGTGAAGAGACAG 3298
Qy 3263 GCTGAGACACCGTGGGGGACATGAGGGGCTGCGGGGCACTACCTGTTGTAATTCAG 3322
Db 3299 GCTGAGACACCGTGGGGGACATGAGGGGCTGCGGGGCACTACCTGTTGTAATTCAG 3358
Qy 3323 GGATTAAGTTCCTGTGATCGGCTCAAGAGCTCGGTGAGGGGTATGCTGTGGGCCCC 3382
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Qy 3383 AACCTTACCAAAATTCATGAGCTTCATGCTTTCGCACTCCGCACTCCGCTCTG 3442
Db 3419 AACCTTACCAAAATTCATGAGCTTCATGCTTTCGCACTCCGCACTCCGCTCTG 3478
Qy 3443 TGTGTGACCTGACATGAGAGAGGGGCGACGGGCTCAAGGTCTATATGCTCTCAAGTC 3502
Db 3479 TGTGTGACCTGACATGAGAGAGGGGCGACGGGCTCAAGGTCTATATGCTCTCAAGTC 3538
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Qy 3563 TCCAGAGCCAGATCAACGCCCATGTCATCTTCTCCCAACACCGACCGCATGAG 3622
Db 3599 TCCAGAGCCAGATCAACGCCCATGTCATCTTCTCCCAACACCGACCGCATGAG 3658
Qy 3623 TGTCTGTGTGCTACGAGACGAGGGTGTCTACGTCAACAGTACGGGGCATCATTAAG 3682
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Qy 3683 ATGTGTGTGTGAGTGGGGGGGAGATGCTACTTGTGTGCTCAATCTGTCCAAACAG 3742
Db 3719 ATGTGTGTGTGAGTGGGGGGGAGATGCTACTTGTGTGCTCAATCTGTCCAAACAG 3778
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Qy 3803 GGGTCTTATGACAAACGAGCTCAGAGGCTCAAGTTCTGTGTGAGCGGAATGACAAAG 3862
Db 3839 GGGTCTTATGACAAACGAGCTCAGAGGCTCAAGTTCTGTGTGAGCGGAATGACAAAG 3898
Qy 3863 TGTTTTGTGCTCAGTCCGCTCTGGGGGGGAGAGCCAAAGTTTCACTTCACTGAAAC 3922
Db 3899 TGTTTTGTGCTCAGTCCGCTCTGGGGGGGAGAGCCAAAGTTTCACTTCACTGAAAC 3958
Qy 3923 GTTACTGTCATGAACTGTTGAAAGGCG 3951
Db 3959 GTTACTGTCATGAACTGTTGAAAGGCG 3987

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; Sequence 11, Application US/10725329
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: MYRTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/10/725,329
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US/09/688,188B
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 4133
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-725-329-11

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Query Match 92.0%; Score 3635; DB 54; Length 4133;
Best Local Similarity 95.9%; Pred. No. 0;
Matches 3824; Conservative 0; Mismatches 15; Indels 150; Gaps 3;

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Qy 170 TCATGATGTGTACCGAGAGACGAGAGAGATCAACAGAGATCAACATGCTGAAA 229
Db 62 TCATGATGTGTACCGAGAGACGAGAGAGATCAACAGAGATCAACATGCTGAAA 121
Qy 220 AGTACTTCACACCGGCAACATGCGCACCTTACTAGAGGCTTCAATCAAGAAAGCCCC 289
Db 122 AGTACTTCACACCGGCAACATGCGCACCTTACTAGAGGCTTCAATCAAGAAAGCCCC 181
Qy 290 CGGGAACGATGACCAAGCTCTGGGCTGTGATGAGATGCTGTGTGCTGCTCAAGTCA 349
Db 182 CGGGAACGATGACCAAGCTCTGGGCTGTGATGAGATGCTGTGTGCTGCTCAAGTCA 241
Qy 350 ACTGTGTAAAGAACCAAAAGCGCAACGCCCTGAAGAGAGACTGTATCGCTATATCTG 409
Db 242 ACTGTGTAAAGAACCAAAAGCGCAACGCCCTGAAGAGAGACTGTATCGCTATATCTG 301
Qy 410 GGGAGATCTTCAAGGGGTCTGGCCCATCTTCATGCCCAAGAGTATCCATGAGACATCA 469
Db 302 GGGAGATCTTCAAGGGGTCTGGCCCATCTTCATGCCCAAGAGTATCCATGAGACATCA 361
Qy 470 AGGGGCAAGTGTGTGCTGACAGAGATGTCAGAGGTCAAGCTAGTGAATTTGGGGTGA 529
Db 362 AGGGGCAAGTGTGTGCTGACAGAGATGTCAGAGGTCAAGCTAGTGAATTTGGGGTGA 421
Qy 530 GTGCTCAGCTGAGCCGCAACCGTGGGCAACGGAACACTTTATTGGAGCTCCCTACTGA 589
Db 422 GTGCTCAGCTGAGCCGCAACCGTGGGCAACGGAACACTTTATTGGAGCTCCCTACTGA 481
Qy 590 TGGCTCAGAGGTATCGCTGTGTGATGAGAACCTGTATGCCACTTATATTAACAGAGTG 649
Db 482 TGGCTCAGAGGTATCGCTGTGTGATGAGAACCTGTATGCCACTTATATTAACAGAGTG 541
Qy 650 ATATTGTGCTCTAGGAATCAAGCATGAGATGCGAGAGGGAGCCGCCCTCTGTGTG 709
Db 542 ATATTGTGCTCTAGGAATCAAGCATGAGATGCGAGAGGGAGCCGCCCTCTGTGTG 601
Qy 710 ACATGACCCCATGAGAGCCCTCTTCTCATTTCTCGAACCCTTCGCGCAAGCTCAAGT 769
Db 602 ACATGACCCCATGAGAGCCCTCTTCTCATTTCTCGAACCCTTCGCGCAAGCTCAAGT 661
Qy 770 CCAAGAGTGTCTAAGAAATTCATTAATTTGATGACATGTTTCAATCAAGACTTACC 829

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Db	662	CCAAAGACTGCTTAAGAAAGTTTCATGTACCTTCATGTAGACAAATGTCATCAAGACTTAC	721
Qy	830	TGAGCGCCCAACCCACGAGACACTTGAAGTTTCCCTTCATCCGGACCAAGCCACCG	889
Db	722	TGAGCGCCCAACCCACGAGCACTACTGAAGTTTCCCTTCATCCGGACCAAGCCACCG	781
Qy	890	AGCGGCAAGTCCGCAATCGAGCTTAAAGGACCATTTGACCGAATCCCGGAAGAAAGCGGGGTG	949
Db	782	AGCGGCAAGTCCGCAATCGAGCTTAAAGGACCATTTGACCGAATCCCGGAAGAAAGCGGGGTG	841
Qy	950	AGAAAGAGAAACAGAAATATGAGTACACCGGACGAGAGAGAAATACAGCCATGAG	1009
Db	842	AGAAAGAGAAACAGAAATATGAGTACACCGGACGAGAGAGAAATGACAGCCATGAG	901
Qy	1010	AGGAAGAGAGCCAAAGCTCCATCATGAAAGTGCTGAGAGTGCATCTACCGCGAGT	1065
Db	902	AGGAAGAGAGCCAAAGCTCCATCATGAAAGTGCTGAGAGTGCATCTACCGCGAGT	961
Qy	1070	TTCTTCGGGCTCAGAGAGAAATAAGACCATCAGAGGCTTTAAACAGCAGCAGCAGC	1129
Db	962	TTCTTCGGGCTCAGAGAGAAATAAGACCATCAGAGGCTTTAAACAGCAGCAGCAGC	1021
Qy	1130	TGCAGACAGCAGCAGCAGGAGACCCCGAGGACACATGAAACCTGTGTCACCGCGGAC	1189
Db	1022	TGCAGACAGCAGCAGCAGGAGACCCCGAGGACACATGAAACCTGTGTCACCGCGGAC	1081
Qy	1190	AGCGGCGCATAGAGAGCAGAAAGAGAGCGCGCGCGCTGAGAGAGCAACAGCGCGGG	1249
Db	1082	AGCGGCGCATAGAGAGCAGAAAGAGAGCGCGCGCGCTGAGAGAGCAACAGCGCGGG	1141
Qy	1250	AGCGGAGACAGCGGAAAGCTGCAGAGAAAGAGCAGCAGCGCGGCTTGAGAGACATGCAAG	1309
Db	1142	AGCGGAGACACCGMAAGCTGCAGAGAAAGAGCAGCAGCGCGGCTTGAGAGACATGCAAG	1201
Qy	1310	CTCTGGCGGAGAGAGAGAGCGGCGGCGCAGCGGAGCTGAGACA-----	1352
Db	1202	CTCTGGCGGAGAGAGAGAGCGGCGGCGCAGCGGAGCTGAGACA-----	1261
Qy	1353	-----	1352
Db	1262	GGCTTAGAGAGAGAGACGAGCAAGCTCGAGATCTTCAACAAACGTCGCCAGAAACAG	1321
Qy	1353	-----GGAATACAGCGGAAAGCAGCTGAGAGAGCAGCGGACGTTCAGAACTCTCC	1402
Db	1322	CCCTGCTGCTGAATACAAAGCGAAAGCAGCTGAGAGAGCAGCGGACGTTCAGAACTCTCC	1381
Qy	1403	AGAGGCAAGCTGACAGAGAGACATGCTTACCTTCAGTCCCTGACAGCAGCAACAGCAGC	1462
Db	1382	AGAGGCAAGCTGACAGAGAGACATGCTTACCTTCAGTCCCTGACAGCAGCAACAGCAGC	1441
Qy	1463	AGCAGCTTCAGAAACAGAGCAGCAGCAGCTCTCTCTGAGGAGCAGAAAGCCCTGTAC	1522
Db	1442	AGCAGCTTCAGAAACAGAGCAGCAGCAGCTCTCTCTGAGGAGCAGAAAGCCCTGTAC	1501
Qy	1523	ATTATGCTCGGGGCAATGATCCCGCTGCAACACAGCCTGAGGCCGAGAGGTAGAGAGA	1582
Db	1502	ATTATGCTCGGGGCAATGATCCCGCTGCAACACAGCCTGAGGCCGAGAGGTAGAGAGA	1561
Qy	1583	GAAACAAGATGAAACAGCAGCAGAACTCTCTTGGCCAAAGAGCAGCAGCAGCAGCAGG	1642
Db	1562	GAAACAAGATGAAACAGCAGCAGAACTCTCTTGGCCAAAGAGCAGCAGCAGCAGCAGG	1621
Qy	1643	GGCGTGAAGCCCCCATCCCGCAGGCTCTCCCAAGGGCCCCCAGGAACCCCTTCCGAGCTC	1702
Db	1622	GGCGTGAAGCCCCCATCCCGCAGGCTCTCCCAAGGGCCCCCAGGAACCCCTTCCGAGCTC	1681
Qy	1703	CTCCTATGACAGAGCGCGGTGAGCCCAAGAGGACCGCACAC-----	1744
Db	1682	CTCCTATGACAGAGCGCGGTGAGCCCAAGAGGACCGCACAC-----	1741
Qy	1745	-----AGTCCCTGACGACCAAGC-----	1762
Db	1742	GGGTCCCACTGAGACCATATGACAGCCTGTACCCCAATCCCAAGTCCCTGACGAGACCAAGC	1801

QY	1763	CCACCCTGAAACTGGCTGCTTCCAGAGCTTCCCATGAACCCCGACCTGCTCATCCCCGAC	1822
Db	1802	CCACCCTGAAACTGGCTGCTTCCAGAGCTTCCCATGAACCCCGACCTGCTCATCCCCGAC	1861
QY	1823	CCACTGCGACCGCCAGTGGCCCGAGAGAGCTGTCACTCCGACGAATTCAGACCCCACTCTG	1882
Db	1862	CCACTGCGACCGCCAGTGGCCCGAGAGAGCTGTCACTCCGCGAGAAATTCAGACCCCACTCTG	1921
QY	1883	AAGGACTTGGCCCCAGCCCCGAAATCCCCAGCCCTGGTCCGCGCAGATTAACAGGCCCCAC	1942
Db	1922	AAGGACTTGGCCCCAGCCCCGAAATCCCCAGCCCTGGTCCGCGCAGATTAACAGGCCCCAC	1981
QY	1943	CCAAAGTCTCTAGAGAGACCTCATATGTGCCACTGCCCCCTTAAACACAGTGGGGCCGAG	2002
Db	1982	CCAAAGTCTCTAGAGAGACCTCATATGTGCCACTGCCCCCTTAAACACAGTGGGGCCGAG	2041
QY	2003	GGTCCCCGCGCAGCCCCAGGAGTCCGTCGACAGACTTGGACGAACTCCGCCCTGGCAATCT	2062
Db	2042	GGTCCCCGCGCAGCCCCAGGAGTCCGTCGACAGACTTGGACGAACTCCGCCCTGGCAATCT	2101
QY	2063	ATCTGCAAAAGGCGGGCAGAGCCGGGACCCCAAGCCTCCAGGGCCCCCTCTCAGCCCC	2122
Db	2102	ATCTGCAAAAGGCGGGCAGAGCCGGGACCCCAAGCCTCCAGGGCCCCCTCTCAGCCCC	2161
QY	2123	CTGGCCGCGCCAAACGCTCTAGTAACCCCGACCTCAGAGAGACGACCTGGCTGGGAC	2182
Db	2162	CTGGCCGCGCCAAACGCTCTAGTAACCCCGACCTCAGAGAGACGACCTGGCTGGGAC	2221
QY	2183	GCTCGGACAGGCTCTTCCAGGCTCTCAGGGGACCTCCCCAGGGCTGCTCACTGGAGC	2242
Db	2222	GCTCGGACAGGCTCTTCCAGGCTCTCAGGGGACCTCCCCAGGGCTGCTCACTGGAGC	2281
QY	2243	GGAAACCGGTGGAGGCTCTCTCAAACTGSAAGAGTCCCTGTGCTCTCCCTGGGATA	2302
Db	2282	GGAAACCGGTGGAGGCTCTCTCAAACTGSAAGAGTCCCTGTGCTCTCCCTGGGATA	2341
QY	2303	AAGCCAAAGCCCGACGACCAACGCTCAACGCGCAGGGCCGCGCCGAGACTTGTGTGCTGA	2362
Db	2342	AAGCCAAAGCCCGACGACCAACGCTCAACGCGCAGGGCCGCGCCGAGACTTGTGTGCTGA	2401
QY	2363	AAAGACCGGACTTGGACGAGGCCCCCTGGGCTTCCCAAGAAAGGCAATGAGCTACTCTGCT	2422
Db	2402	AAAGACCGGACTTGGACGAGGCCCCCTGGGCTTCCCAAGAAAGGCAATGAGCTACTCTGCT	2461
QY	2423	CCAGGAGAGAGGTGGAAAGACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2482
Db	2462	CCAGGAGAGAGGTGGAAAGACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2521
QY	2483	AGGGGAGCAGAGATTAACCTCGGGGGCCGCGAGCGATGGGGATACAGCAGCTAGCAACA	2542
Db	2522	AGGGGAGCAGAGATTAACCTCGGGGGCCGCGAGCGATGGGGATACAGCAGCTAGCAACA	2578
QY	2543	TGTTGGTTCACGACGTCCGAGAGATCACCGGAGCCAGGCCCTCAATACGGGGGGCGACCA	2602
Db	2579	TGTTGGTTCACGACGTCCGAGAGATCACCGGAGCCAGGCCCTCAATACGGGGGGCGACCA	2638
QY	2603	TGTTGGTTCACGAGCAACCTCGTAAGAGAGACCGGAACCTGCTGCAATGCTGACAGCAATGGGT	2662
Db	2639	TGTTGGTTCACGAGCAACCTCGTAAGAGAGACCGGAACCTGCTGCAATGCTGACAGCAATGGGT	2698
QY	2663	ACACAAACCTGCTTAAGTGTCTCAGCCCAAGCACTCACACCAACCGAAGAACGAAAGGCC	2722
Db	2699	ACACAAACCTGCTTAAGTGTCTCAGCCCAAGCACTCACACCAACCGAAGAACGAAAGGCC	2758
QY	2723	AAAGCCCAACCTCGAAGATGGGAGTGTGACTACCAAGTCTCGTGGGCTGGTAAAGGCC	2782
Db	2759	AAAGCCCAACCTCGAAGATGGGAGTGTGACTACCAAGTCTCGTGGGCTGGTAAAGGCC	2818
QY	2783	CTGGCAAGAGCTGTTACAGATGTTTGTGGATCTAAGGATCTACAGGCTTGGAGGCGAGTG	2842
Db	2819	CTGGCAAGAGCTGTTACAGATGTTTGTGGATCTAAGGATCTACAGGCTTGGAGGCGAGTG	2878



QY 2843 GGGAGCAGATCCCATCAAGCCCTAGTGGTGAGAGGGCACTCGGCTCGACAGCTGC 2902  
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 QY 2903 AGTACGACGTGAGAAAGGTTCTGTGTCTCAAGTGAATCCCAACACCCGGGGCCACA 2962  
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 DB 2999 GTGAGACCCCTGAGATCCGGAAGTACAAGACGATTCACATCCGAGATCTCTGTGAG 3058  
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 DB 3299 GCTGACCAACCGTGGGGGACATGAGAGGCTGCGGGACATACCTGTGTTGAAATACAGC 3358  
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 DB 3899 TGTTTTGGTCTCAGTCCGCTCTGGGGGAGAGCAAGTACTTACTTCAATGACCTGAAC 3958  
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DB 3959 GTAACCGCATCATGAATGTGTGACGGGGC 3987  
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 US-10-725-330-11  
 ; Sequence 11, Application US/10725330  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PLOWMAN, GREGORY  
 ; APPLICANT: MARTINEZ, RICARDO  
 ; APPLICANT: WHYTE, DAVID  
 ; TITLE OF INVENTION: STEP20-RELATED PROTEIN KINASES  
 ; FILE REFERENCE: 038602/0328  
 ; CURRENT APPLICATION NUMBER: US/10/725,330  
 ; PRIOR FILING DATE: 2003-12-02  
 ; PRIOR APPLICATION NUMBER: US/09/688,188B  
 ; PRIOR FILING DATE: 2000-10-16  
 ; PRIOR APPLICATION NUMBER: 09/291,417  
 ; PRIOR FILING DATE: 1999-04-14  
 ; PRIOR APPLICATION NUMBER: 60/081,784  
 ; PRIOR FILING DATE: 1998-04-14  
 ; NUMBER OF SEQ ID NOS: 155  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 11  
 ; LENGTH: 4133  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-725-330-11  
 Query Match 92.0%; Score 3635; DB 54; Length 4133;  
 Best Local Similarity 95.9%; Pred. No. 0;  
 Matches 3824; Conservative 0; Mismatches 15; Indels 150; Gaps 3;  
 QY 110 CCTACGACAGGTGTACAAAGGTTGGGATGTCAAGACGGGGAGCTGGCTGCATCAAG 169  
 DB 2 CATTTGGGAGGTGTATAGAGGTGCGCATGTCAACCGGGCAGCTGGCTGCATCAAG 61  
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 DB 62 TCATGATGTATCGAGAGACGAGAGAGAGATCAACAGAGATCAACATGCTGAAA 121  
 QY 220 AGTACTTCAACACGCAACATCGCACCTTACTACGAGGCTTCAATCAAGAGAGCCCC 289  
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 DB 182 CGGGAACGATGACCAAGCTGCGCTGATGAGAGTTCTGTGTGCTGCTCAAGTACTG 241  
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 DB 362 AGGGCAGAAATGTGTGCTGACAGAGATGTGAGGTCAAGCTAGTGAATTTGGGGTGA 421  
 QY 530 GTGCTCAGCTGACCGACCGTGGGACAGACGAAACATTTGATTTGGAATCTGGA 589  
 DB 422 GTGCTCAGCTGACCGACCGTGGGACAGACGAAACATTTGATTTGGAATCTGGA 481  
 QY 590 TGGCTCAAGAGTCAATGCTGTGTGATGAAACCTGTATGCCATATATTAACAGAGTG 649  
 DB 482 TGGCTCAAGAGTCAATGCTGTGTGATGAAACCTGTATGCCATATATTAACAGAGTG 541  
 QY 650 ATATTGTCTCTAGGATCAAGCATCGATGAGTGGCAGAGGAGCCCCCTGTGTG 709  
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OY	710	ACATGACACCCAGTCGAGACCCCTCTTCCCTCATTTCTCTGGAAGCCCTCGCCAGGCTCAAGT	769
Db	602	ACATGCAACCCCATGAGGCCCTTCTCTCATTTCTCTGGAAACCTTCGCGCCAGGCTCAAGT	661
OY	770	CCAGAAATGGCTCTAAGAAATTCATTGACTTCATTGACACATGTCTCATCAAGACTTAC	829
Db	662	CCAGAAATGGCTCTAAGAAATTCATTGACTTCATTGACACATGTCTCATCAAGACTTAC	721
OY	830	TGAGCGCGCCCAACCCAGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACAGCCACAG	889
Db	722	TGAGCGCGCCCAACCCAGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACAGCCACAG	781
OY	890	AGCGGCAAGTCCGCATCCAGCTTAAAGACACATTTGACCGATCCCGGAAGACGGGGT	949
Db	782	AGCGGCAAGTCCGCATCCAGCTTAAAGACACATTTGACCGATCCCGGAAGACGGGGT	841
OY	950	AGAAAGAGAGACACAGAAATATGAGTACACCGGAGAGAGAGAGATGACAGCCATGAG	1009
Db	842	AGAAAGAGAGACACAGAAATATGAGTACACCGGAGAGAGAGAGATGACAGCCATGAG	901
OY	1010	AGGAAGAGAGACCAAGCTCCATCATGAAGTGCCTGAGAGTGACTCTAGCGCGGAGT	1069
Db	902	AGGAAGAGAGACCAAGCTCCATCATGAAGTGCCTGAGAGTGACTCTAGCGCGGAGT	961
OY	1070	TTCTTCGGGCTCCAGCAGGAAAAATAAAGCAACTCAGAGGCTTTAAACAGCAGCAGC	1129
Db	962	TTCTTCGGGCTCCAGCAGGAAAAATAAAGCAACTCAGAGGCTTTAAACAGCAGCAGC	1021
OY	1130	TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACATCAACACTCTGTGCACCGCGG	1189
Db	1022	TGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACATCAACACTCTGTGCACCGCGG	1081
OY	1190	AGCGGCGCATTGAAGAGCAAGAGAGAGAGCGGCGCGCGGTGGAGAGCAACAGCGCGG	1249
Db	1082	AGCGGCGCATTGAAGAGCAAGAGAGAGAGCGGCGCGCGGTGGAGAGCAACAGCGCGG	1141
OY	1250	AGCGGAGCAGCGGAAAGCTGCAAGAAAGAGCAGCAGCGCGGCTGAGAGCATGACAG	1309
Db	1142	AGCGGAGCAGCGGAAAGCTGCAAGAAAGAGCAGCAGCGCGGCTGAGAGCATGACAG	1201
OY	1310	CTCTGCGGCGGAGAGAGAGCGGCGGCAAGCGGAGCTGAGCA-----	1357
Db	1202	CTCTGCGGCGGAGAGAGAGCGGCGGCAAGCGGAGCTGAGCA-----	1261
OY	1353	-----	1357
Db	1262	GGCTAAGAGAGAGCAGCGACGCTCGAGATCTTTCAGCAACGCTGCTCCAGGAACAG	1321
OY	1353	-----GGAAATCAAGCGGAAAGCAGCTGAGAGAGCAGCGGCAAGTCAAGACTCTCC	1402
Db	1322	CCCTGCTCTGGAAATCAAGCGGAAAGCAGCTGAGAGAGCAGCGGCAAGTCAAGACTCTCC	1381
OY	1403	AGAGGAGCTGCAAGAGAGCATGCTCTTCAAGTCCCTGCAAGCAGCAGCAGCAGC	1462
Db	1382	AGAGGAGCTGCAAGAGAGCATGCTCTTCAAGTCCCTGCAAGCAGCAGCAGCAGCAGC	1441
OY	1463	AGGACCTTCAAGAAACAGCAGCAGCAGCGCTCTGCGGGGAGAGAAAGCCCTGTAC	1522
Db	1442	AGGACCTTCAAGAAACAGCAGCAGCAGCGCTCTGCGGGGAGAGAAAGCCCTGTAC	1501
OY	1523	ATTATGATCGGGGCAATGATCCCGCTGCAAAACAGCCTGTGGCCCGAGAGGTAGAGAG	1582
Db	1502	ATTATGATCGGGGCAATGATCCCGCTGCAAAACAGCCTGTGGCCCGAGAGGTAGAGAG	1561
OY	1583	GAACAGAGATGAACAAGCAGCAAACTCTCTTGGCCAGAGCAGCGCAGCAGCAGG	1642
Db	1562	GAACAGAGATGAACAAGCAGCAAACTCTCTTGGCCAGAGCAGCGCAGCAGCAGG	1621
OY	1643	GGCCGGAACCCCAATCCGCCAGGCGCTCCCAAGGGCCCAAGAAACCCCTTCCAGATC	1702
Db	1622	GGCCGGAACCCCAATCCGCCAGGCGCTCCCAAGGGCCCAAGAAACCCCTTCCAGATC	1681
OY	1703	CTCCTATGAGAGCCGGTGAAGCCCAAGAGGAGCCGACAC-----	1744

[illegible]

Db 2759 AAAGCCCACTCGAAGGATGGAGTGTGATCAACAGTCTGTGGGCTGTAAAGCCC 2818  
 Qy 2783 CTGGCAAGGCTCTGTCAGATGTTGTGTGATCTAGGGATCTAACAGCCTGAGGAGAG 2842  
 Db 2819 CTGGCAAGGCTCTGTCAGATGTTGTGTGATCTAGGGATCTAACAGCCTGAGGAGAG 2878  
 Qy 2843 GGGAGAGATCCCATCACAGCCCTAGTGGTGGAGAGGAGCACTGGCTCGACAGCTGC 2902  
 Db 2879 GGGAGAGATCCCATCACAGCCCTAGTGGTGGAGAGGAGCACTGGCTCGACAGCTGC 2938  
 Qy 2903 AGTACGACGTGAGAAAGGTTCTGTGTCAACGTGATCCACCAACCCGGGCCACCA 2962  
 Db 2939 AGTACGACGTGAGAAAGGTTCTGTGTCAACGTGATCCACCAACCCGGGCCACCA 2998  
 Qy 2963 GTGACACCCCTGATCCCGAAGTACAAAGCATTCACCTCCAGATCCCTGTGCGAG 3022  
 Db 2999 GTGACACCCCTGATCCCGAAGTACAAAGCATTCACCTCCAGATCCCTGTGCGAG 3058  
 Qy 3023 CCCTTTGGGGGGTCAACCTGCTGTGTGGGCAAGGAGAACGGGCTGATGTTGTGACCGAA 3082  
 Db 3059 CCCTTTGGGGGGTCAACCTGCTGTGTGGGCAAGGAGAACGGGCTGATGTTGTGACCGAA 3118  
 Qy 3083 GTGGGCAAGGCAAGGTGTATGATCTCATTTGGGCGGCGAGCTTCCAGCATGATGTGC 3142  
 Db 3119 GTGGGCAAGGCAAGGTGTATGATCTCATTTGGGCGGCGAGCTTCCAGCATGATGTGC 3178  
 Qy 3143 TGGAGGGGCTCAACCTGCTCATCACATTTGAGGAAAGAAACAACTGGCGGTGTAT 3202  
 Db 3179 TGGAGGGGCTCAACCTGCTCATCACATTTGAGGAAAGAAACAACTGGCGGTGTAT 3238  
 Qy 3203 ACCCTGCTGGCTCCGGAACAAGATTTCTGCAATATGACCAAGTGGAGAGAAAGCAGG 3262  
 Db 3239 ACTGTGCTGGCTCCGGAACAAGATTTCTGCAATATGACCAAGTGGAGAGAAAGCAGG 3298  
 Qy 3263 GCTGGAACAACGTTGGGGGACATGAGAGGCTGGGGCACTACCGTGTGTGAATACGAGC 3322  
 Db 3299 GCTGGAACAACGTTGGGGGACATGAGAGGCTGGGGCACTACCGTGTGTGAATACGAGC 3358  
 Qy 3323 GGATTAAGTTCCTGTGTCATCGCCCTTCAAGAGCTCCGTGAGAGGTATGCTGTGGCCCCCA 3382  
 Db 3359 GGATTAAGTTCCTGTGTCATCGCCCTTCAAGAGCTCCGTGAGAGGTATGCTGTGGCCCCCA 3418  
 Qy 3383 AACCCACACAATTCATGAGCTTCCTTTCGAGACCTCCGCCACCGCCCTCTGC 3442  
 Db 3419 AACCCACACAATTCATGAGCTTCCTTTCGAGACCTCCGCCACCGCCCTCTGC 3478  
 Qy 3443 TGGTGAACCTGACAGTAAAGAGAGGGGACGCGCTCAAGGTCACTATGAGCTCAAGTCTG 3502  
 Db 3479 TGGTGAACCTGACAGTAAAGAGAGGGGACGCGCTCAAGGTCACTATGAGCTCAAGTCTG 3538  
 Qy 3503 GCTTCATGCTGTGATGTGACTGCGGGGAAACAGCTATGACATCTTACCTGTGACAA 3562  
 Db 3539 GCTTCATGCTGTGATGTGACTGCGGGGAAACAGCTATGACATCTTACCTGTGACAA 3598  
 Qy 3563 TCCAGAGCAGATCAACGCCCCATGACATCTTCCCTCCCAACCGGAGCATGAGAGA 3622  
 Db 3599 TCCAGAGCAGATCAACGCCCCATGACATCTTCCCTCCCAACCGGAGCATGAGAGA 3658  
 Qy 3623 TCGTGTGTGTACGAGAGAGAGGTTCTACGTCAACAGTACGGGCGCATCATTTAAG 3682  
 Db 3659 TCGTGTGTGTACGAGAGAGAGGTTCTACGTCAACAGTACGGGCGCATCATTTAAG 3718  
 Qy 3683 ATGTGTGTGTGAGTGGGGGAGATGCTTACTTCTGTGGCTTACATCTGCTCAACAGAA 3742  
 Db 3719 ATGTGTGTGTGAGTGGGGGAGATGCTTACTTCTGTGGCTTACATCTGCTCAACAGAA 3778  
 Qy 3743 TATAGGCTGGGGTGAAGAGCAATTGAGTCGCTGTGAGACGGGCACTTCGAGC 3802  
 Db 3779 TATAGGCTGGGGTGAAGAGCAATTGAGTCGCTGTGAGACGGGCACTTCGAGC 3838  
 Qy 3803 GGGTCTTACAGCAAAAGAGCTCAGAGGCTCAAGTTCTGTGTGAGCGGAAATGACAAAG 3862  
 Db 3839 GGGTCTTACAGCAAAAGAGCTCAGAGGCTCAAGTTCTGTGTGAGCGGAAATGACAAAG 3898

Qy 3863 TGTTTTGGCTCAGTCCGCTCTGGGGGACAGCAGCAAGTTACTTATGACTTGAACC 3922  
 Db 3899 TGTTTTGGCTCAGTCCGCTCTGGGGGACAGCAGCAAGTTACTTATGACTTGAACC 3958  
 Qy 3923 GTAACGATCATGAACTGTGAAAGGCG 3951  
 Db 3959 GTAACGATCATGAACTGTGAGCGGCG 3987  
 RESULT 14  
 US-60-081-784-11  
 ; Sequence 11, Application US/60081784  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GREGORY PLOWMAN and  
 ; APPLICANT: RICARDO MARTINEZ  
 ; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
 ; NUMBER OF SEQUENCES: 95  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FastSeq for Windows 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/60/081,784  
 ; FILING DATE: Filed Herewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 232/279  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4133 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; FEATURE:  
 ; OTHER INFORMATION: Mammalian (Human) ZC3  
 ; US-60-081-784-11  
 Query Match 92.0%; Score 3635; DB 64; Length 4133;  
 Best Local Similarity 95.9%; Pred. No. 0;  
 Matches 3824; Conservative 0; Mismatches 15; Indels 150; Gaps 3;

Qy 110 CCTACGACAGGTGTAACAAGGTTGGGATGTCAAGACGGGGGAGCTGAGCTGCATCAAGG 169  
 Db 2 CATTTGGGAGGTGTATAGAGGTGGGATGTCAAGACGGGGGAGCTGAGCTGCATCAAGG 61  
 Qy 170 TCATGATGTCAACGAGAGAGAGAGAGATCAACAGAGATCAACATGTGAAAA 229  
 Db 62 TCATGATGTCAACGAGAGAGAGAGAGATCAACAGAGATCAACATGTGAAAA 121  
 Qy 220 AGTACTTCAACCAACGCAATCGCACCTTACTACGAGCCTTCACTCAAGAAAGCCCCC 289  
 Db 122 AGTACTTCAACCAACGCAATCGCACCTTACTACGAGCCTTCACTCAAGAAAGCCCCC 181



QY	290	GGGGAAGAATGACACAGCTCTGGGCTGGTGAATGAGTCTCTGGTCTGGTTCAGACACG	349
Db	182	CGGAAAGATGACCAAGCTCTGGCTGGTGAATGAGTCTCTGGTCTGGTTCAGACACG	241
QY	350	ACCTGGTAAAGAACAAAGGCAACGCCCTGAAGAGAGACTGTATCGCTATATCTGCA	409
Db	242	ACCTGGTAAAGAACAAAGGCAACGCCCTGAAGAGAGACTGTATCGCTATATCTGCA	301
QY	410	GGGAGATCTCAGAGGCTCTGGCCATCTTCATGCCACAAAGGTGATCCATCGACATCA	469
Db	302	GGGAGATCTCAGAGGCTCTGGCCATCTTCATGCCACAAAGGTGATCCATCGACATCA	361
QY	470	AGGGGCAAAATGTGCTGTGACAGAGAAATGCTGAAGTCAAGTAACTTTTGGGCTGA	529
Db	362	AGGGGCAAAATGTGCTGTGACAGAGAAATGCTGAAGTCAAGTAACTTTTGGGCTGA	421
QY	530	GTGCTCAGCTGGAACCGCAACCGTGGGACAGACGGAACTTTCAATTGGACTCCCTACTGGA	589
Db	422	GTGCTCAGCTGGAACCGCAACCGTGGGACAGACGGAACTTTCAATTGGACTCCCTACTGGA	481
QY	590	TGGCTCCAGAGTCAATCGCTGTGTGATGAAACCTGATGCCACTATGATTAACAGAGTG	649
Db	482	TGGCTCCAGAGTCAATCGCTGTGTGATGAAACCTGATGCCACTATGATTAACAGAGTG	541
QY	650	ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGAGCCCCCTCTGTGTG	709
Db	542	ATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGAGCCCCCTCTGTGTG	601
QY	710	ACATGCAACCCATGGAGCCCTCTTCCTCAATTCCTGGAAACCTCGGCCAGGCTCAAGT	769
Db	602	ACATGCAACCCATGGAGCCCTCTTCCTCAATTCCTGGAAACCTCGGCCAGGCTCAAGT	661
QY	770	CCAAGAAATGTGCTTAAGAAATTCATTTGACTTATGACACATGTCTCATCAAGACTTAC	829
Db	662	CCAAGAAATGTGCTTAAGAAATTCATTTGACTTATGACACATGTCTCATCAAGACTTAC	721
QY	830	TGAGCCGCCACCCACGGAGCACTAGAAATTTCCCTTCAATCGGAGCAAGCCACAG	889
Db	722	TGAGCCGCCACCCACGGAGCACTAGAAATTTCCCTTCAATCGGAGCAAGCCACAG	781
QY	890	AGCGGAGGTCGCAATCCAGCTTAAGCAATTAACGATCCCGGAAGAAAGCGGGGTG	949
Db	782	AGCGGAGGTCGCAATCCAGCTTAAGCAATTAACGATCCCGGAAGAAAGCGGGGTG	841
QY	950	AGAAAGAGGACAGAAATATGATGATCAACGGCAGCGAGAGAGAAATGACAGCCATGAG	1009
Db	842	AGAAAGAGGACAGAAATATGATGATGATCAACGGCAGCGAGAGAGAAATGACAGCCATGAG	901
QY	1010	AGGAAGAGAGCCAAAGCTCATCATGAACGTGCTGAGAGTGCATCTACGCCGAGT	1069
Db	902	AGGAAGAGAGCCAAAGCTCATCATGAACGTGCTGAGAGTGCATCTACGCCGAGT	961
QY	1070	TTCTTCGGGCTCCAGCAGGAAATTAAGACCACTCAGAGGCTTTAAACAGCAGCAGCAGC	1129
Db	962	TTCTTCGGGCTCCAGCAGGAAATTAAGACCACTCAGAGGCTTTAAACAGCAGCAGCAGC	1021
QY	1130	TGCAGCAGCAGCAGCAGGAGACCCCGAGGCAACATCAAAACCTGTGTCACGACGCG	1189
Db	1022	TGCAGCAGCAGCAGCAGGAGACCCCGAGGCAACATCAAAACCTGTGTCACGACGCG	1081
QY	1190	AGCGGCGCATGAGAGAGCAGAAAGAGCGGCGCGCGCTGAGAGAGCAACAGCGCGCG	1249
Db	1082	AGCGGCGCATGAGAGAGCAGAAAGAGCGGCGCGCGCTGAGAGAGCAACAGCGCGCG	1141
QY	1250	AGCGGAGCAGCCGAAAGCTGCAAGAGAAAGACAGCAGCGCGCTGAGAGCAATGCAAG	1309
Db	1142	AGCGGAGCAGCCGAAAGCTGCAAGAGAAAGACAGCAGCGCGCTGAGAGCAATGCAAG	1201
QY	1310	CTCTGCGGCGGAGAGAGCGGCGGCGCAGCGAGCTGAGCA-----	1352
Db	1202	CTCTGCGGCGGAGAGAGCGGCGGCGCAGCGAGCTGAGCA-----	1261
QY	1353	-----	1352

Db	1262	GGCTAGAGGAGGAGCGACCACTGCTGAAGATCTTTACGAAACAGCTGCTCCAGGAAACAGG	1321
Qy	1353	-----GGAAATTAACAAGCCGGAACAGCTGAGGAGCAGCGGCACTGAACGTCCTCC	1402
Db	1322	CCCTGCTGCTGGAAATACAAAGCCGAACAGCTGGAGGAGCAGCGGCAAGTCAGAAAGTCCTCC	1381
Qy	1403	AGAGGCAAGTTCAGCAGGAGGAGCATGCTTACTTCAAGTCCCTGCGAGCAGCAGCAACAGAGC	1462
Db	1382	AAAGGCAAGTTCAGCAGGAGGAGCATGCTTACTTCAAGTCCCTGCGAGCAGCAGCAACAGAGC	1441
Qy	1463	AGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCTGCTGGGGAACAGAAACCCCTGTACC	1522
Db	1442	AGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCTGCTGGGGAACAGAAACCCCTGTACC	1501
Qy	1523	ATTATGTCGGGGCATGAATTCCTGTCACAAACAGCTTGCGCCCGAGAGGTGAAGAGA	1582
Db	1502	ATTATGTCGGGGCATGAATTCCTGTCACAAACAGCTTGCGCCCGAGAGGTGAAGAGA	1561
Qy	1583	GAAACAAGGATGAAACAAGCAGCAGCAATCTTCCTTGGCCAAAGAACCCAGGAGCAGCAGG	1642
Db	1562	GAAACAAGGATGAAACAAGCAGCAGCAATCTTCCTTGGCCAAAGAACCCAGGAGCAGCAGG	1621
Qy	1643	GGCCTGAGGCCCCCAATCCCCCAAGGCTCCCCCAAGGGCCCCCAGGAGCCCTTTCCAGATC	1702
Db	1622	GGCCTGAGGCCCCCAATCCCCCAAGGCTCCCCCAAGGGCCCCCAGGAGCCCTTTCCAGATC	1681
Qy	1703	CTCTATGCAAGAGCGCGGTGAGAGCCCCAGAGGGAACCGACA-----	1744
Db	1682	CTCTATGCAAGAGCGCGGTGAGAGCCCCAGAGGGAACCGACAAGCTGTGTGACACACC	1741
Qy	1745	-----AGTCCGTGCAAGAACAGC	1762
Db	1742	GGGTCCCACTGAAGCCATATGCAAGCACTGTATCCCGATTCCAAGTCCCTGTGCAAGAACAGC	1801
Qy	1763	CCACCAGAAACCTGGCTGCTTCCAGCCTCCCATGACCCCGAACCCCTGCATCCCGCAC	1822
Db	1802	CCACCAGAAACCTGGCTGCTTCCAGCCTCCCATGACCCCGAACCCCTGCATCCCGCAC	1861
Qy	1823	CCACTGCGCAAGCCCGAGTCCGAGAGCTGTATCCGCGCAAAATTCAAGACCCCACTCTG	1882
Db	1862	CCACTGCGCAAGCCCGAGTCCGAGAGCTGTATCCGCGCAAAATTCAAGACCCCACTCTG	1921
Qy	1883	AAGGACTGGGCCCGAGCCCGAAATCCCCAGCGCTGGGTCCGCGCCAGATTAACGAGGCCAC	1942
Db	1922	AAGGACTGGGCCCGAGCCCGAAATCCCCAGCGCTGGGTCCGCGCCAGATTAACGAGGCCAC	1981
Qy	1943	CCAAAGTGTCTCAGAGGACCTCATCTTATGCGCATGCTCCCTTAAACACAGTGGGGCCGAG	2002
Db	1982	CCAAAGTGTCTCAGAGGACCTCATCTTATGCGCATGCTCCCTTAAACACAGTGGGGCCGAG	2041
Qy	2003	GGTCCCGGCGACGCCAGGCAATTCCTGTGCGAGACTGTGCAAGCAATCTCGCTGGCAAAATCT	2062
Db	2042	GGTCCCGGCGACGCCAGGCAATTCCTGTGCGAGACTGTGCAAGCAATCTCGCTGGCAAAATCT	2101
Qy	2063	ATCTGCAAAAGGCGGAGAGCGGAGCAACCCCAAAAGCTTCAGAGGACCCCTGCTCAGGCCCC	2122
Db	2102	ATCTGCAAAAGGCGGAGAGCGGAGCAACCCCAAAAGCTTCAGAGGACCCCTGCTCAGGCCCC	2161
Qy	2123	CTGGCCCGCCCAACGCGCTTAGTAAACCCCGACCTTCAGAGAGCGAACCTTGCTGAGAAC	2182
Db	2162	CTGGCCCGCCCAACGCGCTTAGTAAACCCCGACCTTCAGAGAGCGAACCTTGCTGAGAAC	2221
Qy	2183	GCTGGGAGCAGGCTCTTTCCAGGCTTCAGAGGAGCACTCCCGAGGCTGAGTCACTGAGC	2242
Db	2222	GCTGGGAGCAGGCTCTTTCCAGGCTTCAGAGGAGCACTCCCGAGGCTGAGTCACTGAGC	2281
Qy	2243	GGAAACGCGGTGGAGACTCTCTCAAACTTGAACAGCTCCCTGTGCTCTCCCTCGGGAATA	2302
Db	2282	GGAAACGCGGTGGAGACTCTCTCAAACTTGAACAGCTCCCTGTGCTCTCCCTCGGGAATA	2341
Qy	2303	AAAGCAAGCCGAGCAACACGCGCTCAGCGGCGAGGCGCGCCGACAGCTTTGTGTGCTGA	2362

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Db 2342 AAGCAAGCCGACGACCAACGCTCAACGCGACGCGCCGACAGATTGTGTGCTGA 2401
Qy 2343 AAGAGCGACTCTGAGACGAGGCGCTCGGCTCCCAAGAGGCGACTGACTCTGTGT 2422
Db 2402 AAGAGCGACTCTGAGACGAGGCGCTCGGCTCCCAAGAGGCGACTGACTCTGTGT 2461
Qy 2423 CCAGCGAGAGGTGAGAAAGCAGTGAAGACGACGAGAGAGAGAGAGAGAGAGAGAG 2482
Db 2442 CCAAGGAGAGGTGAGAAAGCAGTGAAGACGACGAGAGAGAGAGAGAGAGAGAGAG 2521
Qy 2483 AGGGAGAGAGATACCTCTGGGGGCGGACGATGGGGATACAGACGCTGACAGCA 2542
Db 2522 AGGGAGAGAGATACCTCTGGGGGCGGACGATGGGGATACAGACGCTGACAGCA 2578
Qy 2543 TGTGTGTCAAGACGCTGAGAGATACCGGGAGCCAGCCCATACGGGGGCGGACCA 2602
Db 2579 TGTGTGTCAAGACGCTGAGAGATACCGGGAGCCAGCCCATACGGGGGCGGACCA 2638
Qy 2603 TGTGTGTCAAGACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2662
Db 2639 TGTGTGTCAAGACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2698
Qy 2663 ACACAAACCTGCTGACGCTGCTGACGCTGACGCTGACGCTGACGCTGACGCTGAC 2722
Db 2699 ACACAAACCTGCTGACGCTGCTGACGCTGACGCTGACGCTGACGCTGACGCTGAC 2758
Qy 2723 AAAAGCCACCTCGAAGAGATGGAGATGGAGATGGAGATGGAGATGGAGATGGAG 2782
Db 2759 AAAAGCCACCTCGAAGAGATGGAGATGGAGATGGAGATGGAGATGGAGATGGAG 2818
Qy 2783 CTGGAAGAGCTGCTGACGATGTTGTGATCTAGAGATCTAGAGATCTAGAGAG 2842
Db 2819 CTGGAAGAGCTGCTGACGATGTTGTGATCTAGAGATCTAGAGATCTAGAGAG 2878
Qy 2843 GGGAGAGATCCCATCAACGCTTATGAGTGGAGAGAGAGAGAGAGAGAGAGAG 2902
Db 2879 GGGAGAGATCCCATCAACGCTTATGAGTGGAGAGAGAGAGAGAGAGAGAGAG 2938
Qy 2903 AGTACAGGTGAGAGAGAGGTCTGAGTGTCAAGTGAATCCCAACACCGGGGCGCA 2962
Db 2939 AGTACAGGTGAGAGAGAGGTCTGAGTGTCAAGTGAATCCCAACACCGGGGCGCA 2998
Qy 2963 GTGAGACCCCTGAGATCCGGAAGTACAAAGAGAGATCACTCCGAGATCTCTG 3022
Db 2999 GTGAGACCCCTGAGATCCGGAAGTACAAAGAGAGATCACTCCGAGATCTCTG 3058
Qy 3023 CCTTTGGGGGCTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3082
Db 3059 CCTTTGGGGGCTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3118
Qy 3083 GTGGGCAAGGAGATGATGATCTATGATGGGCGGAGAGCTTCCAGAGATGATG 3142
Db 3119 GTGGGCAAGGAGATGATGATCTATGATGGGCGGAGAGCTTCCAGAGATGATG 3178
Qy 3143 TGGAGGGGCTCAACCTGCTCATCAACATCTCAGGGGAAAAGAAACAACTGCG 3202
Db 3179 TGGAGGGGCTCAACCTGCTCATCAACATCTCAGGGGAAAAGAAACAACTGCG 3238
Qy 3203 ACTGTCTGCTGCTCGGAAACAAGATTCTGCAACATGACCCAGAGTGAAGAG 3262
Db 3239 ACTGTCTGCTGCTCGGAAACAAGATTCTGCAACATGACCCAGAGTGAAGAG 3298
Qy 3263 GCTTGAACCAACGCTGGGGGACATGAGAGGCTGGGGGACATGAGTGTGGAAT 3322
Db 3299 GCTTGAACCAACGCTGGGGGACATGAGAGGCTGGGGGACATGAGTGTGGAAT 3358
Qy 3323 GATTTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3382
Db 3359 GATTTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3418
Qy 3383 AACCTTACCAAAATTCATGCTTCAAGTCTTTTGCAGACCTCCCAACGCGCT 3442
Db 3419 AACCTTACCAAAATTCATGCTTCAAGTCTTTTGCAGACCTCCCAACGCGCT 3478

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Qy 3443 TGTGTGACCTGACAGTAGAGAGAGGAGGAGCGGCTCAAGTTCATATGCTCAAGTCTG 3502
Db 3479 TGTGTGACCTGACAGTAGAGAGAGGAGGAGCGGCTCAAGTTCATATGCTCAAGTCTG 3538
Qy 3503 GCTTCATGCTGTGAGATGCTGCTGCGGAAACAGTATGATCTACATCTCTGTGCA 3562
Db 3539 GCTTCATGCTGTGAGATGCTGCTGCGGAAACAGTATGATCTACATCTCTGTGCA 3598
Qy 3563 TCCAGAGCAGATACCGCCCATGATCATCTTCTCCCAACCGAGCGGATGAGA 3622
Db 3599 TCCAGAGCAGATACCGCCCATGATCATCTTCTCCCAACCGAGCGGATGAGA 3658
Qy 3623 TGTGTGTGTGCTAGAGAGAGAGGATGCTACGTCACACGCTACGCGGATCA 3682
Db 3659 TGTGTGTGTGCTAGAGAGAGAGGATGCTACGTCACACGCTACGCGGATCA 3718
Qy 3683 ATGTGTGCTGACAGTGGGGGAGATGCTTACTTGTGTGCTTACATCTGCTCAAC 3742
Db 3719 ATGTGTGCTGACAGTGGGGGAGATGCTTACTTGTGTGCTTACATCTGCTCAAC 3778
Qy 3743 TAAATGGGCTGGGGTGAAGAACCATGATCCGCTGTGAGAGAGCGGCGCATTAAG 3802
Db 3779 TAAATGGGCTGGGGTGAAGAACCATGATCCGCTGTGAGAGAGCGGCGCATTAAG 3838
Qy 3803 GGGTCTTATGACACAAACGAGCTGAGAGCTCAAGTTCCTGTGTGAGCGGATGA 3862
Db 3839 GGGTCTTATGACACAAACGAGCTGAGAGCTCAAGTTCCTGTGTGAGCGGATGA 3898
Qy 3863 TGTTTTTCCTCAAGTCCGCTCTGCGGGGAGAGAGAGAGAGAGAGAGAGAGAG 3922
Db 3899 TGTTTTTCCTCAAGTCCGCTCTGCGGGGAGAGAGAGAGAGAGAGAGAGAGAG 3958
Qy 3923 GTAACGTGATGATGAACGTGTGAAGGCG 3951
Db 3959 GTAACGTGATGATGAACGTGTGAAGGCG 3987

RESULT 15
US-10-170-235-34328
; Sequence 34328, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; FILE REFERENCE: CLO01380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 34328
; LENGTH: 4436
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-34328

Query Match 92.0%; Score 3635; DB 46; Length 4436;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 3829; Conservative 0; Mismatches 5; Indels 171; Gaps 2;

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[illegible]

QY	1327	GAGCGCGCGCAGCGCGAGCGTATGACAGGAAATCAACCGGAAGAGCTGGAGAGCAACGG	1386
Db	1321	GAGCGCGCGCAGCGCGAGCGCAGCAGGAATTAACAACGGGAAGCAGCTGGAGAGCAACGG	1380
QY	1387	CAGTGAAGACGTCTCCAGAGGAGCTGCAGCAGAGACATGCTTAACCTCAAGTCCCTGAC	1446
Db	1381	CAGTGAAGACGTCTCAGAGGAGCTGCAGCAGAGACATGCTTAACCTCAAGTCCCTGAC	1440
QY	1447	CAGCAGCAACAGCAGCAGCAGCTTCAGAAAACAGCAGCAGCAGCAGCTCTGCTGGGAG	1506
Db	1441	CAGCAGCAACAGCAGCAGCAGCTTCAGAAAACAGCAGCAGCAGCAGCAGCTCTGCTGGGAG	1500
QY	1507	AGGAAGCCCTGTACCATTAATGCTGGGGGCAATGAAATCCGCTGACAAACAGCCTGGGCG	1566
Db	1501	AGGAAGCCCTGTACCATTAATGCTGGGGGCAATGAAATCCGCTGACAAACAGCCTGGGCG	1560
QY	1567	CGAGAGGTAGAAAGAGAAACAAAGATGAAACAGCAGCAGAACTCTCCCTTGGCCAAAGC	1626
Db	1561	CGAGAGGTAGAAAGAGAAACAAAGATGAAACAGCAGCAGAACTCTCCCTTGGCCAAAGC	1620
QY	1627	AAGCCAGGACAGACGGGGCGTACGCCCCCATCCCCAGGCGTCCCCAGGGCCCCCAAGA	1686
Db	1621	AAGCCAGGACAGACGGGGCGTACGCCCCCATCCCCAGGCGTCCCCAGGGCCCCCAAGA	1680
QY	1687	CCCTCTTCCAGACTCTCTCTATGAGAGGCGGCTGAGACCCCAAGAGGAGCCGACA--	1744
Db	1681	CCCTCTTCCAGACTCTCTCTATGAGAGGCGGCTGAGACCCCAAGAGGAGCCGACAAG	1740
QY	1745	-----AG	1746
Db	1741	AGCTGTGTGACACACCGGGTCCCACTGAAGCCATATGACACCTGTACCCCAATCCAG	1800
QY	1747	TCCCTGAGGAACCAAGCCCAACCGGAACCTGGGCTGCTTCCACAGCTTCCATGACCCCGAC	1806
Db	1801	TCCCTGAGGAACCAAGCCCAACCGGAACCTGGGCTGCTTCCACAGCTTCCATGACCCCGAC	1860
QY	1807	CCTGCGCATCCCCGCAACCACTGCACACGCCAGTGCCTCGAGAGCTGTCAATCGCCAGAAT	1866
Db	1861	CCTGCGCATCCCCGCAACCACTGCACACGCCAGTGCCTCGAGAGCTGTCAATCGCCAGAAT	1920
QY	1867	TCAGACCCCACTCTGAAGAGACTTGCCCCACCGGAATCCCCACGCTGGGGTCCGGCCA	1926
Db	1921	TCAGACCCCACTCTGAAGAGACTTGCCCCACCGGAATCCCCACGCTGGGGTCCGGCCA	1980
QY	1927	GATAACAGAGCCCAACCCAGGTGCTTCAGAGGACTCTCAATCTATGCGCACTGCGCTTAAC	1986
Db	1981	GATAACAGAGCCCAACCCAGGTGCTTCAGAGGACTCTCAATCTATGCGCACTGCGCTTAAC	2040
QY	1987	ACCAAGTGGGGCGGAGGGTCCCGGCCAAGCCAGGCAGTCCGTGCAAGACTCGCAACAC	2046
Db	2041	ACCAAGTGGGGCGGAGGGTCCCGGCCAAGGCAGGCAGTCCGTGCG-----	2085
QY	2047	TCCGCTTGCAAAATTAATCTGTCAAAAGGGGGGCAAGCGGGGACCCCAAGCTCCAGGG	2106
Db	2086	-----	2085
QY	2107	CCCCCTGCTAGCCCCCTGAGCCCGCCAAACGCTCTTAAGTAACCCCGACTCAGAGAGAGC	2166
Db	2086	-----AGTAACCCCGACTCAGAGAGAGC	2109
QY	2167	GACCTTGGCTGGGAACGCTTCGGACAGCGTCTTCCAGCCTCTCAAGGGGACCTCCCCAG	2226
Db	2110	GACCTTGGCTGGGAACGCTTCGGACAGCGTCTTCCAGCCTCTCAAGGGGACCTCCCCAG	2169
QY	2227	GCTGGCTCACTGAGCGGAAACGCGCTGGGAGCTCTCCAAACTGGACAGCTCCCTGTG	2286
Db	2170	GCTGGCTCACTGAGCGGAAACGCGCTGGGAGTCTCTCCAAACCGGACAGCTCCCTGTG	2229
QY	2287	CTCTCTCCCTGGGAATAAAGCCACAGCCCGACACACCGCTCACAGGCTCAGGCGGCTCGCA	2346
Db	2230	CTCTCTCCCTGGGAATAAAGCCACAGCCCGACACACCGCTCACAGGCTCAGGCGGCTCGCA	2289

2347 GACTTTGTTGCTGTAAGAGCGAAGCTGAGCGAGCGGCTTCCGAGAGGCG 2406  
2280 GACTTTGTTGCTGTAAGAGCGAAGCTGAGCGAGCGGCTTCCGAGAGGCG 2349  
2407 ATGACTCTCTGCTGCTGAGCGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2466  
2350 ATGACTCTCTGCTGCTGAGCGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2409  
2467 GAAAGCGGCGGCGAGAGGCGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2526  
2410 GAAAGCGGCGGCGAGAGGCGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2469  
2527 GACAGCGTCAAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2586  
2470 GACAGCGTCAAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2529  
2587 TACGGGGGGCGGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2646  
2530 TACGGGGGGCGGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2589  
2647 GCTGACAGAGAGGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2706  
2590 GCTGACAGAGAGGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2649  
2707 GAGAAAGAGAGGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2766  
2650 GAGAAAGAGAGGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2709  
2767 GGGCTGTTAAAGGCGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2826  
2710 GGGCTGTTAAAGGCGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2769  
2827 GAGCTGAGAGGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2886  
2770 GAGCTGAGAGGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2829  
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3007 GAGATCTCTGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3066  
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3127 CAGCAGATGATGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3186  
3070 CAGCAGATGATGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3129  
3187 AATGCGGCGGCTGATGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3246  
3130 AATGCGGCGGCTGATGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3189  
3247 GTGAGAGAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3306  
3190 GTGAGAGAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3249  
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3367 TATGCGTGGGCGGCGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3426  
3310 TATGCGTGGGCGGCGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3369  
3427 CCCACCGGCTCTGCTGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3486

3370 CCGGCGGCTCTGCTGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3429  
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3490 TATGCGTGGGCGGCGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3549  
3607 ACCGAGCGAGAGGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3666  
3550 ACCGAGCGAGAGGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3609  
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3727 ATCTGCTCAACAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3786  
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3787 ACGGCGCAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3846  
3730 ACGGCGCAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3789  
3847 GAGCGGAGAGGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3906  
3790 GAGCGGAGAGGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3849  
3907 TTGATGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3951  
3850 TTGATGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 3894

Search completed: March 2, 2004, 17:00:49  
Job time : 8056 secs

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 09:47:59 ; Search time 9931 Seconds

(without alignments)  
17243.815 Million cell updates/sec

Title: US-10-029-115-1

Perfect score: 3951 1 gccctatcgccgaccagc.....tcacgaactgctgaaggcc 3951

Scoring table:

IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```
GenEmbl:*
1: gb ba:*
2: gb hcg:*
3: gb in:*
4: gb om:*
5: gb ov:*
6: gb pat:*
7: gb ph:*
8: gb pl:*
9: gb pr:*
10: gb ro:*
11: gb sts:*
12: gb sy:*
13: gb un:*
14: gb vi:*
15: em ba:*
16: em fun:*
17: em hum:*
18: em in:*
19: em nu:*
20: em om:*
21: em or:*
22: em ov:*
23: em pat:*
24: em ph:*
25: em pl:*
26: em ro:*
27: em sts:*
28: em un:*
29: em vi:*
30: em hcg_hum:*
31: em hcg_inv:*
32: em hcg_other:*
33: em hcg_mus:*
34: em hcg_pln:*
35: em hcg_rod:*
36: em hcg_mam:*
37: em hcg_vrt:*
38: em ay:*
39: em htgo_hum:*
40: em htgo_mus:*
41: em htgo_other:*
```

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3870.2	98.0	5014	9	BC034673 Homo sapi
2	3635	92.0	4133	6	BD243845 STE20-rel
3	3635	92.0	4133	6	AR435598 Sequence
4	3632.2	91.9	3888	9	AB035698 Homo sapi
5	3601	91.1	4863	9	AB041926 Homo sapi
6	3583.8	90.7	3912	6	AX235361
7	3501.2	88.6	3999	6	AX235359 Sequence
8	3358.2	85.0	3735	6	AX235365
9	3275.6	82.9	3822	6	AX235363
10	3230.8	81.8	4842	10	BC052474 Mus muscu
11	3026.8	76.6	4848	10	AB035697 Mus muscu
12	2992.8	75.7	4873	10	AB041925 Mus muscu
13	2884	73.0	4590	9	HSMB02420
14	2824.2	71.5	4381	10	BC011346
15	2531.6	64.1	3824	6	BD183377
16	1551	39.3	1717	6	AX235422
17	1468.4	37.2	1787	6	AX235419
18	1466	37.1	1482	6	AX235417
19	1463.4	37.0	1649	6	AX235415
20	1440.8	36.5	4483	5	BC055134
21	1407.2	35.6	3996	6	AR316824
22	1407.2	35.6	3996	6	AR316849 Sequence
23	1407.2	35.6	3996	6	AR338483
24	1407.2	35.6	3996	6	AX127187
25	1407.2	35.6	3996	6	AF172265 Homo sapi
26	1391.2	35.2	3972	6	AR316828
27	1391.2	35.2	3972	6	AR316853
28	1391.2	35.2	3972	6	AR338487
29	1391.2	35.2	3972	6	AX127191
30	1391.2	35.2	3972	9	AF172269 Homo sapi
31	1360	34.4	5727	9	AB011123
32	1358.6	34.4	4083	6	AR279571
33	1358.6	34.4	4083	6	AR316823
34	1358.6	34.4	4083	6	AR316848
35	1358.6	34.4	4083	6	AR338482
36	1358.6	34.4	4083	6	AX127186
37	1358.6	34.4	4083	9	AF172264
38	1358.6	34.4	4083	6	BD228669
39	1345.6	34.1	4055	6	BD243844
40	1345.6	34.1	4055	6	AR435597
41	1342.6	34.0	4059	6	AR316826
42	1342.6	34.0	4059	6	AR316851
43	1342.6	34.0	4059	6	AR338485
44	1342.6	34.0	4059	6	AX127189
45	1342.6	34.0	4059	9	AF172267 Homo sapi

## ALIGNMENTS

RESULT 1  
LOCUS BC034673 5014 bp mRNA linear PRI 12-NOV-2003  
DEFINITION Homo sapiens mishapen/NIK-related kinase, transcrip variant 3,  
BC034673  
ACCESSION BC034673  
VERSION mRNA (CDNA clone MGC:21111 IMAGE:438442), complete cds.  
KEYWORDS  
SOURCE MGC:21961594  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 5014)  
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,  
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

FEATURES	source
gene	<p>Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Batat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J.J., Hsieh, F., Datschenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Tothiyakul, S., Camicci, P., Prange, C., Rana, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Boak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wotley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huily, S.W., Villallon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Scherchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywicki, M.I., Skalska, U., Smilins, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.</p> <p>Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences</p> <p>Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)</p> <p>22388257</p> <p>12477932</p> <p>2 (bases 1 to 5014)</p> <p>Strausberg, R.</p> <p>Direct Submission</p> <p>Submitted (24-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA</p> <p>NIH-MGC Project URL: <a href="http://mgc.ncl.nih.gov">http://mgc.ncl.nih.gov</a></p> <p>Contact: MGC help desk</p> <p>Email: <a href="mailto:gcgabs-remail.nih.gov">gcgabs-remail.nih.gov</a></p> <p>Tissue Procurement: Lou Straud</p> <p>cDNA Library Preparation: Life Technologies, Inc.</p> <p>cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)</p> <p>DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center</p> <p>Center code: BCM-HGSC</p> <p>Web site: <a href="http://www.hgsc.bcm.tmc.edu/cdna/">http://www.hgsc.bcm.tmc.edu/cdna/</a></p> <p>Contact: <a href="mailto:amgdbcm.tmc.edu">amgdbcm.tmc.edu</a></p> <p>Gunaratne, P.H., Garcia, A.M., Lu, X., Huily, S.W., Louisse, H., Kovis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Navarette, A.N., Gibbs, R.A.</p> <p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a></p> <p>Series: IRAP Plate: 26 Row: N Column: 8</p> <p>This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27436915.</p> <p>Location/Qualifiers</p> <p>1. 5014</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="MGC:21111 IMAGE:4384442"</p> <p>/tissue_type="Lymph, Lymphoma"</p> <p>/clone_id="NHL_MGC_85"</p> <p>/lab_host="DH10B"</p> <p>/note="Vector: pCMV-SPORT6"</p> <p>1. 5014</p> <p>/gene="MINK"</p> <p>/note="Synonym: MGC21111"</p> <p>/db_xref="LocusID:50488"</p> <p>197. 4195</p> <p>/codon_start=1</p> <p>/product="mishapen/NIK-related kinase, isoform 3"</p> <p>/protein_id="AAH34673.1"</p> <p>/db_xref="GI:21961595"</p> <p>/db_xref="LocusID:50488"</p> <p>/translation="MGDPAPARSDDIDLSALRDPAGIFELVEVNGGTGYGVYKGRHVKTKDLAIKMDVDEDEBEIKOINLKYSHRNINATYGAFIKSPGNDQDLMLVMEFCGASVTDLVKTKGNALKECDICATCEITLIGATLHAHAKYTHDICONLTLTNAEYKUDFVSAQIDRTVRYGNFTIGTFPYMAPEVYACDENPDATIDRYDYSLGITNAEACAPPLCDMHPRAFLFPRNPPLKPKSKKCIDIDTCLITVYS</p>

Query Match	98.0%: Score 3870.2; DB 9; Length 5014;
Best Local Similarity	98.4%: Pred. No. 0;
Matches 3942; Conservative	0; Mismatches 3; Indels 60; Gaps 1;
7 ATGGGCGACCCAGCCCGCCCGCAGCCTGAGCAGCATGCACTGTCGCGCTTCGGCGGAC	66
197 ATGGGCGACCCAGCCCGCCCGCAGCCTGAGCAGCATGCACTGTCGCGCTTCGGCGGAC	256
67 CTGCTGGGATCTTGAAGCTTTGAGGTGGTGGCAATGGAACCTTACGACAGGTGAC	126
257 CTGCTGGGATCTTGAAGCTTTGAGGTGGTGGCAATGGAACCTTACGACAGGTGAC	316
127 AAGGTTGGGATGTCAGACAGGGGCACTGGCTGCATCAAGCTCAGTATGTCAGGAG	186
317 AAGGTTGGGATGTCAGACAGGGGCACTGGCTGCATCAAGCTCAGTATGTCAGGAG	376
187 GACAGAGAGAAAGATCAAAACAGAGATCAACATGCTGAAAAAGTACTCTCAACACGC	246
377 GACAGAGAGAAAGATCAAAACAGAGATCAACATGCTGAAAAAGTACTCTCAACACGC	436
247 AACATGCGCACTTACGAGAGCTTCAATCAAGAGAGCCCGCGGAAAACGATGACAG	306
437 AACATGCGCACTTACGAGAGCTTCAATCAAGAGAGCCCGCGGAAAACGATGACAG	496
307 CTGCTGGGATGTCAGAGCTTTGAGGTGGTGGCAATGGAACCTTACGACAGGTGAC	366
497 CTGCTGGGATGTCAGAGCTTTGAGGTGGTGGCAATGGAACCTTACGACAGGTGAC	556
367 AAGGCAAGCCCTGAGAGAGAGCTGATGCTTATATGCAAGGAGATCTCAGGGGT	426
557 AAGGCAAGCCCTGAGAGAGAGCTGATGCTTATATGCAAGGAGATCTCAGGGGT	616
427 CTGGCCCATCTCCATGCTCAACAGGTATCTATGAGACATCAAGGGGCAAGATGTCTG	486
617 CTGGCCCATCTCCATGCTCAACAGGTATCTATGAGACATCAAGGGGCAAGATGTCTG	676
487 CTGACAGGAATGTTGAGCTCAAGCTATGAGATTTTGGGTGAGTGTCTCAGCTGGACGC	546



Db 677 CTGACAGAAATGCTGAGGTCAAGCTAGTGAATTTTGGGGTGAAGTCTCAAGTCGACCCG 736  
Qy 547 ACCGTGGGACAGACGGAACATTTTCAATGAGACTCTCTA CTGAGATGCTTCAGAGGTCAATC 606  
Db 737 ACCGTGGGACAGACGGAACATTTTCAATGAGACTCTCTA CTGAGATGCTTCAGAGGTCAATC 796  
Qy 607 GCGCTGTGTGAAGAACCCCTGATGCGCACTTATGATTTACAGAGATGATATTTTGGTCTCTAGGA 666  
Db 797 GCGCTGTGTGAAGAACCCCTGATGCGCACTTATGATTTACAGAGATGATATTTTGGTCTCTAGGA 856  
Qy 667 ATCACAGCCATCGAGATGCGACAGAGGAGCCGCCCTCTGTGTGACATGACCCCATGCGA 726  
Db 857 ATCACAGCCATCGAGATGCGACAGAGGAGCCGCCCTCTGTGTGACATGACCCCATGCGA 916  
Qy 727 GCCCTCTTCTCTATTCCTGGAACCTTCGCGCCAGAGCTCAAGTCCAGAAAGTGTCTAAG 786  
Db 917 GCCCTCTTCTCTATTCCTGGAACCTTCGCGCCAGAGCTCAAGTCCAGAAAGTGTGTAAAG 976  
Qy 787 AAGTTCAATTTGACTTCAATTTGACACATGTCATCAATCAAGACTTAACCTGAGCGGCCACCCACG 846  
Db 977 AAGTTCAATTTGACTTCAATTTGACACATGTCATCAAGACTTAACCTGAGCGGCCACCCACG 1036  
Qy 847 GAGCAGCTACTGAAGTTTCCCTTCAATCCGAGACAGCCACAGAGCGGCAAGTCCGATC 906  
Db 1037 GAGCAGCTACTGAAGTTTCCCTTCAATCCGAGACAGCCACAGAGCGGCAAGTCCGATC 1096  
Qy 907 CAGCTTAAAGACCAATTTGACCGATCCCGAAAGAGCGGGGTGAGAAAGAGAGACAGAA 966  
Db 1097 CAGCTTAAAGACCAATTTGACCGATCCCGAAAGAGCGGGGTGAGAAAGAGAGACAGAA 1156  
Qy 967 TATAGATCACCGGACGAGAGAGAGAGATGACAGCCATGAGAGAGAGAGAGCAAGC 1026  
Db 1157 TATAGATCACCGGACGAGAGAGAGAGATGACAGCCATGAGAGAGAGAGAGCAAGC 1216  
Qy 1027 TCCATCATGAACTGTCCTGAGAGTGACTCACTACCCCGGAGTTTCTCCGCTCCAGAG 1086  
Db 1217 TCCATCATGAACTGTCCTGAGAGTGACTCACTACCCCGGAGTTTCTCCGCTCCAGAG 1276  
Qy 1087 GAAATTAAGACCAATCTGAGAGCTTTAAACAGCAGCAGCAGCTGACAGCAGCAGCAG 1146  
Db 1277 GAAATTAAGACCAATCTGAGAGCTTTAAACAGCAGCAGCAGCTGACAGCAGCAGCAG 1336  
Qy 1147 CGAAGCCCCGAGGACACATCAAAACCTGCTGACACCGGCGGCGGCGGATGAGAG 1206  
Db 1337 CGAAGCCCCGAGGACACATCAAAACCTGCTGACACCGGCGGCGGCGGATGAGAG 1366  
Qy 1207 CAGAAGGAGAGCGGCGGCGGCTGAGAGACAGCGGCGGAGCGGAGCGAGCGAG 1266  
Db 1397 CAGAAGGAGAGCGGCGGCGGCTGAGAGACAGCGGCGGAGCGGAGCGGAGCGAG 1456  
Qy 1267 CTGCAAGAGAGAGCAGCAGCGCGGCTGAGAGACATGCAAGCTCTGCGGCGGAGAG 1326  
Db 1457 CTGCAAGAGAGAGCAGCAGCGCGGCTGAGAGACATGCAAGCTCTGCGGCGGAGAG 1516  
Qy 1327 GAGCGGCGGACGCGGCGGAGCGTGAAGAGAAATCAAGCGGAGCAGCTGAGAGAGAG 1386  
Db 1517 GAGCGGCGGACGCGGCGGAGCGTGAAGAGAAATCAAGCGGAGCAGCTGAGAGAGAG 1576  
Qy 1387 CAGTCAGAACGTCTCTCAAGGACAGCTGAGCAGCAGCTAGCTTCAAGTCTCTGAG 1446  
Db 1577 CAGTCAGAACGTCTCTCAAGGACAGCTGAGCAGCAGCTAGCTTCAAGTCTCTGAG 1636  
Qy 1447 CAGCAGCAACAGCAGCAGCAGCTTCAAGAAACAGCAGCAGCAGCAGCTCTGCGGAG 1506  
Db 1637 CAGCAGCAACAGCAGCAGCAGCTTCAAGAAACAGCAGCAGCAGCAGCTCTGCGGAG 1696  
Qy 1637 AGGAAAGCCCTGTACCAATTAATGTCGCGGCAATGAATCCCGTGAACAAACAGCCCTGAG 1756  
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Qy 1687 CCCCTTTCCAGACTCTCTCTATGACAGAGCGGCTGAGAGCCCAAGAGAGAGCCGACA - 1744  
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Qy 1745 -----AG 1746  
Db 1937 AGCCGTGAGCAGACCGGGTCCCACTGAAGCATATGACAGACCTGTACCCGATCCGAG 1996  
Qy 1747 TCCCTGAGAGACAGAGCCCAACCCGAAACCTGTGCTCTTCCAGGCTCCATGAAGCCGAG 1806  
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Qy 1867 TCAGACCCCACTCTGAAGACCTGAGCCCAAGCCGAAATCCCAAGCTGAGTCCGCCA 1926  
Db 2117 TCAGACCCCACTCTGAAGACCTGAGCCCAAGCCGAAATCCCAAGCTGAGTCCGCCA 2176  
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Qy 2287 CTCTCCCTGGGAATTAAGCCAGAGCCGAGAGACACCGCTCAACCGGCGGCGGCGCA 2346  
Db 2537 CTCTCCCTGGGAATTAAGCCAGAGCCGAGAGACACCGCTCAACCGGCGGCGGCGCA 2596  
Qy 2347 GACTTTGTGTGCTGAAGAGCGGACTCTGGAACAGAGCCCTCGGCTCTCCAGAAAGGC 2406  
Db 2597 GACTTTGTGTGCTGAAGAGCGGACTCTGGAACAGAGCCCTCGGCTCTCCAGAAAGGC 2656  
Qy 2407 ATGGAATACTGCTGTCACAGGAGAGGTGAAAGAGTGAAGAGCAGAGAGAGAAAGGC 2466  
Db 2657 ATGGAATACTGCTGTCACAGGAGAGGTGAAAGAGTGAAGAGCAGAGAGAGAAAGGC 2716  
Qy 2467 GAAAGCGGCGCAGAGAGGGGAGCAGAGATACCCCTGAGGGGCGGACAGATGGGATACA 2526  
Db 2717 GAAAGCGGCGCAGAGAGGGGAGCAGAGATACCCCTGAGGGGCGGACAGATGGGATACA 2776  
Qy 2527 GACAGGTCACAGCAGATGATGATCAAGAGTCAAGAGTCAACCGGAGCCCAAGCCGCA 2586  
Db 2777 GACAGGTCACAGCAGATGATGATCAAGAGTCAAGAGTCAACCGGAGCCCAAGCCGCA 2836  
Qy 2587 TACGGGGGCGGACCAATGATGATCAAGAGCAGCCCTGAAGAGAGCGGAACTGTCTCAT 2646  
Db 2837 TACGGGGGCGGACCAATGATGATCAAGAGCAGCCCTGAAGAGAGCGGAACTGTCTCAT 2896





QY 350 ACCTGTAAAGAACAAAGGCAAGCCCTGAGAGAGACTGTTATCCCTTATCTGCA 409  
DB 242 ACCGTGTAAAGAACAAAGGCAAGCCCTGAGAGAGACTGTTATCCCTTATCTGCA 301  
QY 410 GGGAGATCTTCAAGGGGCTGGCCCATCTCAATGCCCAAGAGTGTATCCATGAGACATCA 469  
DB 302 GGGAGATCTTCAAGGGGCTGGCCCATCTCAATGCCCAAGAGTGTATCCATGAGACATCA 361  
QY 470 AGGGGCAAGATGTCTGTGTCAGAGAAATGCTGAGAGTCAAGTGTATTTGGGGTGA 529  
DB 362 AGGGGCAAGATGTCTGTGTCAGAGAAATGCTGAGAGTCAAGTGTATTTGGGGTGA 421  
QY 530 GTGCTCAGCTGAGACCGCAGCCGTGGCAGACGGAACTTTTATTTGGGACTCCCTTACTGA 589  
DB 422 GTGCTCAGCTGAGACCGCAGCCGTGGCAGACGGAACTTTTATTTGGGACTCCCTTACTGA 481  
QY 590 TGGCTCCAGAGAGTATGCTGTGTATGAGAAACCTGATGCACTTATTAACAGAGAGT 649  
DB 482 TGGCTCCAGAGAGTATGCTGTGTATGAGAAACCTGATGCACTTATTAACAGAGAGT 541  
QY 650 ATATTTGGTCTCTAGGATCAACAGCATGAGATGGCAGAGAGAGCCCTCTGTGTG 709  
DB 542 ATATTTGGTCTCTAGGATCAACAGCATGAGATGGCAGAGAGAGCCCTCTGTGTG 601  
QY 710 ACATGCAACCCATGCGAGCCCTCTTCTCATTTCTCGGAAACCTTCCCGCAGGCTCAAGT 769  
DB 602 ACATGCAACCCATGCGAGCCCTCTTCTCATTTCTCGGAAACCTTCCCGCAGGCTCAAGT 661  
QY 770 CCAAGAGTGTCTTAAAGTTCATTAAGCTTCACTTGAACATGTCTCATGAAGCTTACC 829  
DB 662 CCAAGAGTGTCTTAAAGTTCATTAAGCTTCACTTGAACATGTCTCATGAAGCTTACC 721  
QY 830 TGAAGCCGCCCAACCCAGAGAGAGCTTAAAGTTCCTTCACTCGGAGCAGAGCCACAG 889  
DB 722 TGAAGCCGCCCAACCCAGAGAGAGCTTAAAGTTCCTTCACTCGGAGCAGAGCCACAG 781  
QY 890 AGCCGCAAGTTCGCATCTCAGCTTAAAGCAACATTTGACCGATCCCGAAGAGCGGGTGG 949  
DB 782 AGCCGCAAGTTCGCATCTCAGCTTAAAGCAACATTTGACCGATCCCGAAGAGCGGGTGG 841  
QY 950 AGAAGAGAGAGAGATATGATGACAGCGGACAGCGAGAGAGATGACAGCCATGAG 1009  
DB 842 AGAAGAGAGAGAGATATGATGACAGCGGACAGCGAGAGAGATGACAGCCATGAG 901  
QY 1010 AGAAGAGAGAGAGCTCCTCATGAACTGTCTGAGAGTCACTTACCGCGGAGT 1069  
DB 902 AGAAGAGAGAGAGCTCCTCATGAACTGTCTGAGAGTCACTTACCGCGGAGT 961  
QY 1070 TTCTCCGCTCTCAGCAGGAAATTAAGACCACTAGAGGCTTTAAACAGCAGCAGCAGC 1129  
DB 962 TTCTCCGCTCTCAGCAGGAAATTAAGACCACTAGAGGCTTTAAACAGCAGCAGCAGC 1021  
QY 1130 TGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1189  
DB 1022 TGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1081  
QY 1190 AGCCGCGCATTAAG 1249  
DB 1082 AGCCGCGCATTAAG 1141  
QY 1250 AGCCGAG 1309  
DB 1142 AGCCGAG 1201  
QY 1310 CTCTGCGCGGAG 1352  
DB 1202 CTCTGCGCGGAG 1261  
QY 1353 ----- 1352  
DB 1262 GGCTTAAG 1321

QY 1353 -----GGAATACAGCGGAG 1402  
DB 1322 CCTGTGCTGAGATTAAG 1381  
QY 1403 AGAGGAG 1462  
DB 1382 AGAGGAG 1441  
QY 1463 AGCAGCTTCAAGAAACAGCAG 1522  
DB 1442 AGCAGCTTCAAGAAACAGCAG 1501  
QY 1523 ATATGCTGGGGAGATGAATCCGCTGACAAACAGCTGGGGCCGAGAGGTAAAGAGA 1582  
DB 1502 ATATGCTGGGGAGATGAATCCGCTGACAAACAGCTGGGGCCGAGAGGTAAAGAGA 1561  
QY 1583 GAAACAAGATGAACAGCAG 1642  
DB 1562 GAAACAAGATGAACAGCAG 1621  
QY 1643 GGCCTGAGCCCTCATATCCCGAGGCTTCCCGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1702  
DB 1622 GGCCTGAGCCCTCATATCCCGAGGCTTCCCGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1681  
QY 1703 CTCTATGACAGAGGCGGTGAGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1744  
DB 1682 CTCTATGACAGAGGCGGTGAGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1741  
QY 1745 -----AGTCCCTGAG 1762  
DB 1742 GGGTCCACATGAAGCCATATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1801  
QY 1763 CCAACCGAAG 1822  
DB 1802 CCAACCGAAG 1861  
QY 1823 CCACTGAG 1882  
DB 1862 CCACTGAG 1921  
QY 1883 AAGGACCTGAG 1942  
DB 1922 AAGGACCTGAG 1981  
QY 1943 CCAAGGTGCTCAG 2002  
DB 1982 CCAAGGTGCTCAG 2041  
QY 2003 GGTCCCGGAG 2062  
DB 2042 GGTCCCGGAG 2101  
QY 2063 ATCTGCAAG 2122  
DB 2102 ATCTGCAAG 2161  
QY 2123 CTGAGCCGCGCAAGCCTTATGATACCCGAGCCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 2182  
DB 2162 CTGAGCCGCGCAAGCCTTATGATACCCGAGCCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 2221  
QY 2183 GCTTCGAG 2242  
DB 2222 GCTTCGAG 2281  
QY 2243 GGAACGCGGTGAG 2302  
DB 2282 GGAACGCGGTGAG 2341  
QY 2303 AAGCAGAGCCGAG 2362  
DB 2342 AAGCAGAGCCGAG 2401  
QY 2363 AAGAGCGAGATCTGAG 2422

Db	2402	AAAGACCGAGCTTGTGACGAGGCGCTCTGGCCTTCCCAAGAGGCATATGACTATCTGTCTGT	2461
OY	2423	CCAGCGAGAGAGTGGAAAACATGTAGAGACGACGAGAGAGAAAGCGAAAGCGGCGCACGAG	2482
Db	2462	CCAGCGAGAGAGTGGAAAAGCAGTAGGAGCGACGAGAGAGAAAGCGAAAGCGGCGCACGAG	2521
OY	2483	AGGGAGCGAGAGATATTCCTCTGGGGGGCCCGCACCGATCTGGGGATATACAGACAGCGCTCAGACCA	2542
Db	2522	AGGGAGCGAGAGATATTCCTCTGGGGGGCCCGCACCGATCTGGGGATATACAGACAGCGCTCAGACCA	2578
OY	2543	TGTGTGTCTCAGACGCTCGAGAGAGATCAACCGGAGACCCAGCCCATATCGAGGGCGCGACCA	2602
Db	2579	TGTGTGTCTCAGACGCTCGAGAGAGATCAACCGGAGACCCAGCCCATATCGAGGGCGCGACCA	2638
OY	2603	TGTGTGTCTCAGCGCACCCCTTGAAGAGAGCGGAACTGTCTGCATGTCTGACAGCAATGGGT	2662
Db	2639	TGTGTGTCTCAGCGCACCCCTTGAAGAGAGCGGAACTGTCTGCATGTCTGACAGCAATGGGT	2698
OY	2663	ACACAAACCTGCTGAGCGTGGTCCAGGCCAGCGCACTGACCCACCGAGAAACGACAAAGGCC	2722
Db	2699	ACACAAACCTGCTGAGCGTGGTCCAGGCCAGCGCACTGACCCACCGAGAAACGACAAAGGCC	2758
OY	2723	AAAGCCCACTCTCGAAGGATGGAGGTGTGACTACCACTCTGTGTGGCTGTGTAAAGGCC	2782
Db	2759	AAAGCCCACTCTCGAAGGATGGAGGTGTGACTACCACTCTGTGTGGCTGTGTAAAGGCC	2818
OY	2783	CTGGCAAGAGCTCTTTACAGATGTTTGTGTGATCTTAGGATCTTACACGCTTGAAGAGCAGTG	2842
Db	2819	CTGGCAAGAGCTCTTTACAGATGTTTGTGTGATCTTAGGATCTTACACGCTTGAAGAGCAGTG	2878
OY	2843	GGGACAGCATCCCCATCAACAGCCCTAGTGGGTGAGAGAGGACACTCGGCTCAGCAGCTGC	2902
Db	2879	GGGACAGCATCCCCATCAACAGCCCTAGTGGGTGAGAGAGGACACTCGGCTCAGCAGCTGC	2938
OY	2903	AGTACGACGTAGAGAAAGGGTTCTGTGTCAAAGTGAATCCACCAACACCCGGGCCACA	2962
Db	2939	AGTACGACGTAGAGAAAGGGTTCTGTGTCAAAGTGAATCCACCAACACCCGGGCCACA	2998
OY	2963	GTGAGACCCCTGAGATTCGGGAAAGTACAGAAAGCCATTCACTCCGAGATTCCTCTGTGTAG	3022
Db	2999	GTGAGACCCCTGAGATTCGGGAAAGTACAGAAAGCCATTCACTCCGAGATTCCTCTGTGTAG	3058
OY	3023	CCCTTTGGGGGGGTCAACTGTCTGTGTGGGACAGGAGAAAGGGCTGTATTTCTGTGACCGAA	3082
Db	3059	CCCTTTGGGGGGGTCAACTGTCTGTGTGGGACAGGAGAAAGGGCTGTATTTCTGTGACCGAA	3118
OY	3083	GTGGCGAGGCGAAGGTGTATGAGCTCATTTGGGCGGCGACGCTTCCAGCAGATGTGATGTGC	3142
Db	3119	GTGGCGAAGGCGAAGGTGTATGAGCTCATTTGGGCGGCGACGCTTCCAGCAGATGTGATGTGC	3178
OY	3143	TGGAGGGGCTCAACTGTCTCATCAACATCTCAGGGGAAAGGAAACAAATCGGGGGGTATTT	3202
Db	3179	TGGAGGGGCTCAACTGTCTCATCAACATCTCAGGGGAAAGGAAACAAATCGGGGGGTATTT	3238
OY	3203	ACTGTGCTGTGCTCCGGAACAAGATTTCTGCACAATGACCCAGAAGTGGAGAAAGACAGG	3262
Db	3239	ACTGTGCTGTGCTCCGGAACAAGATTTCTGCACAATGACCCAGAAGTGGAGAAAGACAGG	3298
OY	3263	GCTGAGACCAACGCTGGGGGACATGAGAGGCGTGGGGCACTACCTGTGTGTGAATATCGAGC	3358
Db	3299	GCTGAGACCAACGCTGGGGGACATGAGAGGCGTGGGGCACTACCTGTGTGTGAATATCGAGC	3384
OY	3323	GGATTAAAGTTCCTGTGATTCGCCCTCAAGAGCTCGTGTGAAGGTATCTCGGGGCCCA	3382
Db	3359	GGATTAAAGTTCCTGTGATTCGCCCTCAAGAGCTCGTGTGAAGGTATCTCGGGGCCCA	3418
OY	3383	AAACCTTACCAAAATTCATGTGCTTCAAGTCTTTGCCGACCTTCCCAACCGCCTCTGC	3442
Db	3419	AAACCTTACCAAAATTCATGTGCTTCAAGTCTTTGCCGACCTTCCCAACCGCCTCTGC	3478
OY	3443	TGCTGACCTGACGTAGAGAGGGGCGAGCGGCTCAAGTCACTATATGGCTTCAATGTCTG	3502

[illegible]

Db	182	CGGAAACGATGACCAAGCTCTGGCTGGTATGGAAGTTCTGTGTCGTGGTTCAGTGAAGTCTG	241
OY	350	ACCTGTGAAGAACACAAAGAGCAACGCCCTGAGAGAGACTGTATCGCCATATATCTGCA	409
Db	242	ACCTGTGAAGAACACAAAGAGCAACGCCCTGAGAGAGACTGTATCGCCATATATCTGCA	301
OY	410	GGGAATCTCAGGGGCTGTGGCCCATCTTCATGCCCCAAGGTATCCATGAGACATCA	469
Db	302	GGGAATCTCAGGGGCTGTGGCCCATCTTCATGCCCCAAGGTATCCATGAGACATCA	361
OY	470	AGGGGCAAAATGTGTGCTGACAGAGAAATGCTGAAGTCAAGTAACTGTGATTTTGGGGTGA	529
Db	362	AGGGGCAAAATGTGTGCTGACAGAGAAATGCTGAAGTCAAGTAACTGTGATTTTGGGGTGA	421
OY	530	GTGCTCAGCTGGACCGCAACCGTGGGACAGCGAGACATTTCTATTTGGGACTCCCTACTGSA	589
Db	422	GTGCTCAGCTGGACCGCAACCGTGGGACAGCGAGACATTTCTATTTGGGACTCCCTACTGSA	481
OY	590	TGGCTCCAGAGGTCAATCGCTGTGTATGAAACCTTGATGCCACTATGATTACAGAGTGG	649
Db	482	TGGCTCCAGAGGTCAATCGCTGTGTATGAAACCTTGATGCCACTATGATTACAGAGTGG	541
OY	650	ATATTTGGTCTCTAGGAATCAACAGCATGAGATGGCAGAGGAGACCCCCCTGTGTGTG	709
Db	542	ATATTTGGTCTCTAGGAATCAACAGCATGAGATGGCAGAGGAGACCCCCCTGTGTGTG	601
OY	710	ACATGCACCCCATGGAGCCCTCTTCTCTCATATTCCTCGGAACCTCGGCCAGGCTCAAGT	769
Db	602	ACATGCACCCCATGGAGCCCTCTTCTCTCATATTCCTCGGAACCTCGGCCAGGCTCAAGT	661
OY	770	CCAGAAGTGTCTTAAGAAATTCAATTGACTTGAACATGTCTCATCAAGACTTAC	829
Db	662	CCAGAAGTGTGTCTTAAGAAATTCAATTGACTTGAACATGTCTCATCAAGACTTAC	721
OY	830	TGAGCCGCCCAACCCACGAGAGGCTATGGAAGTTCCCTTCATCCGGGACCAAGCCCAAG	889
Db	722	TGAGCCGCCCAACCCACGAGAGGCTATGGAAGTTCCCTTCATCCGGGACCAAGCCCAAG	781
OY	890	AGCGGCAAGTCCGCATCTCAGCTTAAGAACACATTGACCGATCCCGAAGAAAGCGGGTGG	949
Db	782	AGCGGCAAGTCCGCATCTCAGCTTAAGAACACATTGACCGATCCCGAAGAAAGCGGGTGG	841
OY	950	AGAAAGAGAGACAGAAATATGATGACAGCGGACGAGAGAGAGAGATGACAGCCATGGAG	1009
Db	842	AGAAAGAGAGACAGAAATATGATGATGACAGCGGACGAGAGAGAGAGATGACAGCCATGGAG	901
OY	1010	AGAAAGAGAGACCAAGCTTCATCATGAACGTGCTTGAGAGTTCGACTTACGCGCGGAGT	1068
Db	902	AGAAAGAGAGACCAAGCTTCATCATGAACGTGCTTGAGAGTTCGACTTACGCGCGGAGT	961
OY	1070	TTCTCCGGCTCAGAGAGAAAATAAGACCACTCAGAGGCTTTAAACAGCAGCAGCAGC	1128
Db	962	TTCTCCGGCTCAGAGAGAAAATAAGACCACTCAGAGGCTTTAAACAGCAGCAGCAGC	1021
OY	1130	TGCAAGCAGCAGCAGCAGCAGACCCCGAGGCAACATCAAAACACTGTGTCGACACGCGAC	1188
Db	1022	TGCAAGCAGCAGCAGCAGCAGACCCCGAGGCAACATCAAAACACTGTGTCGACACGCGAC	1081
OY	1190	AGCGGCGCATAGAGAGCAAGAGAGAGCGGCGCGCGGTGAGAGACACGCGCGGG	1248
Db	1082	AGCGGCGCATAGAGAGCAAGAGAGAGCGGCGCGCGGTGAGAGACACGCGCGGG	1141
OY	1250	AGCGGGAACAGCGGAAGCTGACGAGAAAGGAGCAGCAGCGCGGTGAGAGACATGCAAG	1309
Db	1142	AGCGGGAACAGCGGAAGCTGACGAGAAAGGAGCAGCAGCGCGGTGAGAGACATGCAAG	1201
OY	1310	CTCTGCGCGGAGAGAGCAGCGCGGCAAGCGGACCTGAGC-----	1352
Db	1202	CTCTGCGCGGAGAGAGCAGCGCGGCAAGCGGACCTGAGC-----	1261
OY	1353	-----	1355
Db	1262	GGCTTAGAGAGAGCAGCGACACTCTGAGATCTTCAAGCAACGCTGCTCAGGAACAG	1321

QY	1353	-----GGAATTAACAAGCGGAAAGCAGCTTGGAGAGACAGCGGACAGTCCAGAACTCTCC	1402
Db	1322	CCCTGCTGGTGAATTAACAAGCGGAAAGCAGCTGGAGAGACAGCGGACAGTCCAGAACTCTCC	1391
QY	1403	AGAGGACAGCTCAGACGAGGAGCATGCTCACTCAAGTCCCTTCAGACGACGAAACGACAGC	1462
Db	1382	AGAGGACAGCTCAGACGAGGAGCATGCTCACTCAAGTCCCTTCAGACGACGAAACGACAGC	1441
QY	1463	AGCAGCTTCAGAAA CAGCAGACGACGACGCTCTGCTGGGACAGGAGCCCTGTATCC	1522
Db	1442	AGCAGCTTCAGAAA CAAACAGCAGCAGCAGCTCTGCTGGGAGAGGAGCCCTGTATCC	1501
QY	1523	ATTATGTGCTGGGGGATGAATCCCGCTGACAAACAAGCTGGGGCCCGAAGGTTAGAAAGA	1582
Db	1502	ATTATGTGCTGGGGGATGAATCCCGCTGACAAACAAGCTGGGGCCCGAAGGTTAGAAAGA	1561
QY	1583	GAACAAGGATGAACAAGCAGCAGAACTCTCTTGTGGCCAGAGGAGACGACGACGAGCAGG	1642
Db	1562	GAACAAGGATGAACAAGCAGCAGAACTCTCTTGTGGCCAGAGGAGACGACGACGAGCAGG	1621
QY	1643	GGCTGAGCCCCCAATCCCCCAGGCTCTCCAGGGCCCCCAGAGACCCCTTTCCAGACTC	1702
Db	1622	GGCTGAGCCCCCAATCCCCCAGGCTCTCCAGGGCCCCCAGAGACCCCTTTCCAGACTC	1681
QY	1703	CTCCATATGACAGGCGGGTGGAGCCCCAGAGGGAGCCGACCA-----	1744
Db	1682	CTCCATATGACAGGCGGGTGGAGCCCCAGAGGGAGCCGACCAAGAGCTGGTGGACACAC	1741
QY	1745	-----AGTCCCTGACGAGCCAGC	1762
Db	1742	GGGTCCCACTGAACCATATGACACACCTGTACCCCGCATCCCAATGCTCTGACGAGACAGC	1801
QY	1763	CCACCCGAGAAACCTAGGCTGCTTCCAGGCTCCCATGACCCCGGACCTGGCCATCCCGGAC	1822
Db	1802	CCACCCGAGAAACCTAGGCTGCTTCCAGGCTTCCCATGACCCCGGACCTGGCCATCCCGGAC	1861
QY	1823	CCACTGACACCCCGCAGTGCCTCCAGAGAGCTGTATCCGACAGAAATTGAGACCCCACTCTG	1882
Db	1862	CCACTGACACCCCGCAGTGCCTCCAGAGAGCTGTATCCGACAGAAATTGAGACCCCACTCTG	1921
QY	1883	AAGGACTGTGCCCCCAGGCCCCGAAATCCCCAGCTGGGTTCCGCCAGATTAAGAGGCCCAAC	1942
Db	1922	AAGGACTGTGCCCCCAGGCCCCGAAATCCCCAGCTGGGTTCCGCCAGATTAAGAGGCCCAAC	1981
QY	1943	CCAAAGTATCCCTCAGAGGACTCATCTATATGCGCATGTGCTCTTAACACAGTGGGCGGAG	2002
Db	1982	CCAAAGTATCCCTCAGAGGACTCATCTATATGCGCATGTGCTCTTAACACAGTGGGCGGAG	2041
QY	2003	GGTCCCGGCCAGGCCAGGCAGTCCGTGCGAGACTTCGACGAACCTCCGCTGGCAATCT	2062
Db	2042	GGTCCCGGCCAGGCCAGGCAGTCCGTGCGAGACTTCGACGAACCTCCGCTGGCAATCT	2101
QY	2063	ATCTGCAAAAGCGGGGACAGAGGGGGACCCCAAAGCTTCAGAGGGCCCCCTGCTCAGCCCC	2122
Db	2102	ATCTGCAAAAGCGGGGACAGAGGGGGACCCCAAAGCTTCAGAGGGCCCCCTGCTCAGCCCC	2161
QY	2123	CTGACCCGCGCAAGCGCTCTGTATTAACCCCGACCTCAGAGAGGAGGACCTTGCTGGGAAAC	2182
Db	2162	CTGACCCGCGCAAGCGCTCTGTATTAACCCCGACCTCAGAGAGGAGGACCTTGCTGGGAAAC	2221
QY	2183	GCTTGGAACAGCTCTCTTCAGGCTCTCAGGGGACCTTCCCAAGCTTGCTCATCTGAGAC	2242
Db	2222	GCTTGGAACAGGCTCTCTTCAGGCTCTCAGGGGACCTTCCCAAGCTTGCTCATCTGAGAC	2281
QY	2243	GGAAACGCGGTGGAGGCTCTCTCAAACTGACAGACTCCCTGTGCTCTCCCTGGGATA	2302
Db	2282	GGAAACGCGGTGGAGGCTCTCTCTCAAACTGACAGACTCCCTGTGCTCTCCCTGGGATA	2341
QY	2303	AAGCCAAGCCGACGACCAACGCTCAGCGGCGGCGGCGGCGGACCTTGTGTTGCTGA	2362
Db	2342	AAGCCAAGCCGACGACCAACGCTCAGCGGCGGCGGCGGCGGACCTTGTGTTGTTGCTGA	2401

OY	2353	AAAGACCGGACTCTGGACGAGAGCCCTCTGGGCTCCCTCCAAAGACCAATGGAATCACTCTGCTCT	2422
Db	2402	AAAGACCGGACTCTGGACGAGAGCCCTCTGGGCTCCCTCCAAAGACCAATGGAATCACTCTGCTCT	2461
OY	2423	CCAGCGAGAGAGTGGAAAAGCATGTGAGACGACGACGAGAGAGAGCGAAGCGCGGCGACAG	2482
Db	2462	CCAGCGAGAGAGTGGAAAAGCATGTGAGACGACGAGAGAGAGAGCGAAGCGCGGCGACAG	2521
OY	2483	AGGGGAGCAGAGATACCCCTTGGGGGGCGGACGATGGGGATACAGACAGGCTCAGACACCA	2542
Db	2522	AGGGGAGCAGAGATACCCCTTGGGGGGCGGACGATGGGGATACAGACAGGCTCAGACACCA	2578
OY	2543	TGTTGGTCCACGACGTCGAGGAGATACACGGGACCCAGCCCTCAACGAGGGCGGACACCA	2602
Db	2579	TGTTGGTCCACGACGTCGAGGAGATACACGGGACCCAGCCCTCAACGAGGGCGGACACCA	2638
OY	2603	TGTTGGTCCAGCGGCAACCCCTGTAAGAGAGCGGAACCTGCTGACATGCTGACAGCAATGGGT	2662
Db	2639	TGTTGGTCCAGCGGCAACCCCTGTAAGAGAGCGGAACCTGCTGACATGCTGACAGCAATGGGT	2698
OY	2663	ACACAAACCTGCTTGAAGCTGTGATCCAGCCGACCACTCACCCACGAGAAACAGCAAAAGGCC	2722
Db	2699	ACACAAACCTGCTTGAAGCTGTGATCCAGCCGACCACTCACCCACGAGAAACAGCAAAAGGCC	2758
OY	2723	AAAGCCCAACCTCGAAGAGTGGAGATGGTGACTACCAATCTGCTGGGCTGGTAAAGGCC	2782
Db	2759	AAAGCCCAACCTCGAAGAGTGGAGATGGTGACTACCAATCTGCTGGGCTGGTAAAGGCC	2818
OY	2783	CTGGCAAGAGCTGCTTCAAGATGTTTGTGATCTAAGGATCTAACAGCTTGGAGGCACTG	2842
Db	2819	CTGGCAAGAGCTGCTTCAAGATGTTTGTGATCTAAGGATCTAACAGCTTGGAGGCACTG	2878
OY	2843	GGGACAGACATCCCAATCAACGCCATGAGGGGGAGAGAGGGAATCTGGCTGACACAGCTGC	2902
Db	2879	GGGACAGACATCCCAATCAACGCCATGAGGGGGAGAGAGGGAATCTGGCTGACACAGCTGC	2938
OY	2903	AGTACGAGCTGAGGAAGGGTTCTGTGTCTCAACGTGAATCCCAACCAACCCGGGCCACA	2962
Db	2939	AGTACGAGCTGAGGAAGGGTTCTGTGTCTCAACGTGAATCCCAACCAACCCGGGCCACA	2998
OY	2963	GTGAGACCCCTGTGATATCCGGAAGTACAGAAAGCATTAACCTCCAGATCTCTGTGTGAG	3022
Db	2999	GTGAGACCCCTGTGATATCCGGAAGTACAGAAAGCATTAACCTCCAGATCTCTGTGTGAG	3058
OY	3023	CCCTTTGGGGGGGTCAACCGTCGTGGGGGCAAGGAGAGGGGCTGATGTTGTCGACCGAA	3082
Db	3059	CCCTTTGGGGGGGTCAACCGTCGTGGGGGCAAGGAGAGGGGCTGATGTTGTCGACCGAA	3118
OY	3083	GTGGGCAAGGCGAAGGTGTATGGAATCATTTGGGCGGCGACGCTTCAGACAGATGATGTGC	3142
Db	3119	GTGGGCAAGGCGAAGGTGTATGGAATCATTTGGGCGGCGACGCTTCAGACAGATGATGTGC	3178
OY	3143	TGAGAGGGGCTCAACTGCTCATACCAATCTCAGGGAAAAAGAACAAATCTGGGGGTATTT	3202
Db	3179	TGAGAGGGGCTCAACTGCTCATACCAATCTCAGGGAAAAAGAACAAATCTGGGGGTATTT	3238
OY	3203	ACCTGTCCGTGGCTCGGGAACAAAGATTCTGACCAATGACCCAGAAATGAGAGAAAGCAGG	3262
Db	3239	ACCTGTCCGTGGCTCGGGAACAAAGATTCTGACCAATGACCCAGAAATGAGAGAAAGCAGG	3298
OY	3263	GCTGAGACCAACGTTGGGGGACATGAGAGGGCTGCGGCACTACCGTGTGTGAAATACGAGC	3322
Db	3299	GCTGAGACCAACGTTGGGGGACATGAGAGGGCTGCGGCACTACCGTGTGTGAAATACGAGC	3358
OY	3323	GGATTAAAGTTCTTGGTCAATCGCCCTCAAGAGCTCCGTGAGAGTGTATGCTTGGGGCCCCA	3382
Db	3359	GGATTAAAGTTCTTGGTCAATCGCCCTCAAGAGCTCCGTGAGAGTGTATGCTTGGGGCCCCA	3418
OY	3383	AAACCTTACCAAAATTCAATGAGCTTCAAGTCTTTGGCGGACCTTCCCAACGCGCTCTGCG	3442
Db	3419	AAACCTTACCAAAATTCAATGAGCTTCAAGTCTTTGGCGGACCTTCCCAACGCGCTCTGCG	3478
OY	3443	TGGTGAACCTGACAGTAAAGAGAGGGGCAAGCGGCTCAAGGATCTTAATGGCTTCACAGTCTG	3502

Db	3419	TGCTCGACCTGACAGTAGAGAGAGGGGCGAGCGGCTCAAGGTCATCTATGGGCTCCAGTGGCTG	3538
Qy	3503	GCTTCATGCTGTGGATGTGCACTTCGGGGAAACAGCTATGACATTTAATCTCCCTGTGCACA	3562
Db	3539	GCTTCATGCTGTGGATGTGCACTTCGGGGAAACAGCTATGACATTTAATCTCCCTGTGCACA	3598
Qy	3553	TCGAGAGCGAGATGACGGCCCCATGCGATTCCTCCATCCCGCAACCGACGGATGAGAGA	3622
Db	3599	TCGAGAGCGAGATGACGGCCCCATGCGATTCCTCCATCCCGCAACCGACGGATGAGAGA	3658
Qy	3623	TGCTGCTGTGCTACGAGGACGAGGGGTGTCTACGTCAACACGCTACGGGCGCATCTTAAGG	3682
Db	3659	TGCTGCTGTGCTACGAGGACGAGGGGTGTCTACGTCAACACGCTACGGGCGCATCTTAAGG	3718
Qy	3683	ATGTGATGCTGCAGTGGGGGGAGATGCCCTACTTGTGGGCTTACATCTGCTCCAACGAGA	3742
Db	3719	ATGTGATGCTGCAGTGGGGGGAGATGCCCTACTTGTGGGCTTACATCTGCTCCAACGAGA	3788
Qy	3743	TAAATGGGCTGGGGGTGAGAAAGCCATTGAGATCCGCTCTGAGGAGACGGGGCCACCTCGACG	3802
Db	3779	TAAATGGGCTGGGGGTGAGAAAGCCATTGAGATCCGCTCTGAGGAGACGGGGCCACCTCGACG	3838
Qy	3803	GAGCTTCATGACCAAAAGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGATGACAAAGG	3862
Db	3839	GAGCTTCATGACCAAAAGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGATGACAAAGG	3898
Qy	3863	TGTTTTTTCCTCAGTCGCTCTTGGGGGCGACGACCCAAATTACTTCATGACTCTGAACC	3922
Db	3899	TGTTTTTTCCTCAGTCGCTCTTGGGGGCGACGACCCAAATTACTTCATGACTCTGAACC	3958
Qy	3923	GTAACGATCATGACATGCTGTGAAAGGCG	3951
Db	3959	GTAACCGATCATGACATGCTGTGAAAGGCGGCGC	3987

RESULT 4				PRI 18-APR-2000
AB035698				
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ACCESSION	AB035698			
VERSION				
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ORGANISM	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases)			
	Dan,I., Watanabe,N.M., Kobayashi,T., Yamashita-Suzuki,K., Fukagawa,Y., Kajikawa,E., Kimura,W.K., Nakashima,T.M., Matsumoto,K., Ninomiya-Tsuji,J. and Kusumi,A.			
TITLE	Molecular cloning of MNK, a novel member of mammalian GCK family kinases, which is up-regulated during postnatal mouse cerebral development			
JOURNAL	FEBS Lett. 469 (1), 19-23 (2000)			
MEDLINE	20175403			
PUBMED	10708748			
REFERENCE	2 (bases 1 to 3888)			
AUTHORS	Dan,I., Watanabe,N.M. and Kusumi,A.			
TITLE	Direct Submission			
JOURNAL	Submitted (10-DEC-1999) Ippelita Dan, ERATO, Kusumi Membrane Organizer Project; 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail:dangebio.nagoya-u.ac.jp, Tel.:81-52-789-2497, Fax:81-52-789-2368)			
FEATURES	Location/Qualifiers			

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AUTHORS	Dan, I., Watanabe, N.M., Kobayashi, T., Yamashita-Suzuki, K., Fukagaya, Y., Kajikawa, E., Kimura, W.K., Nakashima, T.M., Matsumoto, K., Niinomiya-Tsujii, J., and Kusumi, A.				
TITLE	Molecular cloning of MINK, a novel member of mammalian GCK family kinases, which is up-regulated during postnatal mouse cerebral development				
JOURNAL	FEBS Lett. 469 (1), 19-23 (2000)				
MEDLINE	20175403				
PUBMED	10708748				
AUTHORS	2 (bases 1 to 4863)				
TITLE	Watanabe, N.M., Dan, I., and Kusumi, A.				
JOURNAL	Direct Submission				
FEATURES	Submitted (16-APR-2000) Ippelita Dan, Nagoya University, Dept. of Biological Science; Chikusa-ku, Furo-cho, Nagoya, Aichi 464-8602, Japan (E-mail: dangebio.nagoya-u.ac.jp, URL: http://www.supra.bio.nagoya-u.ac.jp/DNM/, Tel: 81-52-789-2497, Fax: 81-52-789-2368)				
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Db	1205	TC CATCATGAAGCGTGCCTGGAGAGTGCATCAAGCCGGAGGTTTCTCCGCTCCAGCAG	1264
QY	1087	GA AAA TTAAGCAACTCAGAGGCTTTTAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAG	1146
Db	1285	GA AAA TTAAGCAACTCAGAGGCTTTTAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCAG	1324
QY	1147	CGAGACCCCGGAGGCA CACATCAACCTGTCGACCAAGCGGCGAGCGGCGCATGAGAGAG	1206
Db	1325	CGAGACCCCGGAGGCA CACATCAACCTGTCGACCAAGCGGCGAGCGGCGCATGAGAGAG	1384
QY	1207	CAGAA GAGAGAGCGCGCGCGCTGTGAGGAGCA CAGCGGCGGAGCGGAGCA CCGAGCAG	1266
Db	1385	CAGAA GAGAGAGCGCGCGCGCTGTGAGGAGCA CAGCGGCGGAGCGGAGCA CCGAGCAG	1444
QY	1287	CTG CAGAGAAAGAGCAGCAGCAGCGCGCTGCGTGAAGACATGCA GCGCTCTGCGCGGAGAGAG	1326
Db	1445	CTG CAGAGAAAGAGCAGCAGCAGCGCGCTGCGTGAAGACATGCA GCGCTCTGCGCGGAGAGAG	1504
QY	1327	GAGCGGCGGCGAGCGGAGCGTGTGAGAGGAATCAAGCGGAAAGCAGCTGGAGAGCAGCGG	1386
Db	1505	GAGCGGCGGCGAGCGGAGCGTGTGAGAGGAATCAAGCGGAAAGCAGCTGGAGAGCAGCGG	1564
QY	1387	CAGTCAGAA CGTCTTCAGAGGCA GCTGCAGCAGAGACATGCTCA CTCTCAATCTCTCTGACG	1446
Db	1565	CAGTCAGAA CGTCTTCAGAGGCA GCTGCAGCAGAGACATGCTCA CTCTCAATCTCTCTGACG	1624
QY	1447	CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCTGCTGGGAGAC	1506
Db	1625	CAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCTGCTGGGAGAC	1684
QY	1507	AGGAA GCGCCCTGTATCCATTATGTGTGGGGCATGAAATCCCGCTGACAAACAGACCTGTGGCC	1566
Db	1685	AGGAA GCGCCCTGTATCCATTATGTGTGGGGCATGAAATCCCGCTGACAAACAGACCTGTGGCC	1744
QY	1567	CGAGAGGTAGAA GAGAGAAACAGAGATGAAACAGCAGCAGAACTCTCCCTTGCCCAAGAC	1626
Db	1745	CGAGAGGTAGAA GAGAGAAACAGAGATGAAACAGCAGCAGAACTCTCCCTTGCCCAAGAC	1804
QY	1627	AA GCGCAGCAGCAGCAGCGGCGCTGAGCGCCCGCCCATCCCGCAGGCGCTCCCAAGGAGAGG	1686
Db	1805	AA GCGCAGCAGCAGCAGCGGCGCTGAGCGCCCGCCCATCCCGCAGGCGCTCCCAAGGAGAGG	1864
QY	1687	CC CCGTTTCCAGACTCTCTCTTATGACAGCGCGGTGAGCGCCCAAGAGAGAGCCGACACA -	1744
Db	1865	CC CCGTTTCCAGACTCTCTCTTATGACAGCGCGGTGAGCGCCCAAGAGAGAGCCGACACA -	1924
QY	1745	-----AG	1746

Db	1925	AGCCTGGTGGCAACCGGGTCCCACTGAAGCATTGACAGACCTGTAACTCCCATCCGAC	1984
Qy	1747	TCCTTCGAGAGCAAGCCCACTCGAACTTGCTGCTTTCCAGCTCTCCATTGACCCCGAC	1806
Db	1985	TCCTTCGAGAGCAAGCCCACTCGAACTTGCTGCTTTCCAGCTCTCCATTGACCCCGAC	2044
Qy	1807	CCTGCAATCCCGGCAACCACTGCCAACCCTGATGCCGAGAGGTGATCTCCGCAAT	1866
Db	2045	CCTGCAATCCCGGCAACCACTGCCAACCCTGATGCCGAGAGGTGATCTCCGCAAT	2104
Qy	1867	TCAGACCCCACTCTGAAGAAGCACTGGCCCAAGCCCAATCCCAAGCTGGTCCGCCA	1926
Db	2105	TCAGACCCCACTCTGAAGAAGCACTGGCCCAAGCCCAATCCCAAGCTGGTCCGCCA	2164
Qy	1927	GATTAAGAGGCCCAACCCAAAGTGCCTTCAAGAGACTTATCTATGCGCACTGCCCTTAA	1986
Db	2165	GATTAAGAGGCCCAACCCAAAGTGCCTTCAAGAGACTTATCTATGCGCACTGCCCTTAA	2224
Qy	1987	ACCAATGGGGCCGAGAGGTCCCCGCGACCTCAAGGCACTTCGTGCGAACACTCCGAGCAAC	2046
Db	2225	ACCAATGGGGCCGAGAGGTCCCCGCGACCTCAAGGCACTTCGTGCGAACACTCCGAGCAAC	2269
Qy	2047	TCCGCTGGCAATCTATCTGCAAAAGGCGGCGAGAGCGGGCAACCCCAAGCTCAGAGG	2106
Db	2270	-----	2269
Qy	2107	CCCCCTGCTCAGCCCCCTGGCCCGCCCAACCGCTCTAATAACCCCGACCTTCAGAGGAGC	2166
Db	2270	-----AGTAACTCCGACTTCAGAGGAGC	2293
Qy	2167	GACCTTGGCTGGAAACGCTCGGACAGCGTCTTTCACGCTTTCACCGGCACTCTCCCGAC	2226
Db	2294	GACCTTGGCTGGAAACGCTCGGACAGCGTCTTTCACGCTTTCACCGGCACTCTCCCGAC	2353
Qy	2227	GCTGGCTACTGGAAGCGGACCGGCTGGAGACTCTTCAAACTGGAACAGCTCCCTGTG	2286
Db	2354	GCTGGCTACTGGAAGCGGACCGGCTGGAGACTCTTCAAACTGGAACAGCTCCCTGTG	2413
Qy	2287	CTCTCCCTGGGAATTAAGCCCAAGCCCGACGACACCGCTCACCGGCGAGGCGCGCCGA	2346
Db	2414	CTCTCCCTGGGAATTAAGCCCAAGCCCGACGACACCGCTCACCGGCGAGGCGCGCCGA	2473
Qy	2347	-----GACTTGTGTTCTGAAAGCGGACTCTTGACGAG	2382
Db	2474	AGCTAATAGCAGCAATGTTGTGAGGACTTTGTGTCGAAAGCGGACTCTTGACGAG	2533
Qy	2383	GCCCCCTGGGCTCCCAAGAAGCCATGGAATCTACTGCTGCTCAGCGAGAGGTGGAAGC	2442
Db	2534	GCCCCCTGGGCTCCCAAGAAGCCATGGAATCTACTGCTGCTCAGCGAGAGGTGGAAGC	2593
Qy	2443	AGTGAAGACGACGAGGAGGAAGGCGGAAGCGGCGACGAGAGGGGAGCAGATACCTT	2502
Db	2594	AGTGAAGACGACGAGGAGGAAGGCGGAAGCGGCGACGAGAGGGGAGCAGATACCTT	2653
Qy	2503	GGGGGCGCAGCGATGGGGAATACAGACGCGTCAACCATGTTGTTCACGACGTCGTGAG	2562
Db	2654	GGGGGCGCAGCGATGGGGAATACAGACGCGTCAACCATGTTGTTCACGACGTCGTGAG	2713
Qy	2563	GAGATCAACCGGACCCCAACCCCTCATACGGGGGCGGCAACATGTTGTTCACGACCCCT	2622
Db	2714	GAGATCAACCGGACCCCAACCCCTCATACGGGGGCGGCAACATGTTGTTCACGACCCCT	2773
Qy	2623	GAAAGAGAGCGGAACCTGCTGATGCTGACAGCAATGGGTCACAAACTTGCCTGACGTG	2682
Db	2774	GAAAGAGAGCGGAACCTGCTGATGCTGACAGCAATGGGTCACAAACTTGCCTGACGTG	2833
Qy	2683	GTTCAGCCCAAGCACTCAACCCAGAGAACGCAAAAGGCCCAAGCCCACTTCGAAGAT	2742
Db	2834	GTTCAGCCCAAGCACTCAACCCAGAGAACGCAAAAGGCCCAAGCCCACTTCGAAGAT	2893
Qy	2743	GGAGTGGTGAATCAAGTCTTGTTGGCTGGTAAAGGCTCTGGCAAGACTTCTTCAAG	2802

Db	2894	GGGAGTGGTGA CTG CCACTCTGTTGGCTGGTAAAGGCCCTGGCAAGAGCTCGTTACG	2953
Qy	2803	ATGTTTGTGATCTTAGGGATCTACAGCTTGAGAGGCAAGTGGGAGACGATCCCATACA	2862
Db	2954	ATGTTTGTGATCTTAGGGATCTACAGCTTGAGAGGCAAGATCCCATACA	3013
Qy	2863	GGCCTAGTGGGTGGAGAGGGGCACTCCGCTGACCAAGCTGCAGTACGATGAGGAAGGGT	2922
Db	3014	GGCCTAGTGGGTGGAGAGGGGCACTCCGCTGACCAAGCTGCAGTACGATGAGGAAGGGT	3073
Qy	2923	TCTGTGCTCAAGTGAATCCACCAACACCCGGGCCCAAGTGAAGCCCTGAAGTCCGG	2982
Db	3074	TCTGTGCTCAAGTGAATCCACCAACACCCGGGCCCAAGTGAAGCCCTGAAGTCCGG	3133
Qy	2983	AAGTACAAAGAACGATTCACCTCGAGATCTCTGTGACGCCCTTGGGGGGTCAACCTG	3042
Db	3134	AAGTACAAAGAACGATTCACCTCGAGATCTCTGTGACGCCCTTGGGGGGTCAACCTG	3193
Qy	3043	CTGTGTGGGCAAGAGAAAGGGCTGATGTTGGCTGACCGAAGTGGGCAAGGCAAGGTGAT	3102
Db	3194	CTGTGTGGGCAAGAGAAAGGGCTGATGTTGGCTGACCGAAGTGGGCAAGGCAAGGTGAT	3253
Qy	3103	GGACTCATTTGGGCGGCGACGCTTCCAGAGATGATGTGCTGAGAGGGGCTCAACCTGCTC	3162
Db	3254	GGACTCATTTGGGCGGCGACGCTTCCAGAGATGATGTGCTGAGAGGGGCTCAACCTGCTC	3313
Qy	3163	ATCACCATCTTCAGGGAAAAAGAACAACTGGCGGGTATTAACCTGTGCTCCGGAAC	3222
Db	3314	ATCACCATCTTCAGGGAAAAAGAACAACTGGCGGGTATTAACCTGTGCTCCGGAAC	3373
Qy	3223	AAGATTTCTGCACATGACCCGAGAAATGAGAAAGACAGGGCTGGAACAACCTGGGGAC	3282
Db	3374	AAGATTTCTGCACAATGACCCGAGAAATGAGAAAGACAGGGCTGGAACAACCTGGGGAC	3433
Qy	3283	ATGAGGGGCTGCGGGCACTACCGATTTGTAATACGAGCGGATTAAGTTCTGTGCTATC	3342
Db	3434	ATGAGGGGCTGCGGGCACTACCGATTTGTAATACGAGCGGATTAAGTTCTGTGCTATC	3493
Qy	3343	GGCCTCAAGACCTCGGTGAGAGGTGATGCTGGGCGCCCAAAACCTTACCAAAATTCAAG	3402
Db	3494	GGCCTCAAGACCTCGGTGAGAGGTGATGCTGGGCGCCCAAAACCTTACCAAAATTCAAG	3553
Qy	3403	GCCTTCAAGTCTTTGCGGACCTCCGCCCAACCGGCTCTGTGCTGTGACCTGACAGTAGAG	3462
Db	3554	GCCTTCAAGTCTTTGCGGACCTCCGCCCAACCGGCTCTGTGCTGTGACCTGACAGTAGAG	3613
Qy	3463	GAGGGGCGCGGCTCAAGGTACATCATGAGCTCAAGTGTGCTTCATGCTGTGGAATGTC	3522
Db	3614	GAGGGGCGCGGCTCAAGGTACATCATGAGCTCAAGTGTGCTTCATGCTGTGGAATGTC	3673
Qy	3523	GACTCGGGGAAACAGTATGACATCTACATCCCTGTGCAATCCAGAGCCAGATCAACGCC	3582
Db	3674	GACTCGGGGAAACAGTATGACATCTACATCCCTGTGCAATCCAGAGCCAGATCAACGCC	3733
Qy	3583	CATGCCATCATCTTCTCTCCCAACACCGACGGCATGAGATGCTGTGCTACGAGGAC	3642
Db	3734	CATGCCATCATCTTCTCTCCCAACACCGACGGCATGAGATGCTGTGCTACGAGGAC	3793
Qy	3643	GAGGCTGCTACGTACACAGTACGAGGGGCACTTAAGATGTGAGTCTGCAAGTGGGG	3702
Db	3794	GAGGCTGCTACGTACACAGTACGAGGGGCACTTAAGATGTGAGTCTGCAAGTGGGG	3853
Qy	3703	GAGATGCTTACTTCTGTGGGCTCAATCTGTCTCAACAGATTAATGGGCTGGGGTGAAGAA	3762
Db	3854	GAGATGCTTACTTCTGTGGGCTCAATCTGTCTCAACAGATTAATGGGCTGGGGTGAAGAA	3913
Qy	3763	GGCATTTGAGATCCGGTCTGTGGAGACGGGGCACTCGACGGGGGTCTTATGACACAAACGA	3822
Db	3914	GGCATTTGAGATCCGGTCTGTGGAGACGGGGCACTCGACGGGGGTCTTATGACACAAACGA	3973
Qy	3823	GCTCAGAGAGCTCAAGTTCTCTGTGTGATGAGGGAAATGACAAAGGTGTTTTTGGCTCAAGTCCGC	3882
Db	3974	GCTCAGAGAGCTCAAGTTCTCTGTGTGATGAGGGAAATGACAAAGGTGTTTTTGGCTCAAGTCCGC	4033

QY	3883	TCGCGGGGCGAGCAGCCAGTTTACTTCATATGACTGTAAACCGTACTGATCATATGAACCTGG	3942
Db	4034	TCGCGGGGCGAGCAGCCAGTTTACTTCATATGACTGTAAACCGTACTGATCATATGAACCTGG	4093
QY	3943	TGAAGGCGC	3951
Db	4094	TGACGGGGC	4102
RESULT 6	AX235361	3912 bp	DNA
LOCUS	AX235361	Sequence 8 from Parent	MO0162928.
ACCESSION	AX235361		
VERSION	AX235361.1	GI:15593893	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
CDS			
QY	7	ATGGGCGACCCAGCCCGCCCGCAGCGCTGGACGACATCGACTCTGCGCCCTGCGGAGC	66
Db	1	ATGGGCGACCCAGCCCGCCCGCAGCGCTGGACGACATCGACTCTGCGCCCTGCGGAGC	60
QY	67	CTGCTGGGAACTTTGAGCTTGTGAGAGTGTGCTGGCAATGGAACCTTACCGACAGTGTAC	126
Query Match	90.7%;	Score 3583.8;	DB 6; Length 3912;
Best Local Similarity	94.9%;	Pred. No. 0;	
Matches 3816;	Conservative	0; Mismatches	12; Indels 195; Gaps 3;

Db	61	CTCTGCGGGATCTTTGAGCTTGTGAGAGTGGTCCGACATGGAACCTACCGACAGGTGAC	120
Qy	127	AAAGGTCGGACATGTCACAACGCGGACGCTGCGCTGCCATCAAGTCTAGATGTCAACGAG	186
Db	121	AAAGGTCGGACATGTCACAACGCGGACGCTGCGCTGCCATCAAGTCTAGATGTCAACGAG	180
Qy	187	GACGAGGAGGAAAGATCAATCAACGAGAGTCAAACTGCTGAAAAAGTACTCTCAACAACGC	246
Db	181	GACGAGGAGGAAAGATCAAAACGAGAGTCAACATGCTGAAAAAGTACTCTCAACAACGC	240
Qy	247	AACATGCGCACTTACTACGAGCCCTTCAACAAGAGCCCCCGGGAAACGATGACGAG	306
Db	241	AACATGCGCACTTACTACGAGCCCTTCAACAAGAGCCCCCGGGAAACGATGACGAG	300
Qy	307	CTCTGCGTGGTGAATGAGAGTTCTGTGTGTCTGTTGATGACTGACCTGTGTAAGAACA	366
Db	301	CTCTGCGTGGTGAATGAGAGTTCTGTGTGTCTGTTGATGACTGACCTGTGTAAGAACA	360
Qy	367	AAAGGCAACGCCCTGAGAGGAGCTGTATCGCTATATCTGACGGAGAACTCTAGGGGT	426
Db	361	AAAGGCAACGCCCTGAGAGGAGCTGTATCGCTATATCTGACGGAGAACTCTAGGGGT	420
Qy	427	CTGCGCCATCTTCATATGCCCAACAGGTGATCCATCGAGACATCAAGGGGACAGATGTGCTG	486
Db	421	CTGCGCCATCTTCATATGCCCAACAGGTGATCCATCGAGACATCAAGGGGACAGATGTGCTG	480
Qy	487	CTGACAGAGATGCTGAGGTCAAGCTTAAGATTTTGGGGTGAAGTCTCAGCTGAGCCG	546
Db	481	CTGACAGAGATGCTGAGGTCAAGCTTAAGATTTTGGGGTGAAGTCTCAGCTGAGCCG	540
Qy	547	ACCGTGGGACAGCGGACAACCTTCAATGAGGACCTCCCTACGTGAGTGGCTCCAGAGGTATC	606
Db	541	ACCGTGGGACAGCGGACAACCTTCAATGAGGACCTCCCTACGTGAGTGGCTCCAGAGGTATC	600
Qy	607	GCGTGTGATGAGAACCTCGATGCCCACTATGATTAACAAGATGTATTTGGTCTCTAGAA	666
Db	601	GCGTGTGATGAGAACCTCGATGCCCACTATGATTAACAAGATGTATTTGGTCTCTAGAA	660
Qy	667	ATCACAGCCATCGAGATGACAGAGGAGCCCCCTCTGTGTGACATGCAACCCATGCGA	726
Db	661	ATCACAGCCATCGAGATGACAGAGGAGCCCCCTCTGTGTGACATGCAACCCATGCGA	720
Qy	727	GCCCTCTTCATATCTCTCGGAAACCTCCGACAGGCTCAAGTCCAAAGTGGTCTAAG	786
Db	721	GCCCTCTTCATATCTCTCGGAAACCTCCGACAGGCTCAAGTCCAAAGTGGTCTAAG	780
Qy	787	AAAGTCATTGACCTTCAATGACACATGTCTCATCAAGACTTACCTGAGCCGCCCAACG	846
Db	781	AAAGTCATTGACCTTCAATGACACATGTCTCATCAAGACTTACCTGAGCCGCCCAACG	840
Qy	847	GAGCAGCTACTGAAAGTTTCCCTTCAATCCGGGACACAGCCACGAGCGGACAGTCCGATC	906
Db	841	GAGCAGCTACTGAAAGTTTCCCTTCAATCCGGGACACAGCCACGAGCGGACAGTCCGATC	900
Qy	907	CAGCTTAAGAACCAATGACCGGATCCCGGAAAGACGCGGGGTGAGAAAGAGAGACAGAA	966
Db	901	CAGCTTAAGAACCAATGACCGGATCCCGGAAAGACGCGGGGTGAGAAAGAGAGACAGAA	960
Qy	967	TATGAGTACAGCGGACGAGGAGGAGAGATGACAGCCCATGAGAGAGAGAGAGC	1026
Db	961	TATGAGTACAGCGGACGAGGAGGAGAGATGACAGCCCATGAGAGAGAGAGAGC	1020
Qy	1027	TCATCATGAACGTGCTGAGAGTGCATCTACCGCGGAGTTTCTCCGCTCCAGCAG	1086
Db	1021	TCATCATGAACGTGCTGAGAGTGCATCTACCGCGGAGTTTCTCCGCTCCAGCAG	1080
Qy	1087	GAAATTAAGAGCACTCAGAGGCTTTAAACACGACGACGACGCTGACACACAGACAG	1146
Db	1081	GAAATTAAGAGCACTCAGAGGCTTTAAACACGACGACGACGCTGACACACAGACAG	1140
Qy	1147	CGAGACCCCGAGGACACATCAAAACCTGTGTCACACGCGGACGCGCATAGAGAG	1206
Db	1141	CGAGACCCCGAGGACACATCAAAACCTGTGTCACACGCGGACGCGCATAGAGAG	1200

QY	1207	CAGAAAGAGACCGCGCCCGCTGTGAGAGACACACAGCGCGCGGACCGGAGACAGCCGAAG	1266
Db	1201	CAGAAAGAGAGCGCGCCCGCTGTGAGAGACACACAGCGCGCGGAGCGGAGACAGCCGAAG	1260
QY	1267	CTGCAGAGGAAAGAGACAGACAGCGCGCTGAGGACATGTGAGAGCTCTGCGCGGAGAGAG	1326
Db	1261	CTGCAGAGGAAAGAGACAGACAGCGCGCTGAGGACATGTGAGAGCTCTGCGCGGAGAGAG	1320
QY	1327	GAGCGCGCGGACGCGGAGCGCTGAGCAGGAAATACAGCGGAGAGCAGCTGAGAGACACCG	1386
Db	1321	GAGCGCGCGGACGCGGAGCGGAGCAGGAAATATTTCTGACAGGCTGAGAGAGACGCG	1380
QY	1387	CAGTCAGAACTCTTCAGAGGACCTGACAGAGAGATGCTTACTTCAATGCTCCCTGAG	1446
Db	1381	CAGTCAGAACTCTTCAGAGGACCTGACAGAGAGATGCTTACTTCAATGCTCCCTGAG	1440
QY	1447	CAGCAGCAACAGCAGACAGAGCTTCAGAAAACAGCAGCAGCAGCAGCTCTGCTGAGGAC	1506
Db	1441	CAGCAGCAACAGCAGCAGAGCTTCAGAAAACAGCAGCAGCAGCAGCTCTGCTGAGGAC	1500
QY	1507	AGGAAGCCCTGTATCAATTATGTCTGGGGACATGAAATCCCGCTGACAAACAGCCTGGGCC	1566
Db	1501	AGGAAGCCCTGTATCAATTATGTCTGGGGACATGAAATCCCGCTGACAAACAGCCTGGGCC	1560
QY	1567	CGAGAGGTAGAAAGAGAGAACAGAGATGAAACAGCAGCAGAACTTCCCTTGGCCMAAGC	1626
Db	1561	CGAGAGGTAGAAAGAGAGAACAGAGATGAAACAGCAGCAGAACTTCCCTTGGCCMAAGC	1620
QY	1627	AAGCAGGACACAGGGGGCTGAGACCCGCCATCCCGAGGCTCCCGCAGGGGCCCCAGGA	1686
Db	1621	AAGCAGGACACAGGGGGCTGAGACCCGCCATCCCGAGGCTCCCGCAGGGGCCCCAGGA	1680
QY	1687	CCCTTTTCCAGACTCCTCTCTATGACAGAGGCGGTGAGGCCACGAGAGGACCGCACAA--	1744
Db	1681	CCCTTTTCCAGACTCCTCTCTATGACAGAGGCGGTGAGGCCACGAGAGGACCGCACAAAG	1740
QY	1745	-----AG 1746	
Db	1741	AGCTGTGTGACACCGGGTCCCACTGAAGCATATGACAGCATCTGTATCCCGCATCCGAC	1800
QY	1747	TCCCTGACAGACAGAGCCACCCCGAAACTGTGCTGCTCCAGCGTCCCATGACCCGAC	1806
Db	1801	TCCCTGACAGACAGAGCCACCCCGAAACTGTGCTGCTCCAGCGTCCCATGACCCGAC	1860
QY	1807	CCTGCATCCCCGACACCACTGCCACGCCAGTCCCGAGAGAGCTGTCAATCCGCAGAAAT	1866
Db	1861	CCTGCATCCCCGACACCACTGCCACGCCAGTCCCGAGAGAGCTGTCAATCCGCAGAAAT	1920
QY	1867	TCAGACCCCACTCTGAAAGACCTTGGCCCCAGCCCGAATCCCCAGCTCGGGTCCGCCCA	1926
Db	1921	TCAGACCCCACTCTGAAAGACCTTGGCCCCAGCCCGAATCCCCAGCTCGGGTCCGCCCA	1980
QY	1927	GATTAACGAGGCCCAACCAAGTGTCTCAAGAGACCTCACTATTCGGCACCTGCCCTTAAC	1986
Db	1981	GATTAACGAGGCCCAACCAAGTGTCTCTCAAGAGACCTCACTATTCGGCACCTGCCCTTAAC	2040
QY	1987	ACCAAGTGGGGCGGAGGGTCCCGGACAGACCAGGACAGTCCGTGCGCAACTCGCAGCAAC	2046
Db	2041	ACCAAGTGGGGCGGAGGGTCCCGGACAGACCAGGACAGTCCGTGCGCAACTCGCAGCAAC	2085
QY	2047	TCCGCTGTGCAATCTATCTGCAAAAGGCGGGCAGAGCGGGCACCCCAAGCCTCGAGG	2106
Db	2086	----- 2085	
QY	2107	CCCCCTGCTACGCCCTGCGCCGCGCCACGCTCTGTATTAACCCCACTCAAGAGAGC	2166
Db	2086	-----AGTAAACCCCACTCAAGAGAGAGC 2109	
QY	2167	GACCTGTGAGGAAAGCTGGAGCAGGGTCTTTCAGAGCTCTCAAGGAGCACTCCCGCAG	2226
Db	2110	GACCTGTGAGGAAAGCTGGAGCAGGGTCTTTCAGAGCTCTCAAGGAGCACTCCCGCAG	2169

Qy	2227	GCTGGCTCACTGAGCGGAAACCGGTGGAGCTCTCTCAAACTGACAGCTCCCTGTG	2286		
Db	2170	GCTGGCTCACTGAGCGGAAACCGGTGGAGCTCTCTCAAACTGACAGCTCCCTGTG	2229		
Qy	2287	CTCTCCCTGGGAAATAAGCCAGACCCGACGACCAACGCTCAAGCCGACCGCCGCA	2346		
Db	2230	CTCTCCCTGGGAAATAAGCCAGACCCGACGACCAACGCTCAAGCCGACCGCCGCA	2289		
Qy	2347	-----GACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG	2382		
Db	2290	AGCTATAAGCGAGCAATTGTGAGGAACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAG	2349		
Qy	2283	GCCCCCTGGGCTCCCAAGAAAGCCATGGAATCTGTGTCAGAGAGAGAGTGAAGC	2442		
Db	2350	GCCCCCTGGGCTCCCAAGAAAGCCATGGAATCTGTGTCAGAGAGAGAGTGAAGC	2409		
Qy	2443	AGTGAAGACGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATACCCCT	2502		
Db	2410	AGTGAAGACGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATACCCCT	2469		
Qy	2503	GGGGGCGGACGATGGGGATATACAGACGCTCAGACCAATGTGTCTCAGAGCTGAG	2562		
Db	2470	GGGGGCGGACGATGGGGATATACAGACGCTCAGACCAATGTGTCTCAGAGCTGAG	2529		
Qy	2563	GAGATCAACGGGACCCGACCCCTACGAGGGGCGGACCAATGTGTCTCAGAGCCCT	2622		
Db	2530	GAGATCAACGGGACCCGACCCCTACGAGGGGCGGACCAATGTGTCTCAGAGCCCT	2589		
Qy	2623	GAAGAGAGCGGAACTGCTGCTGATGTCAGACCAATGGGTACAAACCTGCTGACGTG	2682		
Db	2590	GAAGAGAGCGGAACTGCTGCTGATGTCAGACCAATGGGTACAAACCTGCTGACGTG	2649		
Qy	2683	GTCAGGCCCAAGCCTACCAACCGAGAACAGCAAAAGGCCCAAGCCCTCGAAGAT	2742		
Db	2650	GTCAGGCCCAAGCCTACCAACCGAGAACAGCAAAAGGCCCAAGCCCTCGAAGAT	2709		
Qy	2743	GGGAGTGTGATCTACAGTCTGTGGGTGTGTAAGGCGCCGTGCAAGAGCTGCTACG	2802		
Db	2710	GGGAGTGTGATCTACAGTCTGTGGGTGTGTAAGGCGCCGTGCAAGAGCTGCTACG	2769		
Qy	2803	ATGTTTGTGATCTAGGATCTACAGCCTGAGAGCAGTGGGACAGATCCCATCA	2862		
Db	2770	ATGTTTGTGATCTAGGATCTACAGCCTGAGAGCAGTGGGACAGATCCCATCA	2829		
Qy	2863	GCCCTAGTGGTGAAGAGGACCTCGGCTCGACCAAGCTGCAAGTGAAGAGAGGT	2922		
Db	2830	GCCCTAGTGGTGAAGAGGACCTCGGCTCGACCAAGCTGCAAGTGAAGAGAGGT	2889		
Qy	2923	TCTGTGTCAACGTGAATCCCAACCAACCCGGGCCCCAATGAGACCCCTGAGATCCGG	2982		
Db	2890	TCTGTGTCAACGTGAATCCCAACCAACCCGGGCCCCAATGAGACCCCTGAGATCCGG	2949		
Qy	2983	AAAGTAAAGAAAGCATCTCAAGATCTCTGTGAGAGCCCTTTGGGGGTCAACCTG	3042		
Db	2950	AAAGTAAAGAAAGCATCTCAAGATCTCTGTGAGAGCCCTTTGGGGGTCAACCTG	3009		
Qy	3043	CTGTGTGGGACGAGAAACGGGCTGATGTTGCTGACCGAAGTGGGACAGGAGTGTAT	3102		
Db	3010	CTGTGTGGGACGAGAAACGGGCTGATGTTGCTGACCGAAGTGGGACAGGAGTGTAT	3069		
Qy	3103	GGAATCATTTGGGCGGACGCTTCCAGACATGTGATGCTGTGAGGGGCTCAACTGTC	3162		
Db	3070	GGAATCATTTGGGCGGACGCTTCCAGACATGTGATGCTGTGAGGGGCTCAACTGTC	3129		
Qy	3163	ATCACCATCTCAAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	3222		
Db	3130	ATCACCATCTCAAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	3189		
Qy	3223	AAAGATTTGACAAATGACCCAGAAAGTGAAGAAAGAGAGAGAGAGAGAGAGAGAG	3282		
Db	3190	AAAGATTTGACAAATGACCCAGAAAGTGAAGAAAGAGAGAGAGAGAGAGAGAGAG	3249		
Qy	3283	ATGAGAGGCTGGGGCACTACCGGTGTTGTGAATAACAGCGGATTAAGTTCTGTGATC	3342		

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Db	3250	ATGAGAGGCTGGGGCACTACCGGTGTTGTGAATAACAGCGGATTAAGTTCTGTGATC	3309		
Qy	3343	GCCCTCAAGAGCTCGTGAAGGTGTATGCTGGGCCCCCAAACTTACCAAAATTCAATG	3402		
Db	3310	GCCCTCAAGAGCTCGTGAAGGTGTATGCTGGGCCCCCAAACTTACCAAAATTCAATG	3369		
Qy	3403	GCCCTCAAGTCTTTGGCGACCTCCGACCGGCTGCTGGTGTGACCTGACAGTGAAG	3462		
Db	3370	GCCCTCAAGTCTTTGGCGACCTCCGACCGGCTGCTGGTGTGACCTGACAGTGAAG	3429		
Qy	3463	GAGGGGAGGGGCTCAAGATCATATGATGCTCCAGTCTGAGTCTTCAATGCTGATGTC	3522		
Db	3430	GAGGGGAGGGGCTCAAGATCATATGATGCTCCAGTCTGAGTCTTCAATGCTGATGTC	3489		
Qy	3523	GACTGGGGAAACAGCTATGACATTCATCTCTGTGACATCCAGAGCCAGATCAAGCC	3582		
Db	3490	GACTGGGGAAACAGCTATGACATTCATCTCTGTGACATCCAGAGCCAGATCAAGCC	3549		
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RESULT 7  
AX235359

LOCUS  
AX235359 3999 bp DNA linear PAT 11-SEP-2001

DEFINITION  
Sequence 6 from Patent WO0162928.

ACCESSION  
AX235359

VERSION  
AX235359.1 GI:15593891

KEYWORDS  
Homo sapiens (human)

SOURCE  
Homo sapiens

ORGANISM  
Homo sapiens (human)

REFERENCE  
1 Vernet, C.A., Fernandez, E., Shimkete, R.A., MacDougall, J. and Spaderma, S.K.  
Polypeptides and nucleic acids encoding same  
Patent: WO 0162928-A 6 30-AUG-2001;  
Curagen Corporation (US)

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RESULT 8			
AX235365			
LOCUS	AX235365	3735 bp	DNA
DEFINITION	Sequence 12 from Patent WO0162928.		1linear
ACCESSION	AX235365		
VERSION	AX235365.1	GI:15593897	

SOURCE ORGANISM	Homo sapiens (human)
	Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE	1
AUTHORS	Vernet, C.A., Fernandes, E., Shinkets, R.A., Ma
TITLE	Spaderma, S.K. and nucleic acids encoding same
JOURNAL	Polypeptides and nucleic acids encoding same
	Patent: WO 0162928-A 12 30-AUG-2001;

Curagen Corporation (US)	1. .3735
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Matches 3673; Conservative	0;	Mismatches 38;	Indels 252; Gaps 4;

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Dh 541 ACCGGGGCAGACGGAA CACTTTCA TTGGGACTCCCTA CTGGATGGCT CAGAGGTATC 600  
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Qy 1353 -----GGAATAC 1359  
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 QY 3796 CTGCAAGGGGCTCTTCATGCAACAAAGAGCTCAGAGGCTCAAGTCTCTGTGAGCGGAT 3855  
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 DB 3733 GACAAGGTGTTTTTGGCTCAGTCCGCTCTGGGGGAGCAGAGCCAAAGTTTACTTCAAGT 3792  
 QY 3916 CTGAACCGTAACTGATCATGATGATGGA 3945  
 DB 3793 CTGAACCGTAACTGATCATGATGATGGA 3822

RESULT 10  
 BC052474  
 LOCUS  
 DEFINITION  
 ACCESION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 4842)

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 AUTHORS  
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klusner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Bluetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udell, T.B., Toshiyuki, S., Carninci, P., Prange, C., Kana, S.S., Loguizano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwen, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hult, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shenchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
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 22388257  
 12477932  
 2 (bases 1 to 4842)  
 Strausberg, R.  
 Direct Submission  
 Submitted (15-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Dr. Jim Lin, University of Iowa  
 cDNA Library Preparation: M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)  
 DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant.  
 Web site: <http://genome.uiowa.edu>  
 Contact: [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu); [tom-casavant@uiowa.edu](mailto:tom-casavant@uiowa.edu)  
 Bonaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A., Fishler, K., Keppel, C., Kueba, T., Lebeck, M., Melo, A., Schaefer, K., Scheetz, T., Smith, C., Smith, E., Tack, D., Trout, K., Walters, J., Casavant, T., Soares, M.B.





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QY	3712	ACTTCTGTGGCTATCTGTGCTCCACCAAGATTAATGGGCTGGGTGAAAGAACCAATTGAG	3771
Db	3825	ACTTCTGTGGCTATCTGTGCTCCACCAAGATTAATGGGCTGGGTGAAAGAACCAATTGAG	3884
QY	3772	ATCGGCTCTGTGTGAGACGGGCGCACTTCGACGGGGCTTTCATGCAACAAACGAGCTCAGAG	3831
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RESULT 11
AB035697
LOCUS
DEFINITION Mus musculus mRNA for Mtsnapen/Nks-related Kinase MINK-1,
ACCESSION AB035697
VERSION AB035697.1 GI:6970475
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
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TITLE
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FEATURES
source

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ORIGIN																										
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Beet Local Similarity	86.5%;		Pred. No. 0;																							
Matches 3477;	Conservative 0;		Mismatches 357;		Indels 186;		Gaps 5;																			
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Db	715	ACTGTGGCAGGCGGAAACATTTCAATTGGAAACCCCATCTGGAATGGCTCCAGAGTCAT	774
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QY	667	ATCAACGCAATCGAGATGGCAGAGGGAGACCCCCCTGTGTGTGACATGCAACCCCATGCGA	726
Db	835	ATCAACGCAATTTGAATATGGCAGAGGGAGACCCCCCTGTGTGTGACATGCAACCCCATGCGG	894
QY	727	GCCCTCTTCTCATTTCTCTCGGAAACCTTCGCGCCAGGCTCAAGTCCAAAGATGTGCTAAG	786
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Db	955	AAGTTCACTGACTTCAATGACACGTGTCTCATCAAGACTTACCTGAGTCCGCCACCAAC	1014
QY	847	GAGCAGCTACCTGAAGTTCCCTTCAATCGGGAGCCAGGCCACAGAGCGGCAGGTCCGATC	906
Db	1015	GAACTGTTACTCMAATTCCTCCCTTCAATCCGAGACAGGCCACAGAGCGGCAGGTCCGATC	1074
QY	907	CAGCTTTAAGACCAATTTAGCCGATCCCGGAGAAAGCCGGGTGTGAAAGAGAGACAGAA	966
Db	1075	CAGCTCAAGGACCAATGACCGGCTCCGGAGAAAGCGGGGTGAGAAAGAGAGACAGAG	1134
QY	967	TATGAGTACAGCGGCGCAGAGAGAGAAATGACACCTAGAGAGAAAGGAGACCAAGC	1026
Db	1135	TATGAGTACAGCGGCGCAGTGAAGAGAGAAACACACCTAGAGAGAAAGGAGACCAAGC	1194
QY	1027	TCCATCATGAACGTGCTGCGTGGAGAGTCGACTGACGCGGGAGTTTCTCCGCTCCAGCAG	1086
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QY	1147	CGAGACCCCGAGGCAACATCAACACACTCTGTGCACAGCGGCGAGCGGCGCATGAGAG	1206
Db	1315	CGGACCCCGAGGCAACATCAACACACTCTGTGCACAGCGGCGAGCTGTGATAGAGAG	1374
QY	1207	CAGAAAGAGAGCGCGCGCGGTGGAGAGCAACAGCGCGGAGCGGAGACAGCGAG	1266
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QY	1267	CTGACAGAGAAAGACAGCAGCGCGCGCTGAGAGCATGCAAGGCTCTGCGCGGAGAGAG	1326
Db	1435	CTACAGAGAGAGACACACAGCGGAGATTGGAAAGCATGCAAGCCCTTACAGAGAGAGAA	1494
QY	1337	GAGCGGCGCAGCGCGAGCGGTGAGCAGAAATCAAGCGGAAAGCAGCTGTGAGAGACGCG	1386
Db	1495	GAGAGCGGCGCAGCAGACCGGAGAACAGAAATCAAGCGGAAAGCAGCTGTGAGAGACGCG	1554
QY	1387	CAGTCAGAACGTCTCAGAGGACGTTGACAGCAGAGGACATGCTACCTCAATCCCTGTAG	1446
Db	1555	CAGTCAGAGCGGCTGACAGAAAGCTTGACAGCAGGACAGCGCTTACCTCAAGTCCCTGTAG	1614
QY	1447	CAGCAGCAACAGCAGCAGAGCTTACAGAAACAGCAGCAGCAGCAGC-----TCTGTGCT	1500
Db	1615	CAGCAGCAGCAGCAGCAGCAGCTTCAAGAAAGCAGCAGCAGCAGCAGCAGCAGCATCTGCT	1674
QY	1501	GGGACAGAGAACCCCTGTATCCATTATGTGTGGGGGAGTAAATCCCGCTGACAAACAGCC	1560

Db	1675	GGAGACAGAAAGCCCTGTATCATTTACGGTTCGGGGCTTTAATCTGTGACAAAGCCAGCA	1734
Qy	1561	TGGGCCCCGAGAGTGAAGAGAGAACAGAGATGAACAAGCAGAGAACTCTCTCTTGGCC	1620
Db	1735	TGGGCCCCGAGAGTGAAGAGAGAGCACGGATGAGACAAAGACAGAGAACTCTCTCTTGGCC	1794
Qy	1621	AAGAGCAAGCCAGCAGACACGGGGGCTGAGCCCCCTCCAGCGCTCCCAAGGGCCC	1680
Db	1795	AAGGAAAGCCAAAGAGGTGCGGGGCCAGAACCCCCCACTTCCAGGCTCTCTTAGCCCC	1854
Qy	1681	CCAGAGACCCCTTTCACAGACTCTCTCATGACAGAGCGGTGAGCCCCACAGAGGACCG	1740
Db	1855	CCAGAGACTCTTTCACAGACTCTCTCTTAGCAGAGGCTGTGAGCCCCCAGAGAGACCG	1914
Qy	1741	CACA-----	1744
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Qy	1745	----AGTCCCTGACGAGACACAGCCCAACCCGAAACTGTGCTCCCTCCAGCTCCCATGAC	1800
Db	1975	TCCCAAGTCCCTGACGAGACACGCCCACTTCGAACCTGTGCTCCTTCCAGCTCCCAAGAC	2034
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Db	2035	CCTGACCTGTGCTGTCTCTTACACCCCATGCGCACACAGTCCCGAGAGCTGTATC	2094
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Qy	1978	GCCCTTAACACAGATGGGGGCGAGAGGTTCGGGCAACCCAGGCAAGTCCGTGCAGACT	2037
Db	2215	GCCCTTAACACAGATGGGGGCGAGAGGTTCGGGCAAGTCCGTGTCTGCTGCC-----	2268
Qy	2038	CGCAGCAATTCGGCTGGCAAAATCTATTCGAAAGCGGGCAGAGCGGGGCAACCCCAAG	2097
Db	2269	-----	2268
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Qy	2218	CTCCCCCAGCTGCTCACTGAGCGG-----AACCGGTGGAGGCTCCTCCAAACTG	2271
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Qy	2332	CCAGGCGGGCCCGAGACTTGTGTGCTGAAAGGAGGAGCTCTGAGCGAGGCCCTCGG	2391
Db	2464	CCAGGCGGGCCCGAGACTTGTGTGCTCAAAAGGAGGAGCTCTGATGAGGCCCTTAG	2523
Qy	2362	CCTCCCAAGAGGCGCATGACTCTCGTGTCCAGCGAGAGGTGAAAACAGTGAAGAC	2451
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Db	2584	GAGGAGAGAGAGGCGAATGGGGAGCCGTCAGAGGGGAGCAGAGACACTCTCCGGGGGCGC	2643
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Dp	2644	AGTAGTGGGATACAGACAGCGCTCA	GCAC	CATGTGGTTCATGATGTTGAGAGATATCC	2703	
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Dp	2894	AGCCACTACCTACCTACCTGAGAACAGCAAAAGGTCAAAACCTCCAAACAAAGATGGAGCAGT	2883			
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Dp	2884	GATTACCAAGTCTGTGGGTGTGTAAAGGCCCTGAGAAAGAGCTCAATCCATGATGTTGTG	2943			
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Dp	3004	GGTGGAGAGAGGAGTGTGTGCTGTTGATATCACTGCAAGTTCCATGTGAGAAAGGCTCTGTGGTC	3063			
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Dp	3424	TGCGGGCACTACCGTGTGTGTGAATAACAGCGGATTAAGTTTCTGTGATCGCCTCAAG	3483			
Oy	3352	AGCTTCGTGAGAGTGTATGTCTGTGGGCCCCCAAAACCTTACCAAAATTCATGGCTTTCAAG	3413			
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Dp	3544	TCCTTTTGTGACCTTCCCTCACCGCCTCTTACTGTGTGTGACCTGACAGTATGAGAGGGAGAG	3603			
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Dp	3604	CGGCTCAAGTATCTATGTGCTCCAGTGTGGCTTCATGTCTGTGTGATGTGATTTCTGGG	3663			
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Dp	3664	AAACAGCTATGACATCTATCATCCCTGTATCATATCCAGACCCAGATCACACCCACGCCCATC	3723			
Oy	3592	ATCTTTCTCTCCCAACACCGAGCGGACATGAGATGTCTGTGTGTCTACAGAGAGAGAGGGTGTCT	3653			
Dp	3724	ATCTTTCTCTCCCAACACATGATGAGATGTCTGTGTGTCTATGAAAGATGAGGGGTGTCT	3783			

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OY	3712	ACTTCTGTGGCTTACATCTGCTCCAAACAGTAATGGGCTGGGGGTGAGAAAGCCATTGAG	37711
Db	3844	ACCTCTGTGGCTTACATCTGCTCCAAACAGTAATGGGCTGGGGGTGAGAAAGCCATTGAG	39033
OY	3772	ATCGGCTCTGGAGAGAGGGGCACTCGAAGGGGTCTTATGCAAAACGAGCTCAGAGG	38313
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Db	3964	CTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTGTCTCTGTCGCCGCTCTGGAGGA	40233
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AB041925	4873 bp	mRNA	linear	ROD 22-APR-2000
LOCUS	AB041925	Mus musculus mRNA for GCK family kinase MINK2, complete cds.		
DEFINITION	AB041925			
ACCESSION	AB041925.1	GI:7637418		
VERSION				
KEYWORDS	MINK2.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus. 1 (sites)			
AUTHORS	Dan, I., Watanabe, N.M., Kobayashi, T., Yamashita-Suzuki, K., Fukagaya, Y., Kajikawa, E., Kimura, W.K., Nakashima, T.M., Matsumoto, K., Nishimura-Tsuji, J. and Kusumi, A.			
TITLE	Molecular cloning of MINK, a novel member of mammalian GCK family kinases, which is up-regulated during postnatal mouse cerebral development			
JOURNAL	FEBS Lett. 469 (1), 19-23 (2000)			
MEDLINE	20175403			
PUBMED	10708748			
REFERENCE	2 (bases 1 to 4873)			
AUTHORS	Watanabe, N.M., Dan, I. and Kusumi, A.			
TITLE	Direct Submission			
JOURNAL	Submitted (16-APR-2000) Ippelita Dan, Nagoya University, Dept. of Biological Science, Chikusa-ku, Furo-cho, Nagoya, Aichi 464-8602, Japan (E-mail: dangdbio.nagoya-u.ac.jp, url: http://www.supra.bio.nagoya-u.ac.jp/DNA/, Tel: 81-52-789-2497, Fax: 81-52-789-2968)			
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 Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.  
 Direct Submission  
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 This clone (DKFZp761K18121) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further  
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VERSION	BC011346.1	GI:15030180
KEYWORDS		
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	

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AUTHORS  
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1 (pages 1 to 4381)  
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BOUFFARD, G.G., BLAKESLEY, R.W., TOUNCHMAN, J.W., GREEN, E.D.,  
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BUTERLEI, F.S., KRZYWINSKI, M.I., SKALISA, U., SMILINS, D.E.,  
SCHMERCH, A., SCHEIN, J.E., JONES, S.J., AND MATRA, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
JOURNAL  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE	22388257
PUBMED	12477932
REFERENCE	2 (bases 1 to 4381)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
COMMENT	Contact: MGC help desk

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FEATURES
source
    Email: cgabbs-remail.nih.gov
    Tissue Procurement: Jeffrey Green M.D.
    cDNA Library Preparation: Life Technologies, Inc.
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
    DNA Sequencing by: Baylor College of Medicine Human Genome
    Sequencing Center
    Center code: BCM-HGSC
    Web site: http://www.hgsc.bcm.tmc.edu/cdna/
    Contact: amg@bcm.tmc.edu
    Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louisseed, H.,
    Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
    A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
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            /note="synonyms: B55, MINK, Yek2"
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            <1. .3596

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Query Match	Best Local Similarity	88.2%	Pred. No. 0/	Matches 3180;	Conservative 0;	Mismatches 323;	Indels 102;	Gaps 6;
71.5%; Score 2824.2;	DB 10;	Length 4381;						
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1	ACAAGTGATCATCAGAGATATCAAGGACACAAATGTGCTGCTGACGAGAAATCTCTAAG	60						
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ACCESSION	BD183377			
VERSION	BD183377.1	GI:31875577		
KEYWORDS	JP 2002345492-A/90.			
SOURCE	Homo sapiens (human)			

## REFERENCE

**AUTHORS** Ohara, O., Nagase, T. and Nakajima, D.  
**TITLE** Novel genes and proteins encoded by the genes  
**JOURNAL** Patent: JP 2002345492-A 90 03-DEC-2002;

**COMMENT**

PN JP 2002345492-A/90

## FEATURES

source	1. .3824
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Db	781	AGCAGCGGAGGCTGAGGCGCCCATCCCGAGGAGCTCCCGAGGAGCCCGCAGAGAGAGAGAG	840
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Db	1081	ACCTCTGAGAGAGACTGAGGCGCCAGAGCTCCCAATCCCGAGCTGGGTTCGCGCAGATACAGAG	1140
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Db	1981	GGTGGAGAGGGCACTCGGCTCGACCAAGCTGACAGACGTAACAGACGTGAAGAAAGGTTCTGTGTC	2040
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Db	2041	AACGTGAATCCCAACCAACACCCCGGGCCCAAGTGAAGACCCCTGAAGATCCGGAATCAAG	2100
QY	2992	AAGGATTTCAACTCCGAGATCTCTTGTGCAAGCCTTTGGGGGGTCAACCTGCTGGTGGGC	3051
Db	2101	AAGGATTTCAACTCCGAGATCTCTTGTGCAAGCCTTTGGGGGGTCAACCTGCTGGTGGGC	2160
QY	3052	ACGAGAAACGGGCTGATGTTGCTGGAACGAAAGTGGCAGGGCAAGGTGTATGACTATT	3111
Db	2161	ACGAGAAACGGGCTGATGTTGCTGGAACGAAAGTGGCAGGGCAAGGTGTATGACTATT	2220
QY	3112	GGGCGGCGAGCGCTTCCAGCAGATGATGTGCTGGAGGGGCTCAACCTGCTCATCACATC	3171
Db	2221	GGGCGGCGAGCGCTTCCAGCAGATGATGTGCTGGAGGGGCTCAACCTGCTCATCACATC	2280

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QY 3172 TCAGGAGAAAGGACAAACTGCGGGTGTATTAATCTGTCTCGGCTCCGGAACAAGATTCTG 3231
DB 2281 TCAGGAGAAAGGACAAACTGCGGGTGTATTAATCTGTCTCGGCTCCGGAACAAGATTCTG 2340
QY 3232 CACATATGACCCGAAAGTGGAGAAAGAGCGGGCTGGACCACTGGGGGGAACATGAGAGGCG 3291
DB 2341 CACAAATGACCCGAAAGTGGAGAAAGAGCGGGCTGGACCACTGGGGGGAACATGAGAGGCG 2400
QY 3292 TCGGGGCACTACCGGTGTGAAATACAGCGGATTAAGTTCCTGGTCAATCGCCCTCAAG 3351
DB 2401 TCGGGGCACTACCGGTGTGAAATACAGCGGATTAAGTTCCTGGTCAATCGCCCTCAAG 2460
QY 3352 AGCTCGTGGAGGTGTATGCTGGGCCCCCAAACTTACCAAAATTCATGGGCTTCAAG 3411
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QY 3832 CTCAGTTCTGTGTGAGCGGGAATGACAAAGTGTGTTTGGCTCAGTCCGCTCTGGGGGC 3891
DB 2941 CTCAGTTCTGTGTGAGCGGGAATGACAAAGTGTGTTTGGCTCAGTCCGCTCTGGGGGC 3000
QY 3892 AGCAGCCAAAGTTTACTTCAATGACTGAAACGTAACCTGCATCATGAACTGTGAAAGGGC 3951
DB 3001 AGCAGCCAAAGTTTACTTCAATGACTGAAACGTAACCTGCATCATGAACTGTGAAAGGGC 3060
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Search completed: March 2, 2004, 12:58:38  
Job time : 10015 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 09:47:24 ; Search time 975 Seconds  
(without alignments)  
17215.006 Million cell updates/sec

Title: US-10-029-115-1

Perfect score: 3951  
Sequence: 1 gccctatggcgaccagc.....tcataactggtgaaggc 3951

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

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2: geneseqn19908:.\*  
3: geneseqn20008:.\*  
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6: geneseqn2002as:.\*  
7: geneseqn2003as:.\*  
8: geneseqn2003bs:.\*  
9: geneseqn2003cs:.\*  
10: geneseqn2004as:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3951	100.0	3951	9	ADE34151 Human DNA
2	3792.8	96.0	4033	9	ADE34155 Human DNA
3	3632.2	91.9	3888	6	AA148627 Human ins
4	3632.2	91.7	4133	2	AA240485 Human ZC3
5	3601	91.1	4863	4	AAK52286 Human pol
6	3601	91.1	4863	6	AA148626 Human ins
7	3601	91.1	4863	8	AA161132 Human MIN
8	3583.8	90.7	3912	5	AA17760 Human nov
9	3501.2	88.6	3999	5	AA17759 Human nov
10	3437.2	87.0	4414	9	ADE34153 Human DNA
11	3392.8	85.9	7132	5	AA888207 DNA encod
12	3358.2	85.0	3735	5	AA17762 Human nov
13	3275.6	82.9	3822	5	AA17761 Human nov
14	1502.6	38.0	2345	5	AA240485 Human pan
15	1407.2	35.6	3996	4	AA184940 Nucleotid
16	1391.2	35.2	3972	4	AA184944 Nucleotid
17	1360	34.4	5727	9	AA17765 Human src
18	1358.6	34.4	4083	4	AA184936 Large NIK
19	1358.6	34.4	4083	4	AA184939 Nucleotid
20	1356.8	34.3	4083	6	AA184945 Nucleotid
21	1348.2	34.1	4180	3	AA184946 Human ins
22	1348.2	34.1	4180	3	AA184946 Human pol
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27	1273.4	32.2	3831	4	AA184943 Nucleotid
28	1272	32.2	3897	4	AA184945 Nucleotid
29	1257.4	31.8	3807	4	AA184946 Nucleotid
30	1257.4	31.8	3807	4	AA184946 Nucleotid
31	1240.2	31.4	1964	6	AA184946 Human ins
32	1145.4	29.0	3798	2	AA240483 Human ZC1
33	1094	27.7	3775	5	AA184946 Human ZC1
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35	1065	27.0	3925	5	AA184946 Human ZC1
36	995.2	25.2	3866	3	AA184946 Human ZC1
37	994	25.2	4266	5	AA184946 Human ZC1
38	994	25.2	4266	5	AA184946 Human ZC1
39	891	22.6	3864	5	AA184946 Human ZC1
40	891	22.6	3864	5	AA184946 Human ZC1
41	891	22.6	3864	5	AA184946 Human ZC1
42	871.8	22.1	1131	4	AA184946 Human ZC1
43	871.8	22.1	1131	4	AA184946 Human ZC1
44	818.6	20.7	3786	3	AA240483 Human ZC1
45	790.6	20.0	4969	5	AA184946 Human ZC1

## ALIGNMENTS

RESULT 1	AD34151	standard; DNA; 3951 BP.
XX	AD34151	
AC	AD34151	
DT	29-JAN-2004	(first entry)
XX		
DE	Human DNA encoding misshapen/NIKE-related kinase, Mink3a.	
XX		
KW	Human, misshapen/NIKEs-related kinase; Mink3a; ds; antiinflammatory;	
KW	Immunosuppressive; cytosolic; germinal centre kinase;	
KW	c-UN N-terminal kinase; JNK; extracellular signal response kinase; ERK;	
KW	growth factor induced-ERK activation; proliferation;	
KW	cell proliferation disorder; cell survival;	
KW	intracellular signal transduction; apoptosis; morphological change;	
KW	cell migration; gene therapy; inflammatory disease; autoimmune disease;	
KW	immunodeficiency; cancer.	
OS	Homo sapiens.	
XX		
XX		
FT	Key	Location/Qualifiers
FT	CDS	7...3945
FT		/*tag= a
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XX		
XX	US2003077597-A1.	
XX	24-APR-2003.	
XX	19-OCT-2001; 2001US-00029115.	
XX	19-OCT-2001; 2001US-00029115.	
XX		
PA	(LNUOY) LNUO Y.	
PA	(FUCA/) FU C A.	
PA	(SHEN/) SHEN M.	
XX		
PI	Luo Y, Fu CA, Shen M;	
XX		
XX	WPI; 2003-635076/60.	
DR	P-PSDB; ADE34150.	
XX		
PT	New misshapen/NIKEs-related kinase nucleic acids and proteins useful in	
PT	gene therapy and for treating disorders, e.g. acute and chronic	
PT	inflammatory diseases.	

xx Claim 3: SEQ ID NO 1: 53bp; English.  
ps The invention relates to a recombinant nucleic acid capable of  
xx hybridising to a Human DNA encoding mishapen/NIKs-related kinase  
cc (Mink3a, 3b and 3c, germinal centre kinase proteins) appearing as  
cc ADE34151, ADE34153 and ADE34155, or at least 90% identity to them, or  
cc their complements. Also included are a recombinant polypeptide at least  
cc 95 % sequence identity to Mink3a, 3b or 3c (appearing as ADE34150,  
cc ADE34152 and ADE34154), screening for a candidate bioactive agent capable  
cc of modulating c-JUN N-terminal kinase (JNK) or extracellular signal  
cc response kinase (ERK) phosphorylation or activity, screening for a  
cc candidate bioactive agent capable of modulating growth factor induced-ERK  
cc activation in a mammalian cell, screening for a candidate bioactive agent  
cc capable of modulating proliferation in a mammalian cell, diagnosing a  
cc mammalian cell proliferation disorder, a medicament for treating a  
cc mammalian cell proliferation disorder and screening for a candidate agent  
cc capable of modulating cell survival. The MINK3 (mishapen/NIKs-related  
cc kinase) nucleic acids are useful in the modulation of intracellular  
cc signal transduction, cell proliferation, apoptosis, morphological change  
cc and migration of mammalian cells. MINK3 nucleic acids and proteins are  
cc specifically useful in gene therapy, and for treating, preventing or  
cc diagnosing acute and chronic inflammatory diseases, autoimmune diseases  
cc and diseases characterised by immunodeficiency. The compositions may also  
cc be used to treat MINK3 dysfunction related disorders, e.g. cancer. The  
cc nucleotide sequences may also be used as hybridisation probes, in  
cc chromosome and gene mapping, and in generating antisense RNA and DNA. The  
cc present sequence encodes Mink3a.

xx Sequence 3951 BP; 928 A; 1196 C; 1199 G; 628 T; 0 U; 0 Other;

Query Match 100.0%; Score 3951; DB 9; Length 3951;  
Beet Local Similarity 100.0%; Pred. No. 0;  
Matches 3951; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 CGGAGACCTGCTGGGATCTTTGAGCTTGTGAGGTGTGTGGCAATGGAACCTACGACAG 120  
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DB 421 AGGGGTCTGGCCCATCTCTCATGCTCCACAGAGTGATTCATCGAGACATCAAGGGGAGAT 480  
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DB 481 GTGCTGTGACAGAGAAATGCTGAGGTCAAGCTAGTGAATTTGGGGTGAGTCTCAGCTG 540  
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DB 541 GACCCGACCGTGGGAGAGCGAACAATTTCATTGGGAGCTCCTACTGATGAGCTCCAGAG 600  
QY 601 GTCATGCGCTGTGATGAGAACCTTGATGCACTATGATTAAGAGATGATTTGCTCT 660  
DB 601 GTCATGCGCTGTGATGAGAACCTTGATGCACTATGATTAAGAGATGATTTGCTCT 660  
QY 661 CTAGGAATCAAGCCATGAGATGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
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QY 721 ATGCGAGCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 780  
DB 721 ATGCGAGCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 780  
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DB 1441 CTGACAGCAGCAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1500  
QY 1501 GGGGACAGAGAGCCCTGTAACATTAATGAGTGGGGCATGAATCCGCTGACAAACAGACC 1560  
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RESULT 2  
ADE34155  
ID ADE34155 standard; DNA; 4033 BP.

AC ADE34155;  
DT 29-JAN-2004 (first entry)

XX Human DNA encoding mishapen/NIKs-related kinase, Mink3c.  
XX  
XX Human; mishapen/NIKs-related kinase; Mink3c; de; antiinflammatory;  
XX immunosuppressive; cytoskeletal; germinal centre kinase;  
XX c-UTN N-terminal kinase; JNK; extracellular signal response kinase; ERK;  
XX growth factor induced-ERK activation; proliferation;  
XX cell proliferation disorder; cell survival;  
XX intracellular signal transduction; apoptosis; morphological change;  
XX cell migration; gene therapy; inflammatory disease; autoimmune disease;  
XX immunodeficiency; cancer.

OS Homo sapiens.  
FH Key Location/Qualifiers  
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FT  
XX US2003077597-A1.  
XX  
XX 24-APR-2003.  
XX  
XX 19-OCT-2001; 2001US-00029115.  
XX  
XX 19-OCT-2001; 2001US-00029115.  
XX  
XX (LUDY/) LUD Y.  
XX (FUCA/) FU C A.  
XX (SHEN/) SHEN M.  
XX  
XX Luo Y, Fu CA, Shen M;  
XX  
XX WPI; 2003-635076/60.  
XX P-PSDB; ADE34154.  
XX  
XX New mishapen/NIKs-related kinase nucleic acids and proteins useful in  
XX gene therapy and for treating disorders, e.g. acute and chronic  
XX inflammatory diseases.  
XX  
XX Claim 3; SEQ ID NO 5; 53bp; English.  
XX  
XX The invention relates to a recombinant nucleic acid capable of  
XX hybridizing to a Human DNA encoding mishapen/NIKs-related kinase  
XX (Mink3a, 3b and 3c, germinal centre kinase proteins) appearing as  
XX ADE34151, ADE34153 and ADE34155, or at least 90% identity to them, or  
XX their complements. Also included are a recombinant polypeptide at least  
XX 95 % sequence identity to Mink3a, 3b or 3c (appearing as ADE34150,  
XX ADE34152 and ADE34154), screening for a candidate bioactive agent capable  
XX of modulating c-UTN N-terminal kinase (UNK) or extracellular signal  
XX response kinase (ERK) phosphorylation or activity, screening for a  
XX candidate bioactive agent capable of modulating growth factor induced-ERK  
XX activation in a mammalian cell, screening for a candidate bioactive agent  
XX capable of modulating proliferation in a mammalian cell, diagnosing a  
XX mammalian cell proliferation disorder; a medicament for treating a  
XX mammalian cell proliferation disorder and screening for a candidate agent  
XX capable of modulating cell survival. The MINK3 (mishapen/NIKs-related  
XX kinase) nucleic acids are useful in the modulation of intracellular

CC signal transduction, cell proliferation, apoptosis, morphological change  
CC and migration of mammalian cells. MINK3 nucleic acids and proteins are  
CC specifically useful in gene therapy, and for treating, preventing or  
CC diagnosing acute and chronic inflammatory diseases, autoimmune diseases  
CC and diseases characterised by immunodeficiency. The compositions may also  
CC be used to treat MINK3 dysfunction related disorders, e.g. cancer. The  
CC nucleotide sequences may also be used as hybridisation probes, in  
CC chromosome and gene mapping, and in generating antisense RNA and DNA. The  
CC present sequence encodes Mink3c.  
XX  
XX Sequence 4033 BP, 959 A; 1213 C; 1210 G; 651 T; 0 U; 0 Other;  
SQ

Query Match 96.0%; Score 3792.8; DB 9; Length 4033;  
Best Local Similarity 98.4%; Pred. No. 0;  
Matches 3877; Conservative 0; Mismatches 2; Indels 63; Gaps 2;

OY 64 GACCTGCTGGATCTTTGAGCTGTGAGAGGTGTGCGCAATGGAACCTTACGACAGGTG 123  
DB 95 GACCTGCTGGATCTTTGAGCTGTGAGAGGTGTGCGCAATGGAACCTTACGACAGGTG 154  
OY 124 TACAAAGGTGCGCATGTCAAGACGGGGCAGCTGGTCCATCAAGTCAAGTCAAGTCAAG 183  
DB 155 TACAAAGGTGCGCATGTCAAGACGGGGCAGCTGGTCCATCAAGTCAAGTCAAGTCAAG 214  
OY 184 GAGACGAGAGAGAGAGATCAACAGAGATCAACATGTGAAAGAAAGTACTTCCACAC 243  
DB 215 GAGACGAGAGAGAGAGATCAACAGAGATCAACATGTGAAAGAAAGTACTTCCACAC 274  
OY 244 CGCAACATGCGCCTTACTTACGAGCTTCAATCAAGAAAGACCCCGGGGAAAGATAC 303  
DB 275 CGCAACATGCGCCTTACTTACGAGCTTCAATCAAGAAAGACCCCGGGGAAAGATAC 334  
OY 304 CAGCTGCGCTGGATGAGAGGTTCTGTGCTGCTGTTCACTGATGATGATGATGATGATG 363  
DB 335 CAGCTGCGCTGGATGAGAGGTTCTGTGCTGCTGTTCACTGATGATGATGATGATGATG 394  
OY 364 ACAAAGGACGAGCCCTGAG 423  
DB 395 ACAAAGGACGAGCCCTGAG 454  
OY 424 GGTCTGCGCCATCTTCATATGCCCAAGAGTATCCATGAGACATCAAGAGGGGCAAGATG 483  
DB 455 GGTCTGCGCCATCTTCATATGCCCAAGAGTATCCATGAGACATCAAGAGGGGCAAGATG 514  
OY 484 CTGCTGACAG 543  
DB 515 CTGCTGACAG 574  
OY 544 CGACCGTGGGCGAGACGAGACATCTTCAATGGAGCTCCCTACTGAGATGCTCCAGAGGTC 603  
DB 575 CGACCGTGGGCGAGACGAGACATCTTCAATGGAGCTCCCTACTGAGATGCTCCAGAGGTC 634  
OY 604 ATGCGCTGTATGAGAACCTTGATGCCCACTATGATTTACAGAGTGAATTTTGGTCTCTA 663  
DB 635 ATGCGCTGTATGAGAACCTTGATGCCCACTATGATTTACAGAGTGAATTTTGGTCTCTA 694  
OY 664 GGAATCAGAGCCATGAGATGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 723  
DB 695 GGAATCAGAGCCATGAGATGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 754  
OY 724 CGAGCCCTCTTCTCATCTCTCGAACCCTCGCCAGAGCTCAAGTCCAAAGAGTGTCT 783  
DB 755 CGAGCCCTCTTCTCATCTCTCGAACCCTCGCCAGAGCTCAAGTCCAAAGAGTGTCT 814  
OY 784 AAGAAATTCATTGACTTATTGACATGATCTCATCAAGACTTACTGAGCCGCCACCC 843  
DB 815 AAGAAATTCATTGACTTATTGACATGATCTCATCAAGACTTACTGAGCCGCCACCC 874  
OY 844 ACGAGCAGCTACGAAATTTTCCCTTATCCGGGACGAGCCACGAGAGCGGAGGTCCGC 903  
DB 875 ACGAGCAGCTACGAAATTTTCCCTTATCCGGGACGAGCCACGAGAGCGGAGGTCCGC 934  
OY 904 ATCCAGCTTAAGAGACCAATGACCATCCGGAAGAGAGAGAGAGAGAGAGAGAGAGACA 963



Db 935 ATCCAGCTTTAAGACCACTTGAACGATCCCGGAAGAGCGGGGTGAGAAAGAGAGACA 994  
Qy 964 GAATATGAGTACAGCGGCGAGCGAGAGAGAAATGACAGCCATGAGAGAGAGAGAGCA 1023  
Db 995 GAATATGAGTACAGCGGCGAGCGAGAGAGAAATGACAGCCATGAGAGAGAGAGAGCA 1054  
Qy 1024 AGCTCCATCATGAAAGTGTCTGGAGAGTGAATCTTAACCGCGGAATTTTCTCCGGCTCAG 1083  
Db 1055 AGCTCCATCATGAAAGTGTCTGGAGAGTGAATCTTAACCGCGGAATTTTCTCCGGCTCAG 1114  
Qy 1084 CAGGAATAATTAAGAGCACTCAGAGGCTTTAAACAGCAGCAGCAGCTGACAGAGAGAG 1143  
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Qy 1264 AAGCTGACAGAGAAAGAGAGAGAGCGGCGCTGAGAGACATGCAAGCTCTGCGGCGGAG 1323  
Db 1295 AAGCTGACAGAGAAAGAGAGAGAGCGGCGCTGAGAGACATGCAAGCTCTGCGGCGGAG 1354  
Qy 1324 GAGAGACGCGCGGAG 1383  
Db 1355 GAGAGACGCGCGGAG 1414  
Qy 1384 CGCGAGTACAGAAAGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1443  
Db 1415 CGCGAGTACAGAAAGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1474  
Qy 1444 CAGCAGCAGCAACAGCAG 1503  
Db 1475 CAGCAGCAGCAACAGCAG 1534  
Qy 1504 GACAG 1563  
Db 1535 GACAG 1594  
Qy 1564 GCGCGAG 1623  
Db 1595 GCGCGAG 1654  
Qy 1624 AGCAAG 1683  
Db 1655 AGCAAG 1714  
Qy 1684 GGAAG 1743  
Db 1715 GGAAG 1774  
Qy 1744 A----- 1744  
Db 1775 AAG 1834  
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Db 1835 CAGTCCCTGAG 1894  
Qy 1804 GAGCCTGAG 1863  
Db 1895 GAGCCTGAG 1954  
Qy 1864 AATTCAAG 1923  
Db 1955 AATTCAAG 2014  
Qy 1924 CCAAGTAAAG 1983

Db 2015 CCAAGTAAAG 2074  
Qy 1984 AACACAG 2043  
Db 2075 AACACAG 2134  
Qy 2044 AACACAG 2103  
Db 2135 AACACAG 2194  
Qy 2104 GAG 2163  
Db 2195 GAG 2254  
Qy 2164 AGCGAG 2223  
Db 2255 AGCGAG 2314  
Qy 2224 CAG 2283  
Db 2315 CAG 2374  
Qy 2284 GTGCTCTCCCTGGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2343  
Db 2375 GTGCTCTCCCTGGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2434  
Qy 2344 GCAAGCTTTGT 2403  
Db 2435 GCAAGCTTTGT 2494  
Qy 2404 GCAAGCTTTGT 2463  
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Db 2555 GCGAG 2611  
Qy 2524 ACAG 2583  
Db 2612 ACAG 2671  
Qy 2584 CCATACAG 2643  
Db 2672 CCATACAG 2731  
Qy 2644 CATGCTGACAGCAATGGGTACACAACTGTGCTGACAGCTGCTGACAGCTGCTGACAG 2703  
Db 2732 CATGCTGACAGCAATGGGTACACAACTGTGCTGACAGCTGCTGACAGCTGCTGACAG 2791  
Qy 2704 ACCGAG 2763  
Db 2792 ACCGAG 2851  
Qy 2764 GGTGGGCTGTAAAG 2823  
Db 2852 GGTGGGCTGTAAAG 2911  
Qy 2824 TACAG 2883  
Db 2912 TACAG 2971  
Qy 2884 ACTGGGCTGAG 2943  
Db 2972 ACTGGGCTGAG 3031  
Qy 2944 ACCAAG 3003  
Db 3032 ACCAAG 3091  
Qy 3004 TCCGAGATCTCTGT 3063  
Db 3092 TCCGAGATCTCTGT 3151

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QY 3064 CTGATCTTGTGGAACCGAGTGGGCAAGGTTATGACTCATTTGGGGGGAGCGC 3123
DB 3152 CTGATGTTCTGACGAAAGTGGGCAAGGTTATGACTCATTTGGGGGGAGCGC 3211
QY 3124 TTCAGCAGATGATGCTGAGAGGGGCTCAACCTGCTCATCCATCTCAGGGAAGAAG 3183
DB 3212 TTCAGCAGATGATGATGCTGAGAGGGGCTCAACCTGCTCATCCATCTCAGGGAAGAAG 3271
QY 3184 AACAACTGCGGGTGTATTACTGTCTGCTCGGAAACAAGTTTGTGCAATGACCA 3243
DB 3272 AACAACTGCGGGTGTATTACTGTCTGCTCGGAAACAAGTTTGTGCAATGACCA 3331
QY 3244 GAAAGTGAAGAAGAGGAGGCTGAGACCAAGTGGGGGAGATGAGAGGGCTGCGGGAGCTAC 3303
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QY 3304 CGTGTGTGTAATACAGAGCGATTAAAGTCTGTGTCATCGCCCTCAAGAGCTCCGTGAG 3363
DB 3392 CGTGTGTGTAATACAGAGCGATTAAAGTCTGTGTCATCGCCCTCAAGAGCTCCGTGAG 3451
QY 3364 GTGTATGCTGGGCCCCCAACCCCTACCAAAATTCATGAGCCTTCAAGTCTTTGCGAC 3423
DB 3452 GTGTATGCTGGGCCCCCAACCCCTACCAAAATTCATGAGCCTTCAAGTCTTTGCGAC 3511
QY 3424 CTCGCCCAAGGCTCTGCTGCTGCTGCACTGAGAGAGAGGGGGGAGGGGCTCAAGGTC 3483
DB 3512 CTCGCCCAAGGCTCTGCTGCTGCTGCACTGAGAGAGAGGGGGGAGGGGCTCAAGGTC 3571
QY 3484 ATCTATGCTCCAGTCTGCTGCTTCCATGCTGTGATGTGACTCGGAGGAACAGTATGAC 3543
DB 3572 ATCTATGCTCCAGTCTGCTGCTTCCATGCTGTGATGTGACTCGGAGGAACAGTATGAC 3631
QY 3544 ATCTATGCTCCAGTCTGCTGCTTCCATGCTGTGATGTGACTCGGAGGAACAGTATGAC 3603
DB 3632 ATCTATGCTCCAGTCTGCTGCTTCCATGCTGTGATGTGACTCGGAGGAACAGTATGAC 3691
QY 3604 AACACCGAGGAGTGGAGATGCTGCTGCTGCTGCAAGAGAGAGGGGCTTACAGTCAACAG 3663
DB 3692 AACACCGAGGAGTGGAGATGCTGCTGCTGCTGCAAGAGAGAGGGGCTTACAGTCAACAG 3751
QY 3664 TACGGGCGCATCTTAAAGATGTGTGCTGCTGCAAGTGGGGGAGATGCTTCTGTGGCC 3723
DB 3752 TACGGGCGCATCTTAAAGATGTGTGCTGCTGCAAGTGGGGGAGATGCTTCTGTGGCC 3811
QY 3724 TACATCTGCTCCAAACAGATATATGAGCTGGGGTGAAGAACCTTGAATCCGCTTGTG 3783
DB 3812 TACATCTGCTCCAAACAGATATATGAGCTGGGGTGAAGAACCTTGAATCCGCTTGTG 3871
QY 3784 GAGAGCGGCACTGCAAGGGGCTTCAATGCAAAAGAGTCAAGGCTCAAGTCTCTG 3843
DB 3872 GAGAGCGGCACTGCAAGGGGCTTCAATGCAAAAGAGTCAAGGCTCAAGTCTCTG 3931
QY 3844 TGTGAGCGGATGACAAAGTGTGTTTGTGCTCAGTCCGCTTGTGGGGGAGCAAGGTT 3903
DB 3932 TGTGAGCGGATGACAAAGTGTGTTTGTGCTCAGTCCGCTTGTGGGGGAGCAAGGTT 3991
QY 3904 TACTTCATGACTCTGAACCGTAACTGATCATGAACTGCTGTA 3945
DB 3992 TACTTCATGACTCTGAACCGTAACTGATCATGAACTGCTGTA 4033

RESULT 3
AAL48627
ID AAL48627 standard; cDNA; 3888 BP.
XX
AC AAL48627;
XX
DT 11-OCT-2002 (first entry)
XX
DE Human insulin receptor signaling modifier cDNA SEQ ID NO: 37.
XX
KW Human; insulin receptor signaling; insulin receptor signaling modifier;
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KW ISM; diabetes; metabolic syndrome; antidiabetic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO20025664-A2.
XX
PD 18-JUL-2002.
XX
PF 11-JAN-2002; 2002MO-US001048.
XX
PR 12-JAN-2001; 2001US-0261226P.
PR 12-JAN-2001; 2001US-0261303P.
PR 12-JAN-2001; 2001US-0261304P.
PR 12-JAN-2001; 2001US-0261335P.
PR 12-JAN-2001; 2001US-0261336P.
PR 12-JAN-2001; 2001US-0261361P.
PR 12-JAN-2001; 2001US-0261456P.
PR 12-JAN-2001; 2001US-0261457P.
PR 12-JAN-2001; 2001US-0261458P.
PR 12-JAN-2001; 2001US-0261459P.
PR 12-JAN-2001; 2001US-0261461P.
PR 12-JAN-2001; 2001US-0261518P.
PR 12-JAN-2001; 2001US-0261531P.
PR 12-JAN-2001; 2001US-0261532P.
PR 12-JAN-2001; 2001US-0261589P.
PR 12-JAN-2001; 2001US-0261590P.
PR 12-JAN-2001; 2001US-0261694P.
PR 12-JAN-2001; 2001US-0261695P.
PR 12-JAN-2001; 2001US-0261697P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Seidel-Dugan C, Ferguson KC, Kidd T;
XX
DX WPI; 2002-599664/64.
XX
DR P-PSDB; AAO18508.
XX
PT Identifying an insulin receptor signaling modulator, useful as drug
PT targets for treating diabetes or metabolic disorders, comprises
PT contacting an assay system comprising insulin receptor signaling
PT modifiers with a test agent.
XX
PS Disclosure; Page 118-120; 232pp; English.
XX
CC The present invention relates to a method of identifying a candidate
CC insulin receptor (INR) signaling modulating agent, involving contacting
CC an assay system comprising an insulin receptor signaling modifier (ISM)
CC polypeptide or nucleic acid with a test agent, and detecting a test agent
CC -biased activity of the assay system. The method is useful for
CC identifying candidate INR signaling modulating agents. ISM genes may be
CC used as drug targets for treatment of disorders related to INR signaling
CC such as diabetes or metabolic syndrome. ISM nucleic acids and
CC polypeptides are useful for identifying and testing agents that modulate
CC ISM function and for other applications related to the involvement of ISM
CC in INR signaling, and for identifying subjects having a predisposition to
CC such diseases associated with INR signaling. The present sequence is an
CC ISM coding sequence described in the exemplification of the invention
XX
SQ Sequence 3888 BP; 917 A; 1168 C; 1182 G; 621 T; 0 U; 0 Other;
XX

Query Match 91.9%; Score 3632.2; DB 6; Length 3888;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 3825; Conservative 0; Mismatches 3; Indels 171; Gaps 2;

QY 7 ATGGCGAACCCAGCCCCCGCCGAGCTGAGCAATGACCTGTCCGCCCTGGCGGAGC 66
DB 1 ATGGCGAACCCAGCCCCCGCCGAGCTGAGCAATGACCTGTCCGCCCTGGCGGAGC 60
QY CCTGCTGGGATCTTTGAGCTTGTGAGGTGCTGGGCAATGAACTACGAGAGGTATC 126
DB 61 CCTGCTGGGATCTTTGAGCTTGTGAGGTGCTGGGCAATGAACTACGAGAGGTATC 120
QY 127 AAGGTCGGCATGTCAAGACGAGGAGCTGTGCTGCATCAAGTCAATGATGTCAAGAG 186
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Db 121 AAGGTCGGCATGTCTAGAACGGGCGAGTGGCTGGCATCAAGCTCATGATGTACAGGAG 180
Qy 187 GACGAGGAGGAGGATCTAAACAGAGATCAACATGCTGAAAAGTACTCTCACCACGGC 246
Db 181 GACGAGGAGGAGGATCTAAACAGAGATCAACATGCTGAAAAGTACTCTCACCACGGC 240
Qy 247 AACATGCCCACTTACTAGAGCCTTCTATCAAGAAAGAGCCCCCGGGAAGAGATGACGAG 306
Db 241 AACATGCCCACTTACTAGAGCCTTCTATCAAGAAAGAGCCCCCGGGAAGAGATGACGAG 300
Qy 307 CTCTGGCTGTGATGAGAGTTCTGTGAGTCTGTTCACTGATCACTGCTGTAAGAACACA 366
Db 301 CTCTGGCTGTGATGAGAGTTCTGTGAGTCTGTTCACTGATCACTGCTGTAAGAACACA 360
Qy 367 AAGAGCAACGCCCTTGAAGAGAGACTGATGCTATATCTGACAGGAGATCTTCAGGGGT 426
Db 361 AAGAGCAACGCCCTTGAAGAGAGACTGATGCTATATCTGACAGGAGATCTTCAGGGGT 420
Qy 427 CTGGCCCATCTCCATGCCCCAAGAGTATCATGAGACATCAAGGGGCAAGATGTGCTG 486
Db 421 CTGGCCCATCTCCATGCCCCAAGAGTATCATGAGACATCAAGGGGCAAGATGTGCTG 480
Qy 487 CTGACAGAGATGCTGAGGTCAGAGTATGATTTTGGGGTGAAGTCTCAGCTGACCGC 546
Db 481 CTGACAGAGATGCTGAGGTCAGAGTATGATTTTGGGGTGAAGTCTCAGCTGACCGC 540
Qy 547 ACCGTGGGCAAGCGGAACATTTTCAATGGGACTCCCTACTGAGATGCTCCAGAGTATC 606
Db 541 ACCGTGGGCAAGCGGAACATTTTCAATGGGACTCCCTACTGAGATGCTCCAGAGTATC 600
Qy 607 GCCTGTGATGAAACCTGATGCGCACTTATGATTAAGAGATGATATTGGTCTCTAGGA 666
Db 601 GCCTGTGATGAAACCTGATGCGCACTTATGATTAAGAGATGATATTGGTCTCTAGGA 660
Qy 667 ATCAAGCAATCGAGATGCGAGAGGAGCCCCCTGTGTGATGATCAAGCCCATGCGA 726
Db 661 ATCAAGCAATCGAGATGCGAGAGGAGCCCCCTGTGTGATGATCAAGCCCATGCGA 720
Qy 727 GCCCTCTTCTCATTTCTCGGAACCTCCGCCAGAGCTCAAGTCCAAAGATGTGTTAAG 786
Db 721 GCCCTCTTCTCATTTCTCGGAACCTCCGCCAGAGCTCAAGTCCAAAGATGTGTTAAG 780
Qy 787 AAGTTCAATGACTTATTTGACATGTCTCATCAAGATTACCTGAGCCGCCACCCACG 846
Db 781 AAGTTCAATGACTTATTTGACATGTCTCATCAAGATTACCTGAGCCGCCACCCACG 840
Qy 847 GAGCAGCTACGAGTTTCCCTTATCCGGGACAGGCCACGAGCGGCAAGTCCGATC 906
Db 841 GAGCAGCTACGAGTTTCCCTTATCCGGGACAGGCCACGAGCGGCAAGTCCGATC 900
Qy 907 CAGCTTAAGGACCAATTGACCGATCCGGAAGAGCGGGGTGAGAAAGAGAGACAGAA 966
Db 901 CAGCTTAAGGACCAATTGACCGATCCGGAAGAGCGGGGTGAGAAAGAGAGACAGAA 960
Qy 967 TATGATGACAGCGGACGAGAGAGAGAGATGACAGCCTGAGAGAGAGAGACCAAGC 1026
Db 961 TATGATGACAGCGGACGAGAGAGAGAGATGACAGCCTGAGAGAGAGAGACCAAGC 1020
Qy 1027 TCCATCATGAACTGCGCTGAGAGTTCATCTAGCCGGGAGTTTCCCGGCTCAGAG 1086
Db 1021 TCCATCATGAACTGCGCTGAGAGTTCATCTAGCCGGGAGTTTCCCGGCTCAGAG 1080
Qy 1087 GAAATATAGAGCACTCAGAGGCTTTAAACAGAGACAGAGCTGACAGACAGAG 1146
Db 1081 GAAATATAGAGCACTCAGAGGCTTTAAACAGAGACAGAGCTGACAGACAGAG 1140
Qy 1147 CGAGACCCCGAGGACACATCAAAACCTGCTGACACAGCGGCAAGCGGCTATGAGAG 1206
Db 1141 CGAGACCCCGAGGACACATCAAAACCTGCTGACACAGCGGCAAGCGGCTATGAGAG 1200
Qy 1207 CAGAGAGAGAGCGGCGCGGCTGAGAGAGCAAGCGGCGGAGCGGAGCAAGCGAG 1266

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Db 1201 CAGAGAGAGAGCGGCGCGGCTGAGAGAGCAAGCGGCGGAGCGGAGACAGCGAG 1260
Qy 1267 CTGACAGAGAGAGAGAGAGAGCGGCGGCTGAGAGACATGACAGGCTTCCGGCGGAGAG 1326
Db 1261 CTGACAGAGAGAGAGAGAGAGCGGCGGCTGAGAGACATGACAGGCTTCCGGCGGAGAG 1320
Qy 1327 GAGCGGCGGAGAGGCGTGAACAGAAATCAAGCGGAGAGAGAGAGAGAGAGAGAG 1386
Db 1321 GAGCGGCGGAGAGGCGGAGCGGAGAGAGAAATCAAGCGGAGAGAGAGAGAGAGAG 1380
Qy 1387 CAGTCAAGAGCTCTCAAGAGCAGCTGACAGAGAGAGAGAGAGAGAGAGAGAG 1446
Db 1381 CAGTCAAGAGCTCTCAAGAGCAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Qy 1447 CAGAGCAACAGAGAGAGAGAGCTTCAAGAAACAGAGAGAGAGAGAGAGAGAGAG 1506
Db 1441 CAGAGCAACAGAGAGAGAGAGCTTCAAGAAACAGAGAGAGAGAGAGAGAGAGAG 1500
Qy 1507 AGGAAGCCCTGTACATTAATGTCGGGGCATGAATCCCGTGAACAACAGAGCTGAGGC 1566
Db 1501 AGGAAGCCCTGTACATTAATGTCGGGGCATGAATCCCGTGAACAACAGAGCTGAGGC 1560
Qy 1567 CGAGAGGTAGAGAGAGAGAGAGAGATGAACAAGAGAGAGAGAGAGAGAGAGAG 1626
Db 1561 CGAGAGGTAGAGAGAGAGAGAGAGATGAACAAGAGAGAGAGAGAGAGAGAGAG 1620
Qy 1627 AAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1686
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Qy 1745 -----AG 1746
Db 1741 AGCCTGGTGGAGACAGGGGTCCTCAAGAGCATATGACAGAGCTTACCCGATCCAG 1800
Qy 1747 TCCCTGAGAGACAGAGCCACCCGAAACCTGAGTGTCTTCCGAGCTTCCATGACCCGAG 1806
Db 1801 TCCCTGAGAGACAGAGCCACCCGAAACCTGAGTGTCTTCCGAGCTTCCATGACCCGAG 1860
Qy 1807 CCGGCAATCCCGGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1866
Db 1861 CCGGCAATCCCGGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Qy 1867 TCAAGCCCACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1926
Db 1921 TCAAGCCCACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Qy 1927 GATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1986
Db 1981 GATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
Qy 1987 ACCAGTGGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2046
Db 2041 ACCAGTGGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2085
Qy 2047 TCGGCTGGCAAAATCTATCTGCAAAAGCGGAGAGAGAGAGAGAGAGAGAGAG 2106
Db 2086 ----- 2085
Qy 2107 CCCCCTGCTAGCCCCCTGAGCGGCGGCAAGGCTTATGTAACCCCGAGCTTCAAGAGAGAG 2166
Db 2086 -----AGTAAACCCGAGCTTCAAGAGAGAGAG 2109
Qy 2167 GAGCCTGGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2226
Db 2110 GAGCCTGGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2169
Qy 2227 GCTGGCTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2286
Db 2170 GCTGGCTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2229

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QY 2287 CTCTCCCTGGGAATTAAGCCCAAGCCCGACACACCGCTCAAGGCGCAAGCGCGCCCA 2346  
 DB 2230 CTCTCCCTGGGAATTAAGCCCAAGCCCGACACACCGCTCAAGGCGCAAGCGCGCCCA 2289  
 QY 2347 GACTTTGTTGCTGTAAGAGCGGACTGTGACGAGGCGCCCTCGGCTTCCCAAGAGCC 2406  
 DB 2230 GACTTTGTTGCTGTAAGAGCGGACTGTGACGAGGCGCCCTCGGCTTCCCAAGAGCC 2349  
 QY 2407 ATGACTACTGCTGCTCCAGCGAGAGGTGGAACAATGAGAGACAGAGAGAGAGC 2466  
 DB 2350 ATGACTACTGCTGCTCCAGCGAGAGGTGGAACAATGAGAGACAGAGAGAGAGC 2409  
 QY 2467 GAAGCGCGGCGCAGAGAGAGAGAGATACCCCTGGGCGCGAGCGATGGGATACA 2526  
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 QY 2527 GACACGCTGACGACCATGTGTGTCACGACGTGAGAGATACCGGAGCCGAGCCCA 2586  
 DB 2470 GACACGCTGACGACCATGTGTGTCACGACGTGAGAGATACCGGAGCCGAGCCCA 2529  
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 DB 2530 TACGGGGGGGCGACATGTGTGTCACGACCGCTGAAAGAGAGCGAACTGTGCTCAT 2589  
 QY 2647 GCTGACAGCAATGGGTACACAAACCTGCTGACGTGTCAGCCGACCTCAACCCACC 2706  
 DB 2590 GCTGACAGCAATGGGTACACAAACCTGCTGACGTGTCAGCCGACCTCAACCCACC 2649  
 QY 2707 GAGAA CAGCAAGAGCCCAAGCCCTCTGAGAGATGGAGTGTGTACTACAGTCTGCT 2766  
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 QY 3007 GAGATCCTCTGTCAGGCGCTTTGGGGGGGTCAACCTGCTGTGGGACGAGAAACGGGCTG 3066  
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 QY 3067 ATGTGTCTGACCGAAGTGGGCAAGGAGTGTATGACTCATTTGGGCGGACGCTTTC 3126  
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 QY 3487 TATGCTCTCAGTGTGCTTCCATGCTGTGTGTGTGATGTGACTGTGGGAAACAGCTATGACATC 3546  
 DB 3430 TATGCTCTCAGTGTGCTTCCATGCTGTGTGTGTGATGTGACTGTGGGAAACAGCTATGACATC 3489  
 QY 3547 TACATCTCTGTGACATTCAGAGCCAGATCACGCCCTTCCATCATCTTCTCCCAAC 3606  
 DB 3490 TACATCTCTGTGACATTCAGAGCCAGATCACGCCCTTCCATCATCTTCTCCCAAC 3549  
 QY 3607 ACCGACGCAATGAGATGTCTGTGCTACAGAGACGAGGGGTGTCTAGTCAACACGTAC 3666  
 DB 3550 ACCGACGCAATGAGATGTCTGTGCTACAGAGACGAGGGGTGTCTAGTCAACACGTAC 3609  
 QY 3667 GGGCGCATCATTAAGAGATGTGTGCTGACGTGGGGGAGATGCTACTTGTGGCTTAC 3726  
 DB 3610 GGGCGCATCATTAAGAGATGTGTGCTGACGTGGGGGAGATGCTACTTGTGGCTTAC 3669  
 QY 3727 ATCTGCTCAACACAGATTAATGGGCTGGGTGAGAAAGCCATTGAGATCCGCTGTGTAG 3786  
 DB 3670 ATCTGCTCAACACAGATTAATGGGCTGGGTGAGAAAGCCATTGAGATCCGCTGTGTAG 3729  
 QY 3787 ACGGCGCACCTGACAGGGGCTCTGATGACAAAGAGCTGAGAGCTCAAGTTCCTGTGT 3846  
 DB 3730 ACGGCGCACCTGACAGGGGCTCTGATGACAAAGAGCTGAGAGCTCAAGTTCCTGTGT 3789  
 QY 3847 GAGCGGAATGACAAAGTGTGTTTGTGCTCACTGCTGCTGGGGGACAGCAAGCAATTAC 3906  
 DB 3790 GAGCGGAATGACAAAGTGTGTTTGTGCTCACTGCTGCTGGGGGACAGCAAGCAATTAC 3849  
 QY 3907 TTCAATGACTGTGAACCGTAACTGCAATCAATGAACTGTGTA 3945  
 DB 3850 TTCAATGACTGTGAACCGTAACTGCAATCAATGAACTGTGTA 3888

RESULT 4  
 AA240485  
 ID AA240485 standard; DNA; 4133 BP.  
 XX  
 AC AA240485;  
 XX  
 DT 18-FEB-2000 (first entry)  
 XX  
 DE Human ZC3 DNA.  
 XX  
 KW Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;  
 KW antipsoriatic; antiarteriosclerotic; antidiabetic; immunosuppressive;  
 KW neuropeptide; cardiac; cerebroprotective; cytotatic; antidiabetic;  
 KW vulnery; STE20; protein kinase; STLK2; STLK4; STLK5; STLK6; STLK7;  
 KW ZC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU3; GEX2; PAK4; PAK5; antagolist;  
 KW antibody; gene therapy; rheumatoid arthritis; arteriosclerosis; ashma;  
 KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;  
 KW thinitis; autoimmunity; organ transplantation; multiple sclerosis;  
 KW myocardial infarction; cardiovascular disease; stroke; renal failure;  
 KW oxidative stress-related neurodegenerative disorder; Parkinson's disease;  
 KW amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;  
 KW ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;  
 KW mesangial disorder; growth regulation; wound healing; T cell activation;  
 KW immunosuppressant; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO9953036-A2.  
 XX  
 PD 21-OCT-1999.  
 XX  
 PF 13-APR-1999; 99WO-US008150.





Db 1562 GAACAAGATGAACAAGCAGACAGAACTCTCCCTGGCAAGAGCAAGCAGAGCAGCAG 1621  
Qy 1643 GGCCTGAGGCCCCCAATCCCCCAAGGCTCCCCAAGGGCCCCCAAGAACCCCTTTCCCAAGATC 1702  
Db 1622 GGCCTGAGGCCCCCAATCCCCCAAGGCTCCCCAAGGGCCCCCAAGAACCCCTTTCCCAAGATC 1681  
Qy 1703 CTCCTATGAGAGGCGGTGAGAGCCCAAGAGGAGCCGCA----- 1744  
Db 1682 CTCCTATGAGAGGCGGTGAGAGCCCAAGAGGAGCCGCAAGAACCTGTTGGCAAC 1741  
Qy 1745 -----AGTCCCTGCAAGACAC 1762  
Db 1742 GGGTCCCACTGAAGCCATATGAGCACTGTACCCCGATCCCGAGTCCCTGCAAGAGCAC 1801  
Qy 1763 CCACCCGGAACCTGGGCTGCTTCCCGACCTCCCATAGACCCCGACCTGGCAATCCCGGAC 1822  
Db 1802 CCACCCGGAACCTGGGCTGCTTCCCGACCTCCCATAGACCCCGACCTGGCAATCCCGGAC 1861  
Qy 1823 CCACTGCAAGCCCAAGTGCCTCGAGAGAGTGTCAATCCCGCAAAATTGAGACCCCACTCTG 1882  
Db 1862 CCACTGCAAGCCCAAGTGCCTCGAGAGAGTGTCAATCCCGCAAAATTGAGACCCCACTCTG 1921  
Qy 1883 AAGGACCTGAGCCCAAGCCCAAGTGCCTCGAGAGAGTGTCAATCCCGCAAAATTGAGACCCCA 1942  
Db 1922 AAGGACCTGAGCCCAAGCCCAAGTGCCTCGAGAGAGTGTCAATCCCGCAAAATTGAGACCCCA 1981  
Qy 1943 CCAAGGTGCTCAGAGAGACTATATATGAGCACTGAGCCCTTAAACACATGAGAGCCGAG 2002  
Db 1982 CCAAGGTGCTCAGAGAGACTATATATGAGCACTGAGCCCTTAAACACATGAGAGCCGAG 2041  
Qy 2003 GGTGCCGAGCAGCCAGGAGAGTCCGTGAGCACTGAGCAAACTCGCTGGCAATCT 2062  
Db 2042 GGTGCCGAGCAGCCAGGAGAGTCCGTGAGCACTGAGCAAACTCGCTGGCAATCT 2101  
Qy 2063 ATCTGCAAAAGCGGAGCAAGCGGAGCACTCCCAAGCTTCAGAGGCCCTGCTCAGCCCC 2122  
Db 2102 ATCTGCAAAAGCGGAGCAAGCGGAGCACTCCCAAGCTTCAGAGGCCCTGCTCAGCCCC 2161  
Qy 2123 CTGGCCGAGCAGCCAGGAGAGTCTGATTAACCCGACCTCAGAGAGAGAGCCCTGGGTGGAAAC 2182  
Db 2162 CTGGCCGAGCAGCCAGGAGAGTCTGATTAACCCGACCTCAGAGAGAGAGCCCTGGGTGGAAAC 2221  
Qy 2183 GCTCGGACAGCGTCTTCCAGAGCTCTCAGAGGCACTCCCGCAGCTGAGCTCACTGAGAC 2242  
Db 2222 GCTCGGACAGCGTCTTCCAGAGCTCTCAGAGGCACTCCCGCAGCTGAGCTCACTGAGAC 2281  
Qy 2243 GGAACCGGCTGGAGAGCTCTTCCAACTGAGACAGCTCCCTGTGTCTCTCCCTGGGAATA 2302  
Db 2282 GGAACCGGCTGGAGAGCTCTTCCAACTGAGACAGCTCCCTGTGTCTCTCCCTGGGAATA 2341  
Qy 2303 AAGCCAGAGCCAGCAGCAGCCGCTCAAGCCGAGCCGAGCCGAGCCTTGTGTGTGCTA 2362  
Db 2342 AAGCCAGAGCCAGCAGCAGCCGCTCAAGCCGAGCCGAGCCGAGCCTTGTGTGTGCTA 2401  
Qy 2363 AAGAGGAGACTTGAAGAGAGCCCTCGAGCTTCCCAAGAGCCATGACTACTGCTGT 2422  
Db 2402 AAGAGGAGACTTGAAGAGAGCCCTCGAGCTTCCCAAGAGCCATGACTACTGCTGT 2461  
Qy 2423 CCAAGCAGAGAGTGAAGAGAGCAGTGAAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAG 2482  
Db 2462 CCAAGCAGAGAGTGAAGAGAGCAGTGAAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAG 2521  
Qy 2483 AAGGAGAGAGAGATTAACCTTGGGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2542  
Db 2522 AAGGAGAGAGAGATTAACCTTGGGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2578  
Qy 2543 TGGTGGTTCAGAGAGTGAAGAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2602  
Db 2579 TGGTGGTTCAGAGAGTGAAGAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2638  
Qy 2603 TGGTGGTTCAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2662

Db 2639 TGGTGGTTCAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2698  
Qy 2663 ACACAAACCTGCTGAGAGTGTCCAGCCAGCAGCTCAACCCAGAGAGAGAGAGAGAGAG 2722  
Db 2699 ACACAAACCTGCTGAGAGTGTCCAGCCAGCAGCTCAACCCAGAGAGAGAGAGAGAGAG 2758  
Qy 2723 AAAGCCACCTCGAAG 2782  
Db 2759 AAAGCCACCTCGAAG 2818  
Qy 2783 CTGGAGAGAGCTGCTCAAGAGTGTGTGAGATCTAGAGAGATCTAGAGAGAGAGAGAG 2842  
Db 2819 CTGGAGAGAGCTGCTCAAGAGTGTGTGAGATCTAGAGAGAGATCTAGAGAGAGAGAG 2878  
Qy 2843 GGAAGAGATCCCATCAAGAGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2902  
Db 2879 GGAAGAGATCCCATCAAGAGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2938  
Qy 2903 AGTACAGAGTGAAGAGAGAGAGTGTGTGTCAAGTGAATCCCAACAGAGAGAGAGAGAG 2962  
Db 2939 AGTACAGAGTGAAGAGAGAGAGTGTGTGTCAAGTGAATCCCAACAGAGAGAGAGAGAG 2998  
Qy 2963 GTGAGAGCTGTGAGATCCGAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3022  
Db 2999 GTGAGAGCTGTGAGATCCGAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3058  
Qy 3023 CCTTTGGAGAGAGTCAACTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3082  
Db 3059 CCTTTGGAGAGAGTCAACTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3118  
Qy 3083 GTGGAGAGAGAGAGTGAATGAGACTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3142  
Db 3119 GTGGAGAGAGAGAGTGAATGAGACTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3178  
Qy 3143 TGGAGAGAGTCAACTGCTCAATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3202  
Db 3179 TGGAGAGAGTCAACTGCTCAATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3238  
Qy 3203 ACTGTGCTGAGCTCGAG 3262  
Db 3239 ACTGTGCTGAGCTCGAG 3298  
Qy 3263 GCTGAGACAGCGTGGAG 3322  
Db 3299 GCTGAGACAGCGTGGAG 3358  
Qy 3323 GGAATTAAGTCTGTGATTCGAG 3382  
Db 3359 GGAATTAAGTCTGTGATTCGAG 3418  
Qy 3383 AACCTTACAGAAATTCATGAGCTTCAAGTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 3442  
Db 3419 AACCTTACAGAAATTCATGAGCTTCAAGTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 3478  
Qy 3443 TGGTGAACCTGACAGTGAAG 3502  
Db 3479 TGGTGAACCTGACAGTGAAG 3538  
Qy 3503 GCTTCAATGCTGTGATGTGAG 3562  
Db 3539 GCTTCAATGCTGTGATGTGAG 3598  
Qy 3563 TCCAGAGCAGATCAAG 3622  
Db 3599 TCCAGAGCAGATCAAG 3658  
Qy 3623 TGGTGTGTGCTGAG 3682  
Db 3659 TGGTGTGTGCTGAG 3718  
Qy 3683 ATGTGTGTGCTGAG 3742  
Db 3719 ATGTGTGTGCTGAG 3778





Db 1085 CAGCTTAAAGACCAATTGACCCGGAAGAACGGGGGTGAGAAAAGAGAGACAGA 1144  
Qy 967 TATGAGTACAGCGGAGCGAGGAGGAAGATGACAGCCATTGAGAGAAAGAGACCAAGC 1026  
Db 1145 TATGAGTACAGCGGAGCGAGGAGGAAGATGACAGCCATTGAGAGAAAGAGACCAAGC 1204  
Qy 1027 TCCATCATGAAAGTGCCTGGAGAGTGCATCTACGCGGGAATTTCTCCGCTCCAGCAG 1086  
Db 1205 TCCATCATGAAAGTGCCTGGAGAGTGCATCTACGCGGGAATTTCTCCGCTCCAGCAG 1264  
Qy 1087 GAAATTAAGAGCACTCAGAGGCTTTAAACAGCAGCAGCAGCTGACAGACAGCAG 1146  
Db 1265 GAAATTAAGAGCACTCAGAGGCTTTAAACAGCAGCAGCAGCTGACAGACAGCAGCAG 1324  
Qy 1147 CGAGACCCCGAGGACACATCAAAACCTGCTGACACAGCGGAGCGGAGCGCATAGAGAG 1206  
Db 1325 CGAGACCCCGAGGACACATCAAAACCTGCTGACACAGCGGAGCGGAGCGCATAGAGAG 1384  
Qy 1207 CAGAAAGAGAGACGCGCGCGCTGGAGAGCAACAGCGGAGCGGAGCGGAGCGGAGAG 1266  
Db 1385 CAGAAAGAGAGACGCGCGCGCTGGAGAGCAACAGCGGAGCGGAGCGGAGCGGAGAG 1444  
Qy 1267 CTGCGAGAGAGAGAGAGAGAGCGCGCTGGAGAGCATTCAGGCTTTCGCGCGGAGAGAG 1326  
Db 1445 CTGCGAGAGAGAGAGAGAGAGCGCGCTGGAGAGCATTCAGGCTTTCGCGCGGAGAGAG 1504  
Qy 1327 GAGCGGCGGACAGCGCGGAGCGTGGAGAGAAACAAGCGGAGAGCTGGAGAGAGCAGCG 1386  
Db 1505 GAGCGGCGGACAGCGCGGAGCGAGAGAAATACAGCGGAGAGAGCTGGAGAGAGCAGCG 1564  
Qy 1387 CAGTCAGAAAGCTCTCCAGAGGAGCTGACAGCAGAGCAGCTCCTCAAGTCCCTGAG 1446  
Db 1565 CAGTCAGAAAGCTCTCCAGAGGAGCTGACAGCAGAGCAGCTCCTCAAGTCCCTGAG 1624  
Qy 1447 CAGCAGCAACAGAGAGAGAGCTTCAAAAACAGCAGCAGCAGAGCTCTGCTCGGAGAC 1506  
Db 1625 CAGCAGCAACAGAGAGAGAGCTTCAAAAACAGCAGCAGCAGAGCTCTGCTCGGAGAC 1684  
Qy 1507 AGGAAAGCCCTGTACCATTAATGATCGGGGAGATGAATCCGCTGACAAAACAGCTGGGCG 1566  
Db 1685 AGGAAAGCCCTGTACCATTAATGATCGGGGAGATGAATCCGCTGACAAAACAGCTGGGCG 1744  
Qy 1567 CGAGAGGTAGAAAGAGAGAAACAAGATGAACAAGCAGCAGACATCTTCTTGGCCAAAGAC 1626  
Db 1745 CGAGAGGTAGAAAGAGAGAAACAAGATGAACAAGCAGCAGACATCTTCTTGGCCAAAGAC 1804  
Qy 1627 AAGCCAGGAGCAACGCGGCGCTGAAGCCCTCCATCCCGAGGCTCCCGAGGCGCCAGGA 1686  
Db 1805 AAGCCAGGAGCAACGCGGCGCTGAAGCCCTCCATCCCGAGGCGCCCGAGGA 1864  
Qy 1687 CCCCTTTCCAGACTCTCTATGACAGAGCGGATGAGAGCCCGAGAGGGAACGACACA -- 1744  
Db 1865 CCCCTTTCCAGACTCTCTATGACAGAGCGGATGAGAGCCCGAGAGGGAACGACACAAG 1924  
Qy 1745 -----AG 1746  
Db 1925 AGCCTGTGAGCAACCGGGTCCCACTGAAGCAATATGAGACACTGTACCCCGATCCAG 1984  
Qy 1747 TCCCTGAGAGACCAAGCCGAAACCTGGCTGCTTCCAGAGCTCCCATGAACCCGAGC 1806  
Db 1985 TCCCTGAGAGACCAAGCCGAAACCTGGCTGCTTCCAGAGCTCCCATGAACCCGAGC 2044  
Qy 1807 CCTGGCAATCCCGGACCCGACTGCAAGCGGAGCGGAGGAGCTGTATCCGCGCAGAT 1866  
Db 2045 CCTGGCAATCCCGGACCCGACTGCAAGCGGAGCGGAGGAGCTGTATCCGCGCAGAT 2104  
Qy 1867 TCAGACCCCACTGTGAAGAGACTGCGCCGAGCCCGAATCCCGAGCCTGGGTCCGCCCA 1926  
Db 2105 TCAGACCCCACTGTGAAGAGACTGCGCCGAGCCCGAATCCCGAGCCTGGGTCCGCCCA 2164  
Qy 1927 GATTAACGAGGCCCAACCAAGGTGCTTCAAGAGACCTCATTTATGCGCATGCTGCTTAAC 1986  
Db 2165 GATTAACGAGGCCCAACCAAGGTGCTTCAAGAGACCTCATTTATGCGCATGCTGCTTAAC 2224

Qy 1987 ACGAGTGGGCGCGAGGAGTCCCGGCAAGCCAGGAGTCCGTGCCAGACTTCGAGCAAC 2046  
Db 2225 ACGAGTGGGCGCGAGGAGTCCCGGCAAGCCAGGAGTCCGTGCC----- 2269  
Qy 2047 TCCGCTGGCAATTTATCTGCAAAAGCGGGCAGAGCGGGGACCCCAAGCCTTCAAGG 2106  
Db 2270 ----- 2269  
Qy 2107 CCCCCTGCTCAGCCCCCTGACCCGCAAGCCTTAAGTAAACCCGACCTGAGAGAGC 2166  
Db 2270 -----AGTAAACCCGACCTGAGAGAGC 2293  
Qy 2167 GACCTGTGCTGGAAACGCTGGACAGCGTCTTCCAGCCTTCAAGGCACTTCCCGAG 2226  
Db 2294 GACCTGTGCTGGAAACGCTGGACAGCGTCTTCCAGCCTTCAAGGCACTTCCCGAG 2353  
Qy 2227 GCTGGCTCATCTGAGCGGAAACGCGGTGGAGGCTTCTTCAAACTGGAACAGCTCCCTGTG 2286  
Db 2354 GCTGGCTCATCTGAGCGGAAACGCGGTGGAGGCTTCTTCAAACTGGAACAGCTCCCTGTG 2413  
Qy 2287 CTCTCCCTGGGAAATTAAGCCAAAGCCGAGCAGCAGCAGCTCAAGGCGAGCGGCCCA 2346  
Db 2414 CTCTCCCTGGGAAATTAAGCCAAAGCCGAGCAGCAGCAGCTCAAGGCGAGCGGCCCA 2473  
Qy 2347 -----GACTTGTGTTGCTGAAGACCGGACTTGGAGCAG 2382  
Db 2474 AGCTATAAGCGAGCAATTTGTGAGAGACTTGTGTTGCTGAAGACCGGACTTGGAGCAG 2533  
Qy 2383 GCCCTCGGCTTCCCAAGAGCCATGGAATCTGTGTCTCAAGAGAGAGGTGGAAGC 2442  
Db 2534 GCCCTCGGCTTCCCAAGAGCCATGGAATCTGTGTCTCAAGAGAGAGGTGGAAGC 2593  
Qy 2443 AGTGAAGACAGAGAGAGAGAGAGAGCGGAGCAGAGAGAGAGAGATACCCCT 2502  
Db 2503 AGTGAAGACAGAGAGAGAGAGAGAGCGGAGCAGAGAGAGAGAGATACCCCT 2653  
Qy 2503 GGGGCGCGAGGATGGGATACAGACAGCGTCAACATGTTGTCTCAGACGTGAG 2562  
Db 2654 GGGGCGCGAGGATGGGATACAGACAGCGTCAACATGTTGTCTCAGACGTGAG 2713  
Qy 2563 GAGATCACCGGAGCCAGCCCATACGAGGAGCGGAGCAGATGTTGTCTCAGGACCCCT 2622  
Db 2714 GAGATCACCGGAGCCAGCCCATACGAGGAGCGGAGCAGATGTTGTCTCAGGACCCCT 2773  
Qy 2623 GAAAGAGAGCGGAACTGTGTGATGCTGACAGCAATGGGTACACAAACCTGCTGACGTG 2682  
Db 2774 GAAAGAGAGCGGAACTGTGTGATGCTGACAGCAATGGGTACACAAACCTGCTGACGTG 2833  
Qy 2683 GTCCAGCCCAAGCACTCAACCCAGAGAACAGCAAAAGGCCAAGCCCTGAAAGAT 2742  
Db 2834 GTCCAGCCCAAGCACTCAACCCAGAGAACAGCAAAAGGCCAAGCCCTGAAAGAT 2893  
Qy 2743 GGGAGTGTGACTTCAAGTCTGTGTGGCTGTGTAAGGCCCCCTGGCAAGAGCTCTTCAAG 2802  
Db 2894 GGGAGTGTGACTTCAAGTCTGTGTGGCTGTGTAAGGCCCCCTGGCAAGAGCTCTTCAAG 2953  
Qy 2803 ATGTTGTGATCTTAGGGATCTAACAGCAGCTGAGGAGCATGGGAGCAGCATCCCATCA 2862  
Db 2954 ATGTTGTGATCTTAGGGATCTAACAGCAGCTGAGGAGCATGGGAGCAGCATCCCATCA 3013  
Qy 2863 GCCCTAGTGTGAGAGAGGCACTCGGCTGACACAGCTGCAAGTACGAGTGAAGAGGT 2922  
Db 3014 GCCCTAGTGTGAGAGAGGCACTCGGCTGACACAGCTGCAAGTACGAGTGAAGAGGT 3073  
Qy 2923 TCTGTGTCAACGTGAATTCACCAACCCGGGCGCCAGAGTGAACCCCTGAGATCCGG 2982  
Db 3074 TCTGTGTCAACGTGAATTCACCAACCCGGGCGCCAGAGTGAACCCCTGAGATCCGG 3133  
Qy 2983 AAGTACAAGAGCGATTCAACCTCGAGATCTCTGTGAGAGCCCTTGTGGGGGTCAACCTG 3042  
Db 3134 AAGTACAAGAGCGATTCAACCTCGAGATCTCTGTGAGAGCCCTTGTGGGGGTCAACCTG 3193

QY 3043 CTGGTGGGACGAGAAACGGGCTGATGTTGTGACCGAAGTGGGACGAGGAGGTGAT 3102  
DB 3194 CTGGTGGGACGAGAAACGGGCTGATGTTGTGACCGAAGTGGGACGAGGAGGTGAT 3253  
QY 3103 GGAATCTATTGGGCGGCGACGCTTCCAGCAGATGAGATGATGAGGGGCTCAACCTGCTC 3162  
DB 3254 GGAATCTATTGGGCGGCGACGCTTCCAGCAGATGAGATGATGAGGGGCTCAACCTGCTC 3313  
QY 3163 ATCAACATCTAGGAGAAAGAAACAACTGGGGTGTATTAACCTGTCTCTGCTCCGGAAC 3222  
DB 3314 ATCAACATCTAGGAGAAAGAAACAACTGGGGTGTATTAACCTGTCTCTGCTCCGGAAC 3373  
QY 3223 AAGATTCTGCAATGACCAAGAGTGGAGAAAGAGGAGGCTGGACCAAGTGGGGGAC 3282  
DB 3374 AAGATTCTGCAATGACCAAGAGTGGAGAAAGAGGAGGCTGGACCAAGTGGGGGAC 3433  
QY 3283 ATGAGAGGCTGCGGCGACCTACCGTGTGTGAAATACAGCGAGATTAAGTTCCTGTCATC 3342  
DB 3434 ATGAGAGGCTGCGGCGACCTACCGTGTGTGAAATACAGCGAGATTAAGTTCCTGTCATC 3493  
QY 3343 GCCCTCAAGAGCTCCGTGAGAGGTATGCTGGGCCCCAAACCTTACCAAAATTCATG 3402  
DB 3494 GCCCTCAAGAGCTCCGTGAGAGGTATGCTGGGCCCCAAACCTTACCAAAATTCATG 3553  
QY 3403 GCCCTCAAGAGCTCCGTGAGAGGTATGCTGGGCCCCAAACCTTACCAAAATTCATG 3462  
DB 3554 GCCCTCAAGAGCTCCGTGAGAGGTATGCTGGGCCCCAAACCTTACCAAAATTCATG 3613  
QY 3463 GAGGGGACGCGCTCAAGAGTATGATGCTCAAGTGTGCTTCATGCTGTGAGATGTC 3522  
DB 3614 GAGGGGACGCGCTCAAGAGTATGATGCTCAAGTGTGCTTCATGCTGTGAGATGTC 3673  
QY 3523 GACTCGGGGAAACAGCTATGACATCTACCTCTGTGACATCCAGAGCAATGACGCC 3582  
DB 3674 GACTCGGGGAAACAGCTATGACATCTACCTCTGTGACATCCAGAGCAATGACGCC 3733  
QY 3583 CATGCCATCATCTCTCCCAACACCGGCAATGAGATGCTGTGCTACGAGGAC 3642  
DB 3734 CATGCCATCATCTCTCCCAACACCGGCAATGAGATGCTGTGCTACGAGGAC 3793  
QY 3643 GAGGGTGTCTACGTCACACCTACGAGGCGCATCAATTAAGATGTGCTGCACTGAGG 3702  
DB 3794 GAGGGTGTCTACGTCACACCTACGAGGCGCATCAATTAAGATGTGCTGCACTGAGG 3853  
QY 3703 GAGATGCTTACTTGTGTGCTTACATCTGCTCAACAGATTAATGGGCTGGAGAAA 3762  
DB 3854 GAGATGCTTACTTGTGTGCTTACATCTGCTCAACAGATTAATGGGCTGGAGAAA 3913  
QY 3763 GCCATTAGATCCGCTCTGTGAGACCGGCGCACTCCAGCGGGTCTTCAATCAAAACGA 3822  
DB 3914 GCCATTAGATCCGCTCTGTGAGACCGGCGCACTCCAGCGGGTCTTCAATCAAAACGA 3973  
QY 3823 GCTCAGAGGCTCAAGTTCCTGTGTGAGGGAATGCAAGTGTGCTTCTCAGTCCGC 3882  
DB 3974 GCTCAGAGGCTCAAGTTCCTGTGTGAGGGAATGCAAGTGTGCTTCTCAGTCCGC 4033  
QY 3883 TCTGGGGGACAGCAAGTTCCTCAATGACTGTAACCGTAACTGATGAACTGG 3942  
DB 4034 TCTGGGGGACAGCAAGTTCCTCAATGACTGTAACCGTAACTGATGAACTGG 4093  
QY 3943 TGAAGGGC 3951  
DB 4094 TGACGGGC 4102

RESULT 6  
AAL48626  
ID AAL48626 standard; cDNA; 4863 BP.  
AC AAL48626;  
XX  
XX  
DT 11-OCT-2002 (first entry)

DE Human insulin receptor signaling modifier cDNA SEQ ID NO: 35.  
XX  
KW Human; insulin receptor signaling; insulin receptor signaling modifier;  
KW ISM; diabetes; metabolic syndrome; antidiabetic; gene; ss.  
XX Homo sapiens.  
OS  
PN WO200255664-A2.  
PD 18-JUL-2002.  
XX  
PF 11-JAN-2002; 2002WO-US001048.  
PR 12-JAN-2001; 2001US-0261323P.  
PR 12-JAN-2001; 2001US-0261330P.  
PR 12-JAN-2001; 2001US-0261304P.  
PR 12-JAN-2001; 2001US-0261335P.  
PR 12-JAN-2001; 2001US-0261336P.  
PR 12-JAN-2001; 2001US-0261361P.  
PR 12-JAN-2001; 2001US-0261456P.  
PR 12-JAN-2001; 2001US-0261457P.  
PR 12-JAN-2001; 2001US-0261458P.  
PR 12-JAN-2001; 2001US-0261459P.  
PR 12-JAN-2001; 2001US-0261461P.  
PR 12-JAN-2001; 2001US-0261518P.  
PR 12-JAN-2001; 2001US-0261531P.  
PR 12-JAN-2001; 2001US-0261532P.  
PR 12-JAN-2001; 2001US-0261589P.  
PR 12-JAN-2001; 2001US-0261590P.  
PR 12-JAN-2001; 2001US-0261590P.  
PR 12-JAN-2001; 2001US-0261594P.  
PR 12-JAN-2001; 2001US-0261695P.  
PR 12-JAN-2001; 2001US-0261697P.  
XX  
PA (EXEL-) EXELIXIS INC.  
XX  
PI Setdel-Dugan C, Ferguson KC, Kidd T;  
XX WPI: 2002-599664/64.  
DR P-PSDB; AAO18507.  
XX  
PT Identifying an insulin receptor signaling modulator, useful as drug  
PT targets for treating diabetes or metabolic disorders, comprises  
PT contacting an assay system comprising insulin receptor signaling  
PT modifiers with a test agent.  
XX  
PS Disclosure; Page 110-112; 232pp; English.  
XX  
SS The present invention relates to a method of identifying a candidate  
CC insulin receptor (INR) signaling modulating agent, involving contacting  
CC an assay system comprising an insulin receptor signaling modifier (ISM)  
CC polypeptide or nucleic acid with a test agent, and detecting a test agent  
CC bi-ased activity of the assay system. The method is useful for  
CC identifying candidate INR signaling modulating agents. ISM genes may be  
CC used as drug targets for treatment of disorders related to INR signaling  
CC such as diabetes or metabolic syndrome. ISM nucleic acids and  
CC polypeptides are useful for identifying and testing agents that modulate  
CC ISM function and for other applications related to the involvement of ISM  
CC in INR signaling, and for identifying subjects having a predisposition to  
CC such diseases associated with INR signaling. The present sequence is an  
CC ISM coding sequence described in the exemplification of the invention  
XX  
SQ Sequence 4863 BP; 1072 A; 1509 C; 1447 G; 835 T; 0 U; 0 Other;  
Query Match 91.1%; Score 3601; DB 6; Length 4863;  
Best Local Similarity 95.0%; Pred. No. 0;  
Matches 3829; Conservative 0; Mismatches 5; Indels 195; Gaps 3;  
QY 7 ATGGGCAACCCAGCCCGCCGCGAGCCTGAGACATGCACTGTCCGCCCTGGGAC 66  
DB 185 ATGGGCAACCCAGCCCGCCGCGAGCCTGAGACATGCACTGTCCGCCCTGGGAC 244  
QY CTTGCTGGAGATCTTGTGAGAGGTGTGGCAATGGAACCTACGACAGAGGTATC 126



QY 2227 GCTGGCTCACTGAGCGGAAACCGGCTGGAGGCTCTCTCAAACTGACAGCTCCCTCTG 2286  
 |||||  
 Db 2254 GCTGGCTCACTGAGCGGAAACCGGCTGGAGGCTCTCTCTCAAAACCGGACAGCTCCCTCTG 2413  
 |||||  
 QY 2287 CTCTCCCTGGGAAATTAAGCCAAAGCCGACGACCAACGCTCAACGCGCAAGGCGGCGGCA 2346  
 |||||  
 Db 2414 CTCTCCCTGGGAAATTAAGCCAAAGCCGACGACCAACGCTCAACGCGCGGCGGCGCA 2473  
 |||||  
 QY 2347 -----GACTTGTGTGTTCTGAAAGAGCGGACTCTTGACGAG 2382  
 |||||  
 Db 2474 AGCTATAAGCGAGCAATTTGTAGAGACTTGTGTGCTGAAAGAGCGGACTCTGAGCAG 2533  
 |||||  
 QY 2283 GCCCTGGGCTCCCAAGAGGCGCAATGACTACTGTGTCAAGCGAGAGGTGGAAGC 2442  
 |||||  
 Db 2534 GCCCTGGGCTCCCAAGAGGCGCAATGACTACTGTGTCAAGCGAGAGGTGGAAGC 2593  
 |||||  
 QY 2443 AGTGAAGACGACGAGAGGAGGCGAGGCGGCGGCGGAGAGGAGGAGATACCCCT 2502  
 |||||  
 Db 2594 AGTGAAGACGACGAGAGGAGGCGAGGCGGCGGCGGAGAGGAGGAGATACCCCT 2653  
 |||||  
 QY 2503 GGGGGCCGACGAGTGGGGATACAGACAGCTCAGACCAATGTGTGTCAAGAGTGGAG 2562  
 |||||  
 Db 2654 GGGGGCCGACGAGTGGGGATACAGACAGCTCAGACCAATGTGTGTCAAGAGTGGAG 2713  
 |||||  
 QY 2563 GAGATCAACGGGACCGAGCCGCAATAGCGGGCGGCAATGTGTGTCAAGGACCCCT 2622  
 |||||  
 Db 2714 GAGATCAACGGGACCGAGCCGCAATAGCGGGCGGCAATGTGTGTCAAGGACCCCT 2773  
 |||||  
 QY 2623 GAAAGAGACGGAACCTGCTCATGTGACAGCAATGGGTACAAACCTGCTGACGCTG 2682  
 |||||  
 Db 2774 GAAAGAGACGGAACCTGCTCATGTGACAGCAATGGGTACAAACCTGCTGACGCTG 2833  
 |||||  
 QY 2683 GTCCAGCCGACGACCTCACTCAACGAGAAACAGAAAGGCCAAGCCCTCGAAGAT 2742  
 |||||  
 Db 2834 GTCCAGCCGACGACCTCACTCAACGAGAAACAGAAAGGCCAAGCCCTCGAAGAT 2893  
 |||||  
 QY 2743 GGGAGTGTGACTCACTGCTGTGTGTGTGTAAGGCCCTGGCAAGAGTCTGTCAG 2802  
 |||||  
 Db 2894 GGGAGTGTGACTCACTGCTGTGTGTGTGTAAGGCCCTGGCAAGAGTCTGTCAG 2953  
 |||||  
 QY 2803 ATGTTTGTGATCTTAGGATCTACAGCCTGAGGCGAGTGGGAGCAGCATCCCATCA 2862  
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 Db 2954 ATGTTTGTGATCTTAGGATCTACAGCCTGAGGCGAGTGGGAGCAGCATCCCATCA 3013  
 |||||  
 QY 2863 GCCCTAGTGGTGAAGAGGCGACTGCGCTCAACCACTGTGACGACTGAGGAGAGGCT 2922  
 |||||  
 Db 3014 GCCCTAGTGGTGAAGAGGCGACTGCGCTCAACCACTGTGACGACTGAGGAGAGGCT 3073  
 |||||  
 QY 2923 TCTGTGTCAACGTGATCCCAACCAACCGGGGCCCAAGTGAAGCCCTGAGATCCGG 2982  
 |||||  
 Db 3074 TCTGTGTCAACGTGATCCCAACCAACCGGGGCCCAAGTGAAGCCCTGAGATCCGG 3133  
 |||||  
 QY 2983 AAGTACAAGAAAGCGATTCAACTCCGAGATCTCTGTGAGCCCTTTGGGGGGTCAACTG 3042  
 |||||  
 Db 3134 AAGTACAAGAAAGCGATTCAACTCCGAGATCTCTGTGAGCCCTTTGGGGGGTCAACTG 3193  
 |||||  
 QY 3043 CTGGTGGGCAACGAGAAACGGGCTGATGTTGCTGACCGGAAGTGGGCAAGGTGTAT 3102  
 |||||  
 Db 3194 CTGGTGGGCAACGAGAAACGGGCTGATGTTGCTGACCGGAAGTGGGCAAGGTGTAT 3253  
 |||||  
 QY 3103 GGAATCTTTGGGCGGCGACGCTTCAAGACATGTGATGTGCTGAGGGGGTCAACTGCTC 3162  
 |||||  
 Db 3254 GGAATCTTTGGGCGGCGACGCTTCAAGACATGTGATGTGCTGAGGGGGTCAACTGCTC 3313  
 |||||  
 QY 3163 ATCAACATCTCAAGGAAAGAAACAACTGGGGTGTATTACTGTCTGTGCTCCGGAAC 3222  
 |||||  
 Db 3314 ATCAACATCTCAAGGAAAGAAACAACTGGGGTGTATTACTGTCTGTGCTCCGGAAC 3373  
 |||||  
 QY 3223 AAGATTCTGCACAATGACCCAGAAAGTGAAGAAAGCAAGGCTGACCAACGCTGGGAGAC 3282  
 |||||  
 Db 3374 AAGATTCTGCACAATGACCCAGAAAGTGAAGAAAGCAAGGCTGACCAACGCTGGGAGAC 3433  
 |||||  
 QY 3283 ATGAGAGGCTGGGGGCACTACCGTGTGTGAATAACAGCGGATTAAGTCTCTGTGATC 3342  
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Db 3434 ATGAGAGGCTGGGGGCACTACCGTGTGTGAATAACAGCGGATTAAGTCTCTGTGATC 3493  
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 QY 3443 GCCCTCAAGAGCTCCGTGAGAGGTATATGCTGGGCCCCCAAAACCTTACCAAAATTCAATG 3402  
 |||||  
 Db 3494 GCCCTCAAGAGCTCCGTGAGAGGTATATGCTGGGCCCCCAAAACCTTACCAAAATTCAATG 3553  
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 QY 3403 GCCTTCAAGTCTTTGGCGACCTCCCAACCGGCTCTGCTGTGTGACCTTGAAGTGAAG 3462  
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 Db 3554 GCCTTCAAGTCTTTGGCGACCTCCCAACCGGCTCTGCTGTGTGACCTTGAAGTGAAG 3613  
 |||||  
 QY 3463 GAGGGGAGCGGCTCAAGAGTCACTATAGGCTCAAGTGGCTTCAATGCTGATGATGTC 3522  
 |||||  
 Db 3614 GAGGGGAGCGGCTCAAGAGTCACTATAGGCTCAAGTGGCTTCAATGCTGATGATGTC 3673  
 |||||  
 QY 3523 GACTGGGGAACAGCTATGACATCTCAATCTCTGTGACATCAAGGCGAGATCAACGCC 3582  
 |||||  
 Db 3674 GACTGGGGAACAGCTATGACATCTCAATCTCTGTGACATCAAGGCGAGATCAACGCC 3733  
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 QY 3583 CATGCCATCATCTTCTCCCAACCAACGAGCGGATGAGATGCTGTGTGAAGAGAC 3642  
 |||||  
 Db 3734 CATGCCATCATCTTCTCCCAACCAACGAGCGGATGAGATGCTGTGTGAAGAGAC 3793  
 |||||  
 QY 3643 GAGGCTGTCAACGTCAACAGTACGGGCGCATCATTAAGATGTGTGCTGACGTGGGG 3702  
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 Db 3794 GAGGCTGTCAACGTCAACAGTACGGGCGCATCATTAAGATGTGTGCTGACGTGGGG 3853  
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 QY 3703 GAGATGCTCACTTGTGGCTCAATCTGTCTCAACAGATATGGGCTGGGTGAAGAA 3762  
 |||||  
 Db 3854 GAGATGCTCACTTGTGGCTCAATCTGTCTCAACAGATATGGGCTGGGTGAAGAA 3913  
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 QY 3763 GCCATTGAGATCCGCTCTGTGAGAACGGGCGCACTCGACGGGGTCTTCAATGCAAAACGA 3822  
 |||||  
 Db 3914 GCCATTGAGATCCGCTCTGTGAGAACGGGCGCACTCGACGGGGTCTTCAATGCAAAACGA 3973  
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 QY 3823 GCTCAGAGGCTCAAGTCTGTGTGAGCGGAATGCAAGGTGTTTGGCTCAGTCCGC 3882  
 |||||  
 Db 3974 GCTCAGAGGCTCAAGTCTGTGTGAGCGGAATGCAAGGTGTTTGGCTCAGTCCGC 4033  
 |||||  
 QY 3983 TCTGGGGGAGCAGCAGCAAGTTTACTTGTATGATCTGAAACGTTAATGATCAATCACTGG 3942  
 |||||  
 Db 4034 TCTGGGGGAGCAGCAGCAAGTTTACTTGTATGATCTGAAACGTTAATGATCAATCACTGG 4093  
 |||||  
 QY 3943 TGAAGGCG 3951  
 |||||  
 Db 4094 TGAAGGCG 4102  
 |||||

RESULT 7  
 AAL61132  
 ID AAL61132 standard; DNA; 4863 BP.  
 XX  
 AC AAL61132;  
 XX  
 DT 22-SEP-2003 (first entry)  
 XX  
 DE Human MINK2 antisense transcript DNA.  
 XX  
 KW Transcription; therapy; systemic lupus erythematosus; inflammatory disease;  
 KW cardiovascular; gastrointestinal disease; atherosclerosis; skin disease;  
 KW rheumatoid disorder; autoimmune disease; diabetes; multiple sclerosis;  
 KW cancer; neuroprotective; human; MINK2; antisense; gene; ds.  
 OS Homo sapiens.  
 PN W02003046220-A1.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 11-NOV-2002; 2002WC-IL000904.  
 XX  
 PR 26-NOV-2001; 2001US-00993398.  
 PR 24-JUL-2002; 2002US-00201605.



XX (COMP-) COMPUEN LTD.  
PA Levanon E, Pollock S, Nemzer S, Shoshan A, Khosravi R, Walach S;  
PI Levine Z, Bernstein J, Dahari D, Wasserman A, Rotman G;  
XX WPI; 2003-505211/47.  
XX Identifying putative naturally occurring antisense transcripts, useful  
PT for quantifying gene expression levels, and detecting and/or treating  
PT inflammatory, autoimmune or cardiovascular diseases, diabetes, arthritis  
XX and cancer.  
PS Example; Page 214-216; 230pp; English.  
XX The invention relates to methods and systems for identifying naturally  
CC occurring antisense transcripts. The method is useful for quantifying  
CC gene expression levels and for detecting, quantifying or specifically  
CC regulating antisense and respective sense transcripts thereby enabling  
CC detection and treatment of a wide range or disorders, such as systemic  
CC lupus erythematosus, inflammatory diseases, rheumatoid disorders,  
CC autoimmune diseases, diabetes, multiple sclerosis, cardiovascular and  
CC gastrointestinal diseases, atherosclerosis, skin diseases and cancer. The  
CC present sequence is human MINK2 transcript DNA used to illustrate the  
CC method of the invention  
SQ Sequence 4863 BP; 1072 A; 1509 C; 1447 G; 835 T; 0 U; 0 Other;  
Query Match 91.1%; Score 3601; DB 8; Length 4863;  
Best Local Similarity 95.0%; Pred. No. 0;  
Matches 3829; Conservative 0; Mismatches 5; Indels 195; Gaps 3;  
OY 7 ATGGGCGACCCGACCCCGCCGCGGACCTGAGACATGACCTGCGCCCTGGGGGAGC 66  
DB 185 ATGGGCGACCCGACCCCGCCGCGGACCTGAGACATGACCTGCGCCCTGGGGGAGC 244  
OY 67 CCGTGTGGGATCTTTGAGGCTTGTGAGAGTGTGTGCGCATGAACTTACGAGGTGTAC 126  
DB 245 CCGTGTGGGATCTTTGAGGCTTGTGAGAGTGTGTGCGCATGAACTTACGAGGTGTAC 304  
OY 127 AAGGATCGGCATGTCAAGACGCGGAGCTGTGCTCCATCAAGGTCTATGATGTCAAGAG 186  
DB 305 AAGGATCGGCATGTCAAGACGCGGAGCTGTGCTCCATCAAGGTCTATGATGTCAAGAG 364  
OY 187 GACGAGGAGGAGATCAAGAGATCAAGATCAAGTGAAGAGTCTGATCAAGAGAG 246  
DB 365 GACGAGGAGGAGATCAAGAGATCAAGATCAAGTGAAGAGTCTGATCAAGAGAG 424  
OY 247 AACATCGCACCTTACTACGAGACCTTCAAGAGAGAGCCCGCGGAGAGCATGACAG 306  
DB 425 AACATCGCACCTTACTACGAGAGCCTTCAAGAGAGAGCCCGCGGAGAGCATGACAG 484  
OY 307 CTGTGGCTGTGATGAGAGT 366  
DB 485 CTGTGGCTGTGATGAGAGT 544  
OY 367 AAAGGCAAGCCCTGAAGAGAGCTGTATGCTTATATCTGAGGAGAGTCCGAGGGGT 426  
DB 545 AAAGGCAAGCCCTGAAGAGAGCTGTATGCTTATATCTGAGGAGAGTCCGAGGGGT 604  
OY 427 CTGGCCCATCTTCATGCGCACAAGGTGATCTCAAGATCAAGAGGAGAGATGTGTG 486  
DB 605 CTGGCCCATCTTCATGCGCACAAGGTGATCTCAAGATCAAGAGGAGAGATGTGTG 664  
OY 487 CTGACAGAGATGTGAGGTCAAGGTGATGATGATGATGATGATGATGATGATGATGATG 546  
DB 665 CTGACAGAGATGTGAGGTCAAGGTGATGATGATGATGATGATGATGATGATGATGATG 724  
OY 547 ACCGTGGGAG 606  
DB 725 ACCGTGGGAG 784  
OY 607 GCCTGTGATGAGAACCTGTATGACCTATGATTAAGAGAGAGAGATGATGATGATGATG 666

DB 785 GCCTGTGATGAGAACCTGTATGACCTATGATTAAGAGAGAGATGATGATGATGATGATG 844  
OY 667 ATTCAGAGCATGAGATGAG 726  
DB 845 ATTCAGAGCATGAGATGAG 904  
OY 727 GCCCTCTTCTCATTTCTCGGAACTTCCGCGCAGAGCTCAAGTCCAGAGAGTGTCTAAG 786  
DB 905 GCCCTCTTCTCATTTCTCGGAACTTCCGCGCAGAGCTCAAGTCCAGAGAGTGTCTAAG 964  
OY 787 AAGTTCAATGACTTCAATGACATGATGTCTATCAAGAGTTTACCTGAGCCGCCACCCAG 846  
DB 965 AAGTTCAATGACTTCAATGACATGATGTCTATCAAGAGTTTACCTGAGCCGCCACCCAG 1024  
OY 847 GAGCAGCTACGAGAGTTTCCCTCATCCGGAGCCGACCCAGAGCGGAGAGTCCGATC 906  
DB 1025 GAGCAGCTACGAGAGTTTCCCTCATCCGGAGCCGACCCAGAGCGGAGAGTCCGATC 1084  
OY 907 CAGCTTAAAGACCACTTGAACCGATCCCGAAGAGAGCGGGGTGAAGAGAGAGAGAGAG 966  
DB 1085 CAGCTTAAAGACCACTTGAACCGATCCCGAAGAGAGCGGGGTGAAGAGAGAGAGAGAG 1144  
OY 967 TATGAGTACAGCGGAG 1026  
DB 1145 TATGAGTACAGCGGAG 1204  
OY 1027 TCCATCATGAACTGCTGAGAGAGTGAAGTCAAGCTGAGCGGAGAGTTTCTCGGCTCAGAG 1086  
DB 1205 TCCATCATGAACTGCTGAGAGAGTGAAGTCAAGCTGAGCGGAGAGTTTCTCGGCTCAGAG 1264  
OY 1087 GAAATTAAGAGCACTCAGAGGCTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1146  
DB 1265 GAAATTAAGAGCACTCAGAGGCTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1324  
OY 1147 CGAGACCCCGAGGAG 1206  
DB 1325 CGAGACCCCGAGGAG 1384  
OY 1207 CAG 1266  
DB 1385 CAG 1444  
OY 1267 CTGACAG 1326  
DB 1445 CTGACAG 1504  
OY 1327 GAGCGGCGGAG 1386  
DB 1505 GAGCGGCGGAG 1564  
OY 1387 CAGTCAAGAGAGCTTCAGAGGAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1446  
DB 1565 CAGTCAAGAGAGCTTCAGAGGAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1624  
OY 1447 CAGCAGCAACAGCAGCAG 1506  
DB 1625 CAGCAGCAACAGCAGCAG 1684  
OY 1507 AGGAG 1566  
DB 1685 AGGAG 1744  
OY 1567 CGAG 1626  
DB 1745 CGAG 1804  
OY 1627 AAGCAGCAG 1686  
DB 1805 AAGCAGCAG 1864  
OY 1687 CCCCTTTCCAGAGCTTCTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1744



Db	1865	CCCCCTTCCAGACTCTCTCTTAATGACAGAGCCGGTGTGAGAGCCCCAGAGAGACCCGACAAG	1924
Qy	1745	-----AG	1746
Db	1925	AGCCTGTGTGGACAACCGGGTCCCACTGAAAGCCATATGAGAGCACTGTACCCCGATCCAG	1984
Qy	1747	TCCCTGCAAGACCAAGCCCACTCCGAAACTGTGGTGGCTTTCCAGCTCTCCCATGACCCGAC	1806
Db	1985	TCCCTGCAAGACCAAGCCCACTCCGAAACTGTGGTGGCTTTCCAGCTCTCCCATGACCCCGAC	2044
Qy	1807	CCTGCAATCCCGGACCCCACTGACAGCCGACAGTGGCCGAGAGAGCTGTATCCGACAGAT	1866
Db	2045	CCTGCAATCCCGGACCCCACTGACAGCCGACAGTGGCCGAGAGAGCTGTATCCGACAGAT	2104
Qy	1867	TCAGACCCCACTCTGAAAGAGACTTGGCCCAAGCCGAAATCCCCAGCCCTGGGTCCGCCCA	1926
Db	2105	TCAGACCCCACTCTGAAAGAGACTTGGCCCAAGCCGAAATCCCCAGCCCTGGGTCCGCCCA	2164
Qy	1927	GATTAACGAGGCCCAACCCAGGTGCTCAAGAGACCTCATCTATGCAACTGACCTTAAC	1986
Db	2165	GATTAACGAGGCCCAACCCAGGTGCTCAAGAGACCTCATCTATGCAACTGACCTTAAC	2224
Qy	1997	ACCAATGGGGCCGGAGGGTCCCGGCAACCCAGAGAGTCCGTGCCAGACCTGCAGACAC	2046
Db	2225	ACCAATGGGGCCGGAGGGTCCCGGCAACCCAGAGAGTCCGTGCCAGACCTGCAGACAC	2265
Qy	2047	TCCGCTGGCAATCTATCTGTCAAGAGGGGAGAGCGGGGCAACCCAAAGCTTCAAGG	2106
Db	2270	-----	2265
Qy	2107	CCCCCTGCTCAGCCCCCTGGCCCGCCCAACGCTCTAGTAACCCCGACCTGAGAGAGC	2166
Db	2270	-----AGTAACCCCGACCTCAGAGAGAGC	2293
Qy	2167	GACCTGTGGCTGGGAACGCTTCGAGACGCTCTTCCAGGCTCTCAAGGGCACTTCCCCAG	2226
Db	2294	GACCTGTGGCTGGGAACGCTTCGAGACGCTCTTCCAGGCTCTCAAGGGCACTTCCCCAG	2353
Qy	2227	GCTGGCTCACTGGAGCGGAAACGCGGTGGAGAGCTCTCAAACTGGAACAGCTCCCTGTG	2286
Db	2354	GCTGGCTCACTGGAGCGGAAACGCGGTGGAGAGCTCTCTCAAACTGGAACAGCTCCCTGTG	2413
Qy	2287	CTCTCCCTGGGAATTAAGCCAGCCGACGACCAACGCTCAGCGGCAAGCCCGGCGGCA	2346
Db	2414	CTCTCCCTGGGAATTAAGCCAGCCGACGACCAACGCTCAGCGGCAAGCCCGGCGGCA	2473
Qy	2347	-----GACTTTGTGTGCTGAAAGAGCGGACTCTGAGCAG	2382
Db	2474	AGCTATAAGCAGAGCAATGTGTGAGAGACTTGTGTGCTGAAAGAGCGGACTCTGAGCAG	2533
Qy	2383	GCCCCCTGGGCTCCCCAAGAAGGCCATGGACTACTCGTGTGTCAGGAGAGAGGTGGAAAGC	2442
Db	2514	GCCCCCTGGGCTCCCCAAGAAGGCCATGGACTACTCGTGTGTCAGGAGAGAGGTGGAAAGC	2593
Qy	2443	AGTGAAGACGACGAGGAGGAAAGGCGGAGGCGGACGAGAGGGAGCAGAGATACCCCT	2502
Db	2594	AGTGAAGACGACGAGGAGGAAAGGCGGAGGCGGACGAGAGGGAGCAGAGATACCCCT	2653
Qy	2503	GGGGGCGCAGCGATGGGGATACAGACAGCGTCACAGCACCATGTGTCTCACAGCGTCGAG	2562
Db	2654	GGGGGCGCAGCGATGGGGATACAGACAGCGTCACAGCACCATGTGTCTCACAGCGTCGAG	2713
Qy	2553	GAGATCAACCGGACCCCAAGCCCCCAATAGGGGGCGGACCAATGTGTCTCACAGCGCACCCCT	2622
Db	2714	GAGATCAACCGGACCCCAAGCCCCCAATAGGGGGCGGACCAATGTGTCTCACAGCGCACCCCT	2773
Qy	2623	GAAAGGAGCGGAACTGTGCTATCTGACAGCAATGGGTACAAACTGCTGACGTG	2682
Db	2774	GAAAGGAGCGGAACTGTGCTATCTGACAGCAATGGGTACAAACTGCTGACGTG	2833
Qy	2683	GTTCCAGCCCAAGCACTCAACCCACGAGAAACAGCAAAAGGCCAAAGCCACTTCAAGGAT	2742
Db	2834	GTTCCAGCCCAAGCACTCAACCCACGAGAAACAGCAAAAGGCCAAAGCCACTTCAAGGAT	2893

QY	2743	GGGAGTGTGA	CTAC	CA	AGTCTT	CGTGGG	CTGTGT	AAAGCCCTT	GGC	AAAGCTCT	GTTCACG	2802				
Db	2894	GGGAGTGTGA	CTAC	CA	AGTCTT	CGTGGG	CTGTGT	AAAGCCCTT	GGC	AAAGCTCT	GTTCACG	2953				
QY	2803	ATGTTTGGAGAT	CTAC	AGGATCTT	AC	CAGCTG	AGAGGAG	AGAGGAG	AGAGGAG	AGAGGAG	AGAGGAG	2862				
Db	2954	ATGTTTGGAGAT	CTAC	AGGATCTT	AC	CAGCTG	AGAGGAG	AGAGGAG	AGAGGAG	AGAGGAG	AGAGGAG	3013				
QY	2863	GGCCTT	AGTGGT	AGAGGAG	AGAGGAG	AGAGGAG	AGAGGAG	AGAGGAG	AGAGGAG	AGAGGAG	AGAGGAG	2922				
Db	3014	GGCCTT	AGTGGT	AGAGGAG	AGAGGAG	AGAGGAG	AGAGGAG	AGAGGAG	AGAGGAG	AGAGGAG	AGAGGAG	3073				
QY	2923	TCCTGTGTG	CAAC	CGTGAAT	CCCA	CCAA	CCCGGGCCCA	CA	AGTGA	CA	CCCTGAGA	TC	CGG	2982		
Db	3074	TCCTGTGTG	CAAC	CGTGAAT	CCCA	CCAA	CCCGGGCCCA	CA	AGTGA	CA	CCCTGAGA	TC	CGG	3133		
QY	2983	AAAGTACA	GAAG	AGCATTC	CACTCC	GAGATCTCT	CTGTG	CAGCCCTT	TTGGGGGGT	CA	ACTG	3042				
Db	3134	AAAGTACA	GAAG	AGCATTC	CACTCC	GAGATCTCT	CTGTG	CAGCCCTT	TTGGGGGGT	CA	ACTG	3193				
QY	3043	CTGTGTGG	CAAC	CGGAGAAC	CGGCTG	ATGTTGT	GTGGA	CCGAA	AGTGG	CA	GGGCA	AGTGTAT	3102			
Db	3194	CTGTGTGG	CAAC	CGGAGAAC	CGGCTG	ATGTTGT	GTGGA	CCGAA	AGTGG	CA	GGGCA	AGTGTAT	3253			
QY	3103	GGAC	TCAT	TTGGGGCGGCG	CGCCTTC	CAC	ACAG	TGGA	TGTCGTG	AGGGGG	CTCA	CTCTCTC	3162			
Db	3254	GGAC	TCAT	TTGGGGCGGCG	CGCCTTC	CAC	ACAG	TGGA	TGTCGTG	AGGGGG	CTCA	CTCTCTC	3313			
QY	3163	ATCA	CCATCTT	CAGG	AAAAAGGA	CAAA	CTGGGGGT	ATTAT	CTGTCTGTG	CTCCG	AAAC	3222				
Db	3314	ATCA	CCATCTT	CAGG	AAAAAGGA	CAAA	CTGGGGGT	ATTAT	CTGTCTGTG	CTCCG	AAAC	3373				
QY	3223	AAAGTT	TCG	CAAT	TGAC	CCCA	GAAGTGA	GAAG	AGAGG	CTGGA	CA	CCGTGGGGAC	3282			
Db	3374	AAAGTT	TCG	CAAT	TGAC	CCCA	GAAGTGA	GAAG	AGAGG	CTGGA	CA	CCGTGGGGAC	3433			
QY	3283	ATGAGAGG	CTGCGGG	CACTAC	CCGTGT	TGTGA	ATAATAC	GAGGG	ATTAA	GTTCCT	GTATC	3342				
Db	3434	ATGAGAGG	CTGCGGG	CACTAC	CCGTGT	TGTGA	ATAATAC	GAGGG	ATTAA	GTTCCT	GTATC	3493				
QY	3343	GCCTT	CAAG	AGCTCC	GTGAG	AGGTGTAT	GTCTGGGG	CCCCCA	ACCTTAC	CA	CAAA	TTCAATG	3402			
Db	3494	GCCTT	CAAG	AGCTCC	GTGAG	AGGTGTAT	GTCTGGGG	CCCCCA	ACCTTAC	CA	CAAA	TTCAATG	3553			
QY	3403	GCCTT	CAAG	AGCTCTT	TGCG	AG	CTCCCCCA	CGG	CCCTGTG	CTGTG	CACTG	AC	3462			
Db	3554	GCCTT	CAAG	AGCTCTT	TGCG	AG	CTCCCCCA	CGG	CCCTGTG	CTGTG	CACTG	AC	3613			
QY	3463	GAGGGG	CA	GGGCTT	CAAG	GTATAT	TATGGCT	CCAG	TC	TGGCTT	CA	TGCTGTG	ATGTC	3522		
Db	3614	GAGGGG	CA	GGGCTT	CAAG	GTATAT	TATGGCT	CCAG	TC	TGGCTT	CA	TGCTGTG	ATGTC	3673		
QY	3523	GAC	TC	CGGGG	AAAC	AC	ACTAT	ATCA	TATCC	CGTGTGA	CA	ATCCAG	AC	3582		
Db	3674	GAC	TC	CGGGG	AAAC	AC	ACTAT	ATCA	TATCC	CGTGTGA	CA	ATCCAG	AC	3733		
QY	3583	CATG	CCAT	CACTCTT	CTCC	CCCA	AC	CGG	AGG	AGTGTG	CTGTG	CTAC	AG	3642		
Db	3734	CATG	CCAT	CACTCTT	CTCC	CCCA	AC	CGG	AGG	AGTGTG	CTGTG	CTAC	AG	3793		
QY	3643	GAGGGT	GTCTAC	GTCA	CA	CGTAC	GGGG	CGATCAT	TTAA	GATGTGTGTG	CTG	CA	AGTGGGG	3702		
Db	3794	GAGGGT	GTCTAC	GTCA	CA	CGTAC	GGGG	CGATCAT	TTAA	GATGTGTGTG	CTG	CA	AGTGGGG	3853		
QY	3703	GAGAT	TG	CTACTT	CTGTG	GG	CCCTAC	ATCTGT	CCAA	CCAG	ATAT	TGGGCT	GGGGTGA	3762		
Db	3854	GAGAT	TG	CTACTT	CTGTG	GG	CCCTAC	ATCTGT	CCAA	CCAG	ATAT	TGGGCT	GGGGTGA	3913		
QY	3763	GCCAT	T	AGAT	CCGCTT	GTG	AG	AG	CGGG	CCACTG	CA	CGGGGT	CTTAC	ATG	CA	3822
Db	3914	GCCAT	T	AGAT	CCGCTT	GTG	AG	AG	CG							

QY 3823 GCTCAGAGCTCAAGTCTCTGTGTGAGCGGAGTGAAGTGTGTTTTCCTCACTCCG 3882  
DB 3974 GCTCAGAGCTCAAGTCTCTGTGTGAGCGGAGTGAAGTGTGTTTTCCTCACTCCG 4033  
QY 3883 TCTGGGGGAGGAGGAGGAGTCTTCTGATGATCTGAAACCGTACTGATCACTGAG 3942  
DB 4034 TCTGGGGGAGGAGGAGGAGTCTTCTGATGATCTGAAACCGTACTGATCACTGAG 4093  
QY 3943 TGAAGAGG 3951  
DB 4094 TGACGGGGC 4102

RESULT 8  
AADI17760  
ID AADI17760 standard; DNA; 3912 BP.

10-DEC-2001 (first entry)

Human novel STE20-like protein, NOV-3b encoding DNA.

Human; NOV-X protein; KIAA1233-like protein; STE20-like protein; tumour;  
trypsin inhibitor-like protein; gene therapy; haematopoietic; illness;  
immunological disorder; neurodegenerative disorder; Alzheimer's disease;  
Parkinson's disease; immunomodulatory; pharmacogenomic; haemostatic;  
human immunodeficiency virus; HIV; fertility disorder; neuroprotective;  
cytostatic; neotropic; anti-fertility; cancer; chromosome 17;  
NOV-3b protein; ds.

Homo sapiens.

Key Location/Qualifiers  
1..3912  
/\*tag= a  
/product= "Human novel STE20-like protein, NOV-3b"

W0200162928-A2.

30-AUG-2001.

26-FEB-2001; 2001WO-US006151.

25-FEB-2000; 2000US-0184951P.

28-FEB-2000; 2000US-0185548P.

01-MAR-2000; 2000US-0185967P.

18-APR-2000; 2000US-0197723P.

27-APR-2000; 2000US-0199957P.

23-FEB-2001; 2001US-00789390.

(CURA-) CUBAGEN CORP.

Vernet CAM, Fernandes E, Shinkels RA, Macdougall J, Spaderna SK;

WPI; 2001-582051/65.

P-PSDB; AAE10612.

New isolated KIAA1233-like, STE20-like, or trypsin inhibitor-like

polypeptide for diagnosing and treating pathological disorders, such as

Parkinson's disease and for use in pharmacogenomics.

Claim 9; Page 51-52; 189pp; English.

The invention relates to novel human polypeptides referred as NOV-X and

their corresponding nucleic acid sequences. NOV-X collectively include

NOV-1, NOV-2a and NOV-2b which are novel KIAA1233-like polypeptides, NOV-

3a, NOV-3b, NOV-3c and NOV-3d which are novel STE20-like polypeptides and

NOV-4a, NOV-4b, NOV-4c, NOV-4d and NOV-4e which are novel trypsin

inhibitor-like polypeptides. NOV-X is used to identify a potential

therapeutic agent that can modulate its activity and can be used for

treating a pathology related to aberrant expression or aberrant

physiological interactions of NOV-X. NOV-X or its DNA is used to

CC determine the presence or predisposition to a disease associated with  
CC altered levels of NOV-X. NOV-X, its DNA and its antibody are used to  
CC treat or prevent a pathology associated with NOV-X. The pathological  
CC states that can be treated or prevented are haematopoietic, cancer,  
CC immunological, tumour, neurodegenerative (e.g. Alzheimer's and  
CC Parkinson's disease), human immunodeficiency virus (HIV) illness and  
CC fertility disorders. NOV-X DNA is used in gene therapy. The present  
CC sequence is a DNA encoding human novel STE20-like protein, NOV-3b.  
CC gene is located at chromosome 17  
XX  
SQ Sequence 3912 BP; 924 A; 1171 C; 1187 G; 630 T; 0 U; 0 Other;

Query Match 90.7%; Score 3583.8; DB 5; Length 3912;  
Best Local Similarity 94.9%; Pred. No. 0;  
Matches 3816; Conservative 0; Mismatches 12; Indels 195; Gaps 3;

QY 7 ATGGGCGACCGACCCCGCCGAGCTGAGACGACATCCAGCTGCGCCCTCGGGAC 66  
DB 1 ATGGGCGACCGACCCCGCCGAGCTGAGACGACATCCAGCTGCGCCCTCGGGAC 60  
QY CCTGCTGGGATCTTTGAGCTTGTGAGGTGCTGCGCAATGGAACCTACGACAGGTGAC 126  
DB 61 CTTGCTGGGATCTTTGAGCTTGTGAGGTGCTGCGCAATGGAACCTACGACAGGTGAC 120  
QY 127 AAGGTCGCGCATGTCAAGACGCGGCAAGCTGCTGCGCATCAAGTCAATGATGTCACGAG 186  
DB 121 AAGGTCGCGCATGTCAAGACGCGGCAAGCTGCTGCGCATCAAGTCAATGATGTCACGAG 180  
QY 187 GACGAGAGGAGAGATTAACAGAGATCAACATGCTGGAAGAAAGTCTCACACCGC 246  
DB 181 GACGAGAGGAGAGATTAACAGAGATCAACATGCTGGAAGAAAGTCTCACACCGC 240  
QY 247 AACATGCGCACCTACTACGAGACCTTCTCATCAAGAGAGAGCCCGGGAGAAAGATGACCG 306  
DB 241 AACATGCGCACCTACTACGAGACCTTCTCATCAAGAGAGAGCCCGGGAGAAAGATGACCG 300  
QY 307 CTTGCTGGGATCTTTGAGCTTGTGAGGTGCTGCGCAATGGAACCTACGACAGGTGAC 366  
DB 301 CTTGCTGGGATCTTTGAGCTTGTGAGGTGCTGCGCAATGGAACCTACGACAGGTGAC 360  
QY 367 AAGGCGACCGCCCTGAGAGAGAGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 426  
DB 361 AAGGCGACCGCCCTGAGAGAGAGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
QY 427 CTGGCCCATCTCATGAGCCCAAGAGTATGATGATGATGATGATGATGATGATGATGATG 486  
DB 421 CTGGCCCATCTCATGAGCCCAAGAGTATGATGATGATGATGATGATGATGATGATGATG 480  
QY 487 CTGACAGAGAAATGCTGAGGTCAAGCTAGTGAATTTGGGGTGAAGTCTCACTGACCGC 546  
DB 481 CTGACAGAGAAATGCTGAGGTCAAGCTAGTGAATTTGGGGTGAAGTCTCACTGACCGC 540  
QY 547 ACCGTGGGCAAGCGAACAATTTTCTATTTGGGACTCCCTCTGAGATGCTCCAGAGTCA 606  
DB 541 ACCGTGGGCAAGCGAACAATTTTCTATTTGGGACTCCCTCTGAGATGCTCCAGAGTCA 600  
QY 607 GCGTGTGATGAACCCCTGATGAGCACTATGATTAACAGAGATGATATTTGGTCTCTAGA 666  
DB 601 GCGTGTGATGAACCCCTGATGAGCACTATGATTAACAGAGATGATATTTGGTCTCTAGA 660  
QY 667 ATCAAGGCAATGAGATGAG 726  
DB 661 ATCAAGGCAATGAGATGAG 720  
QY 727 GCGCTTCTCTCATTTCTGAGAACCTTCGCGCAGGCTCAAGTCCAGAAAGTGTCTAG 786  
DB 721 GCGCTTCTCTCATTTCTGAGAACCTTCGCGCAGGCTCAAGTCCAGAAAGTGTGTAG 780  
QY 787 AAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 846  
DB 781 AAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840

OY	847	GAGGAGCTACTGAAGTTTCCCTTCATCCGGGACAGGCTCCAGACGGGACGTC	906
Db	841	GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACAGGCTCCAGACGGGACGTC	900
OY	907	CAGCTTAAGGACCACTTGAACCGATCCCGGAGAAACGGGGTGAAGAAAGACAGAA	966
Db	901	CAGCTTAAGGACCACTTGAACCGATCCCGGAGAAACGGGGTGAAGAAAGACAGAA	960
OY	967	TATGAGTACAGCGGACGAGGAGGAAAGTGAACGCCATGAGAGAAAGAGAGCCAAAG	1026
Db	961	TATGAGTACAGCGGACGAGGAGGAAAGTGAACGCCATGAGAGAAAGAGAGCCAAAG	1020
OY	1027	TCCATCATGAACGTGCTTGAGAGATGCACTCTACGCCGGGAAATTTCTCGGCTCCAGAG	1086
Db	1021	TCCATCATGAACGTGCTTGAGAGATGCACTCTACGCCGGGAAATTTCTCGGCTCCAGAG	1080
OY	1087	GAAATTAAGACACTCAGAGGCTTTAAACACGACGACGACGCTGACAGCAGCAGCAG	1146
Db	1081	GAAATTAAGACACTCAGAGGCTTTAAACACGACGACGACGCTGACAGCAGCAGCAG	1144
OY	1147	CGAGACCCCGAGGCAACAATCAACACTGCTGACACAGCGCAGCGGCGCTAAGAGAG	1206
Db	1141	CGAGACCCCGAGGCAACAATCAACACTGCTGACACAGCGCAGCGGCGCTAAGAGAG	1200
OY	1207	CAGAAAGAGAGACGGGCGCGCTGAGAGACACACGGCGGGAGCGGAGCAGCGAAG	1266
Db	1201	CAGAAAGAGAGACGGGCGCGCTGAGAGACACACGGCGGGAGCGGAGCAGCGAAG	1260
OY	1267	CTGCAGAGAAAGAACAGACAGCGGGGCGTGGAGGACATGCAGGCGCTGCGGGCGGAGAG	1326
Db	1261	CTGCAGAGAAAGAACAGACAGCGGGGCGTGGAGGACATGCAGGCGCTGCGGGCGGAGAG	1320
OY	1327	GAGCGGCGGACAGCGGACCTGTAGCAGGAAATACAGCGGAAACACTGAGAGGACGACGG	1386
Db	1321	GAGCGGCGGACAGCGGACCTGTAGCAGGAAATATTCGTACACAGCTAGAGGACGACGG	1380
OY	1387	CAGTCAGAAAGCTCTCAGAGGCACTGCACGACGAGCATGCTTACATGTCCTTGAG	1446
Db	1381	CAGTCAGAAAGCTCTCAGAGGCACTGCACGACGAGCATGCTTACATGTCCTTGAG	1440
OY	1447	CAGCAGCAACAGCAGCAGCAGCTTGAAACACGACGACGACGACGCTGCTGGGGAC	1506
Db	1441	CAGCAGCAACAGCAGCAGCAGCTTGAAACACGACGACGACGACGCTGCTGGGGAC	1500
OY	1507	AGGAAGCCCTGTACATTTATGTTGGGGACATGATCCCGCTGACAAACACAGCTGGGCC	1566
Db	1501	AGGAAGCCCTGTACATTTATGTTGGGGACATGATCCCGCTGACAAACACAGCTGGGCC	1560
OY	1567	CGAGAGGTAGAAAGAGAGAACAGAGATGAACAGCAGCAGAACTCTCCCTGGCCAAAGGC	1626
Db	1561	CGAGAGGTAGAAAGAGAGAACAGAGATGAACAGCAGCAGAACTCTCCCTGGCCAAAGGC	1620
OY	1627	AAGCCAGGCAACAAGGGGCTTGAAGCCCCCATCCCCAGGCTCCCCAGGGGCCCCCAGGA	1686
Db	1621	AAGCCAGGCAACAAGGGGCTTGAAGCCCCCATCCCCAGGCTCCCCAGGGGCCCCCAGGA	1680
OY	1687	CCCCCTTTCCAGACTCTCTTATGACAGAGCGCGGTGAGGCCCAAGAGAGGACCGGACA--	1744
Db	1681	CCCCCTTTCCAGACTCTCTCTTATGACAGAGCGCGGTGAGGCCCAAGAGAGAGGACCGGACAAG	1744
OY	1745	-----AG	1746
Db	1741	AGCCTGTGGGACACCGGGTCCCACTGAAGCCAATGACGACCTGTACCCCGATCCGAG	1800
OY	1747	TCCCTGACGAGACAGGCCCAACCCGAAACTTGGGTGCTTCCAGGCTCCCATGACCCGAC	1806
Db	1801	TCCCTGACGAGACAGGCCCAACCCGAAACTTGGGTGCTTCCAGGCTCCCATGACCCGAC	1860
OY	1807	CCTGCGAATCCCGGACACCACTGCGCACGCGCCAGTGCACGAGAGAGCTGATCGGACGAAT	1866
Db	1861	CCTGCGAATCCCGGACACCACTGCGCACGCGCCAGTGCACGAGAGAGCTGATCGGACGAAT	1920
OY	1867	TCAGACCCCACTCTGAAGGACCTTGCGCCCAAGCCGAAATCCCCAGCCTGGGTGCGCCA	1926

Db	1921	TCGACCCCACTCTGAGAGACTGAGCCCAAGCCCAATCCCCCACTGGGTCCGCCA	1986
Qy	1927	GATACGAGGCGCCCAACCCAGGTGCTCAGAGACTCATCTATTCGCACTGCCTTAAC	1986
Db	1981	GATACGAGGCGCCCAACCCAGGTGCTCAGAGACTCATCTATTCGCACTGCCTTAAC	2040
Qy	1987	ACCACTGGGGCCGAGGGTCCCGGCACGCCAGGCAATCCCTGCCAGACTTCGACGAAAC	2044
Db	2041	ACCACTGGGGCCGAGGGTCCCGGCAGGCCAGGCAATCCCTGCCAGACTTCGACGAAAC	2085
Qy	2047	TCGCGCTGGCAATATATCTGCAAAAGGGGGGCAAGGGGGGCAOCCCAAGCTTCAAGG	2108
Db	2086	-----	2085
Qy	2107	CCCCCTGCTCAGCCCCCTGCGCCGCCCAACGCTCTAGTAACCCCGACTTCAGAGAGAGC	2166
Db	2086	-----ACTAATCCCGACTCAGAGAGAGC	2109
Qy	2167	GACCTGGCTGGAAAGCGTCGAGACGCTCTTCAAGCTTCTCAAGGACCTTCCCAAG	2228
Db	2110	GACCTGGCTGGAAAGCGTCGAGACGCTCTTCAAGCTTCTCAAGGACCTTCCCAAG	2166
Qy	2227	GCTGGCTCACTGAGCCGGAACCGGTGGGAACCTCTCCAAACTGGACAGCTCCCTGTG	2288
Db	2170	GCTGGCTCACTGAGCCGGAACCGGTGGGAATCTCTCCAAACCGGACAGCTCCCTGTG	2228
Qy	2287	CTCTCCCTGGGAATAAAGCCAAAGCCCAACACACACGCTCAAGGCGCAGGCGCCGCA	2346
Db	2230	CTCTCCCTGGGAATAAAGCCAAAGCCCAACACACGCTCAAGGCGCAGGCGCCGCA	2288
Qy	2347	-----GACTTGTGTGCTGAAGAAGCGGACTCTGAGCGAG	2388
Db	2290	AGCTATAAGCAGCAATGTTGAGGAGCTTTGTGCTGAAGAAGCGGACTCTGAGCGAG	2346
Qy	2383	GCCCCCTGGCTTCCCAAGAAGCCCATGGAATCTACTCTGCTCACAAGAGAGAGTGGAAAGC	2444
Db	2350	GCCCCCTGGCTTCCCAAGAAGCCCATGGAATCTACTCTGCTCACAAGAGAGAGTGGAAAGC	2405
Qy	2443	AGTGAAGACGACGAGAGAGAGGCGGAAGGCGGCGACGACGAGAGGAGCAGAGATCCCTT	2502
Db	2410	AGTGAAGACGACGAGAGAGAGGCGGAAGGCGGCGACGACGAGAGAGTGGAAAGC	2466
Qy	2503	GAGGGGCGCAGCGATGGGGATACAGACAGCTCAGACCATGTGTTCACAGCGTCGAG	2563
Db	2470	GAGGGGCGCAGCGATGGGGATACAGACAGCTCAGACCATGTGTTCACAGCGTCGAG	2522
Qy	2583	GAGATCACCGGGAACCCAGCCCCCATACGAGGGCGGCAACATGTGTTCACAGCCCCCT	2688
Db	2530	GAGATCACCGGGAACCCAGCCCCCATACGAGGGCGGCAACATGTGTTCACAGCCCCCT	2588
Qy	2633	GAAAGGAGGGGAATCTGCTGCAATGCTGACAGCAATGGGTACATAAACTGCTGACGTG	2688
Db	2580	GAAAGGAGGGGAATCTGCTGCAATGCTGACAGCAATGGGTACATAAACTGCTGACGTG	2649
Qy	2683	GTCGAGCCCAAGCACTCAACCCACGAGAACGCAAAAGGCCAAAGCCCACTTCGAAGAT	2742
Db	2650	GTCGAGCCCAAGCACTCAACCCACGAGAACGCAAAAGGCCAAAGCCCACTTCGAAGAT	2709
Qy	2743	GGGAGGTGTCATACAGTCTCTGTGGGTGTGTAAGGCCCTTGGCAAGACTCTTCAAG	2802
Db	2710	GGGAGGTGTCATACAGTCTCTGTGGGTGTGTAAGGCCCTTGGCAAGACTCTTCAAG	2769
Qy	2803	ATGATTTTGATCTAAGGGATCTACAGCTGAGAGGAGAGTGGGGACAGATCCCATCA	2862
Db	2770	ATGATTTTGATCTAAGGGATCTACAGCTGAGAGGAGAGTGGGGACAGATCCCATCA	2829
Qy	2863	GCCCTAGTGGTGAAGAGGAGCACTCGGCTCGACCAAGCTGCAGTAAGAGTGAAGAGGT	2922
Db	2830	GCCCTAGTGGTGAAGAGGAGCACTCGGCTCGACCAAGCTGCAGTAAGAGTGAAGAGGT	2889
Qy	2923	TCTGTGCTCAAGTGAATCCCAACCAACCCGGGCGCAAGTGAAGCCCTGAGATCCGG	2982

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Db 2890 TCTGTGTCAACGTGATCCCAACCAACCCGGGCCACAGTAGAGACCCCTGAGATCCGG 2949
QY 2893 AAGTACAAAGAACGATTTCACTCCGAGATCCTCTGTGCAAGCCCTTTGGGGGGTCAACTG 3042
Db 2950 AAGTACAAAGAACGATTTCACTCCGAGATCCTCTGTGCAAGCCCTTTGGGGGGTCAACTG 3009
QY 3043 CTGTGGGCAAGGAAACGGGCTGATGTGTGTCGACCCGAGAGTGGGCAAGGCTGAT 3102
Db 3010 CTGTGGGCAAGGAAACGGGCTGATGTGTGTCGACCCGAGAGTGGGCAAGGCTGAT 3069
QY 3103 GGAATCTATTTGGGGGCGGAGCTTTCAGACAGATGATGTGTGTCGAGGGGCTCAACTGCTC 3162
Db 3070 GGAATCTATTTGGGGGCGGAGCTTTCAGACAGATGATGTGTGTCGAGGGGCTCAACTGCTC 3129
QY 3163 ATCAACATCTCAGGAAAAAGAACAACTGGCGGGTATTTACCTGTCTGCTCCGGGAC 3222
Db 3130 ATCAACATCTCAGGAAAAAGAACAACTGGCGGGTATTTACCTGTCTGCTCCGGGAC 3189
QY 3223 AAGATTTGCAATGATCCCAAGATGAGAGAGAGAGGCTGGACCAACCTGGGGGAC 3282
Db 3190 AAGATTTGCAATGATCCCAAGATGAGAGAGAGAGGCTGGACCAACCTGGGGGAC 3249
QY 3283 ATGAGAGGCTGCGGCACTACCGTGTGTGAATAAGAGCGGATTAAGTTCGTGTCATC 3342
Db 3250 ATGAGAGGCTGCGGCACTACCGTGTGTGAATAAGAGCGGATTAAGTTCGTGTCATC 3309
QY 3343 GGCCTCAAGAGCTCCGTGAGAGTGTATGCTTGGGCCCCCAACCTTACCAAAATTCATG 3402
Db 3310 GGCCTCAAGAGCTCCGTGAGAGTGTATGCTTGGGCCCCCAACCTTACCAAAATTCATG 3369
QY 3403 GCCTCAAGTCTTTGGCCGACCTCCGCCACCGCCCTGCTGTGTCAGCTGACAGTAGAG 3462
Db 3370 GCCTCAAGTCTTTGGCCGACCTCCGCCACCGCCCTGCTGTGTCAGCTGACAGTAGAG 3429
QY 3463 GAGGGGCAAGCGGCTCAAGGTCATTAAGGCTCAAGTCTGCTGCTTCATGCTGTGATGTC 3522
Db 3430 GAGGGGCAAGCGGCTCAAGGTCATTAAGGCTCAAGTCTGCTGCTTCATGCTGTGATGTC 3489
QY 3523 GACTGGGGGAAACAGCTATTAACATCCCTGTGCAACATCCAGAGCCAGATCAAGGCC 3582
Db 3490 GACTGGGGGAAACAGCTATTAACATCCCTGTGCAACATCCAGAGCCAGATCAAGGCC 3549
QY 3583 CATGCCATCATCTTCTCCCAACACCGAGGAGATGAGATCTGCTGTACAGAGAC 3642
Db 3550 CATGCCATCATCTTCTCCCAACACCGAGGAGATGAGATCTGCTGTGTACAGAGAC 3609
QY 3643 GAGGGTGTCTACGTCAACAGTACGGGCGCATATTAAAGATGTGTGCTGCAAGTGGGG 3702
Db 3610 GAGGGTGTCTACGTCAACAGTACGGGCGCATATTAAAGATGTGTGCTGCAAGTGGGG 3669
QY 3703 GAGATGCCCTACTTCTGTGCGCTTACATCTGCTCAACCAATATATGGGCTGGGGTGA 3762
Db 3670 GAGATGCCCTACTTCTGTGCGCTTACATCTGCTCAACCAATATATGGGCTGGGGTGA 3729
QY 3763 GGCATTGAGATCCGCTGTGAGAGAGCGGCACTTCAGCGGGGTCTTTCAGCAAAACA 3822
Db 3730 GGCATTGAGATCCGCTGTGAGAGAGCGGCACTTCAGCGGGGTCTTTCAGCAAAACA 3789
QY 3823 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAAGTGTGTTTCTCCTCAGTCCG 3882
Db 3790 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAAGTGTGTTTCTCCTCAGTCCG 3849
QY 3883 TTTGGGGGAGAGAGCAAGTTTACTTCAATGATCTGCAACCGTAACTGCAATGAATGG 3942
Db 3850 TTTGGGGGAGAGAGCAAGTTTACTTCAATGATCTGCAACCGTAACTGCAATGAATGG 3909
QY 3943 TGA 3945
Db 3910 TGA 3912

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RESULT 9  
AAD17759

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ID AAD17759 standard; DNA; 3999 BP.
XX
AC AAD17759;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human novel STE20-like protein, NOV-3a encoding DNA.
XX
KW Human; NOV-X protein; KIAA1233-like protein; STE20-like protein; tumour;
KW trypsin inhibitor-like protein; gene therapy; haematopoietic; illness;
KW immunological disorder; neurodegenerative disorder; Alzheimer's disease;
KW Parkinson's disease; immunomodulatory; pharmacogenomic; haemostatic;
KW human immunodeficiency virus; HIV; fertility disorder; neuroprotective;
KW cytosolic; neotropic; anti-fertility; cancer; chromosome 17;
KW NOV-3a protein; ds.
XX
OS Homo sapiens.
XX
FH Key 1..3999 Location/Qualifiers
FT CDS /tag=a
FT /product= "Human novel STE20-like protein, NOV-3a"
PD
PE
PR 25-FEB-2000; 2000US-0184951P.
PR 28-FEB-2000; 2000US-0185548P.
PR 01-MAR-2000; 2000US-0185967P.
PR 18-APR-2000; 2000US-0197723P.
PR 27-APR-2000; 2000US-0199957P.
PR 23-FEB-2001; 2001US-00789390.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Vernet CAM, Fernandes E, Shinkets RA, Macdougall J, Spaderma SK,
XX WPI, 2001-582051/65.
XX DR P-PSDB; AAB10611.
XX
PT New isolated KIAA1233-like, STE20-like, or trypsin inhibitor-like
PT polypeptide for diagnosing and treating pathological disorders, such as
PT Parkinson's disease and for use in pharmacogenomics.
XX
PS Claim 9; Page 44-45; 189pp; English.
XX
CC The invention relates to novel human polypeptides referred as NOV-X and
CC their corresponding nucleic acid sequences. NOV-X collectively include
CC NOV-1, NOV-2a and NOV-2b which are novel KIAA1233-like polypeptides, NOV-
CC 3a, NOV-3b, NOV-3c and NOV-3d which are novel STE20-like polypeptides and
CC NOV-4a, NOV-4b, NOV-4c, and NOV-4e which are novel trypsin
CC inhibitor-like polypeptides. NOV-X is used to identify a potential
CC therapeutic agent that can modulate its activity and can be used for
CC treating a pathology related to aberrant expression or aberrant
CC physiological interactions of NOV-X. NOV-X or its DNA is used to
CC determine the presence or predisposition to a disease associated with
CC altered levels of NOV-X. NOV-X, its DNA and its antibody are used to
CC treat or prevent a pathology associated with NOV-X. The pathological
CC states that can be treated or prevented are haematopoietic, cancer,
CC immunological, tumour, neurodegenerative (e.g. Alzheimer's and
CC Parkinson's disease), human immunodeficiency virus (HIV) illness and
CC fertility disorders. NOV-X DNA and its DNA are used in pharmacogenomics for
CC predictive medicine. NOV-X DNA is used in gene therapy. The present
CC sequence is a DNA encoding human novel STE20-like protein, NOV-3a. NOV-3a
CC gene is located at chromosome 17
XX
SQ Sequence 3999 BP; 948 A; 1195 G; 1215 C; 641 T; 0 U; 0 Other;

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Query Match 88.6%; Score 3501.2; DB 5; Length 3999;  
Best Local Similarity 93.1%; Pred. No. 0;

Matches 3825; Conservative 0; Mismatches 3; Indels 282; Gaps 4;				
Qy	7	ATGGCGAACCAGCCCGCCCGCCGAGCCTGAGCAGCATGACCTGTCCGCCCTGCGGAC	66	
Db	1	ATGGCGAACCAGCCCGCCCGCCGAGCCTGAGCAGCATGACCTGTCCGCCCTGCGGAC	60	
Qy	67	CCTGCTGGGATCTTTGAGCTTGTGAGGTTGTGCGCAATGGAACTTACGAGCAGGTGTAC	126	
Db	61	CCTGCTGGGATCTTTGAGCTTGTGAGGTTGTGCGCAATGGAACTTACGAGCAGGTGTAC	120	
Qy	127	AAGGTCGGCATGTTCAGAACGGGAGAGCTGTGCTGCATCAAGTTCATGATGTCAAGAG	186	
Db	121	AAGGTCGGCATGTTCAGAACGGGAGAGCTGTGCTGCATCAAGTTCATGATGTCAAGAG	180	
Qy	187	GACGAGAGAGAGATCAACAGAGATCAACATGCTGAAAAAGTACTTCAACACCGC	246	
Db	181	GACGAGAGAGAGATCAACAGAGATCAACATGCTGAAAAAGTACTTCAACACCGC	240	
Qy	247	AAACATGCGACCTACTACGAGAGCTTCAATCAAGAAAGAGCCCGGAAAGCATGACAG	306	
Db	241	AAACATGCGACCTACTACGAGAGCTTCAATCAAGAAAGAGCCCGGAAAGCATGACAG	300	
Qy	307	CTCTGCTGTGTGATGAGATTTCTGTGTGTCTGTGTCTGTGTCTGTGTCTGTGTCTGTGT	366	
Db	301	CTCTGCTGTGTGATGAGATTTCTGTGTGTCTGTGTCTGTGTCTGTGTCTGTGTCTGTGT	360	
Qy	367	AAAGGCAACGCTCTGAGAGAGAGCTGTATCCGCTATATCTGTGAGAGAGATCTTCAAGG	426	
Db	361	AAAGGCAACGCTCTGAGAGAGAGCTGTATCCGCTATATCTGTGAGAGAGATCTTCAAGG	420	
Qy	427	CTGGCCCATCTTCATGCGCCCAAGAGGTGATCCATGAGACATCAAGGGGAGAAATGTGTG	486	
Db	421	CTGGCCCATCTTCATGCGCCCAAGAGGTGATCCATGAGACATCAAGGGGAGAAATGTGTG	480	
Qy	487	CTGACAGAGAAATGCTGAGAGTCAAGCTAGTGAATTTTGGGGTGAAGTCTCAGCTGAGCCG	546	
Db	481	CTGACAGAGAAATGCTGAGAGTCAAGCTAGTGAATTTTGGGGTGAAGTCTCAGCTGAGCCG	540	
Qy	547	ACCGTGGGAGAGCGGAAACATTTCAATGGAGACTCCCTCACTGGATGGCTTCAGAGGTCAATC	606	
Db	541	ACCGTGGGAGAGCGGAAACATTTCAATGGAGACTCCCTCACTGGATGGCTTCAGAGGTCAATC	600	
Qy	607	GCCCTGTATGAGAAACCCGTGATGCCACTATGATTAAGAGAGTAAATTTGTGCTCTAGAG	666	
Db	601	GCCCTGTATGAGAAACCCGTGATGCCACTATGATTAAGAGAGTAAATTTGTGCTCTAGAG	660	
Qy	667	ATCAAGGCTATGAGATGAG	726	
Db	661	ATCAAGGCTATGAGATGAG	720	
Qy	727	GCCCTCTTCTCTATTTCTCGGAAACCTTCGCGCAGGCTCAAGTCCAGAAAGTGTCTAAG	786	
Db	721	GCCCTCTTCTCTATTTCTCGGAAACCTTCGCGCAGGCTCAAGTCCAGAAAGTGTCTAAG	780	
Qy	787	AAGTTCATTTGATTTGATGACATGTCTCATCAAGACTTACCTGAGGCCCAACCCACG	846	
Db	781	AAGTTCATTTGATTTGATGACATGTCTCATCAAGACTTACCTGAGGCCCAACCCACG	840	
Qy	847	GAGCAGCTACTGAAAGTTTCCCTTCATCCGGAGACAGGCCACGAGAGAGAGTCCGCAATC	906	
Db	841	GAGCAGCTACTGAAAGTTTCCCTTCATCCGGAGACAGGCCACGAGAGAGAGTCCGCAATC	900	
Qy	907	CAGCTTAAAGACACATTTGACCGATCCCGAAGAAAGCGGAGTGAAGAAAGAGAGACAGAA	966	
Db	901	CAGCTTAAAGACACATTTGACCGATCCCGAAGAAAGCGGAGTGAAGAAAGAGAGACAGAA	960	
Qy	967	TATGATGACAGCGGAGAGAGAGAGAGATGACACCTATGAGAGAGAGAGAGAGAGAGAG	1026	
Db	961	TATGATGACAGCGGAGAGAGAGAGAGATGACACCTATGAGAGAGAGAGAGAGAGAGAG	1020	
Qy	1027	TCCATCAAGAAAGTCTGAGAGAGTCACTCTACGCGGAGAGTTTCTCCGCTCCAGAG	1086	
Db	1021	TCCATCAAGAAAGTCTGAGAGAGTCACTCTACGCGGAGAGTTTCTCCGCTCCAGAG	1080	

Qy	1087	GAATAATAGACACTGAGAGGCTTTAAACAGAGAGACAGCTGACAGACAGAGAG	1146	
Db	1081	GAATAATAGACACTGAGAGGCTTTAAACAGAGAGACAGCTGACAGACAGAGAG	1140	
Qy	1147	CGAGACCCGAGAGACATCAACCACTGTGTGACAGAGCGGAGCGGCTATAGAGAG	1206	
Db	1141	CGAGACCCGAGAGACATCAACCACTGTGTGACAGAGCGGAGCGGCTATAGAGAG	1200	
Qy	1207	CAGAAAGAGAGCGGCGCGCTGTGAGAGAGACAGCGGCGGAGCGGAGACACGGAAG	1266	
Db	1201	CAGAAAGAGAGCGGCGCGCTGTGAGAGAGACAGCGGCGGAGCGGAGACACGGAAG	1260	
Qy	1267	CTGAG	1326	
Db	1261	CTGAG	1320	
Qy	1327	GAGCGGCGAGAGCGGAGCGTGAACA-----	1352	
Db	1321	GAGCGGCGAGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG	1380	
Qy	1353	-----GGAATAC	1359	
Db	1381	CGACAGCTCGAGATCTTACAGCAACAGCTGCTCCAGAGAACAGGCTGCTGGAATAC	1440	
Qy	1360	AAAGGAG	1419	
Db	1441	AAAGGAG	1500	
Qy	1420	GAGCATGCTTCACTCAAGTCCCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1479	
Db	1501	GAGCATGCTTCACTCAAGTCCCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1560	
Qy	1480	CAGCAGCAGAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1539	
Db	1561	CAGCAGCAGAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1620	
Qy	1540	AAATCCCTGTGAG	1599	
Db	1621	AAATCCCTGTGAG	1680	
Qy	1600	CAGCAGAACTTCTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1659	
Db	1681	CAGCAGAACTTCTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1740	
Qy	1660	CCCCAGGCTTCCAG	1719	
Db	1741	CCCCAGGCTTCCAG	1800	
Qy	1720	GTGAG	1744	
Db	1801	GTGAG	1860	
Qy	1745	-----AGTCCCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1779	
Db	1861	TATGAG	1920	
Qy	1780	GCTTTCAGAGCTTCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1839	
Db	1921	GCTTTCAGAGCTTCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1980	
Qy	1840	GCCGAG	1899	
Db	1981	GCCGAG	2040	
Qy	1900	CCGAAATCCCGAGCTGGGAGTCCGCGCAGATTAAGAGAGAGAGAGAGAGAGAGAGAG	1959	
Db	2041	CCGAAATCCCGAGCTGGGAGTCCGCGCAGATTAAGAGAGAGAGAGAGAGAGAGAGAG	2100	
Qy	1960	ACCTCATCTATGCACTGAGCTTTAACAACAGTGGAGAGAGAGAGAGAGAGAGAGAG	2019	
Db	2101	ACCTCATCTATGCACTGAGCTTTAACAACAGTGGAGAGAGAGAGAGAGAGAGAGAG	2160	



OY	2020	GCAGTCCGCTGCAGACCTCTCGACGAACTCCGCTGCGAAATCTATCTGCAAAAGCGGGCA	2079
Db	2161	GCAGTCCGCTGCC-----	2172
OY	2080	GAGCGGGGCACCCAAAAGCTCTCAGAGGCCCCCTGCTCAGCCCCCTGCGCCGCCAAGCGC	2139
Db	2173	-----	2172
OY	2140	TCATGTAACCCCGACTTCAGAGAGGCAACCTTGCTGGGAACGCTCGGACAGCTGCTT	2199
Db	2173	--AGTAACCCCGACTTCAGAGAGGCGAACCTTGCTGGGAACGCTCGGACAGGCTCCTT	2229
OY	2200	CCAGCTCTCAACGGGCACTCTCCCGAGGCTGGCTCACTGGAGCGGAAACGGGTGGGAGCC	2259
Db	2230	CCAGCTCTCAACGGGCACTCTCCCGAGGCTGGCTCACTGGAGCGGAAACGGGTGGGAGTC	2289
OY	2260	TCCTTCAAACTGSAAGCTCCCTTGCTGCTCTCCCTGGGAATTAAGCAACCCCGACGAC	2319
Db	2280	TCCTTCAAAACGGGACAGCTCCCTTGCTGCTCTCCCTGGGAATTAAGCAACCCCGACGAC	2349
OY	2320	CACCGCTCACGCGCCAGGCGCGCCGCA-----GACTTTGTG	2355
Db	2350	CACCGCTCACGCGCCAGGCGCGCCGCACTTAAGCGAGCAATTGGTAGAGACTTTGTG	2409
OY	2356	TTTGCTGAAGAAGCGGCACTCTGAGAGAGGCCCCCTGGCTCCCAAGAAAGCCATGACATAC	2415
Db	2410	TTTGCTGAAGAAGCGGCACTCTGAGAGAGGCCCCCTGGCTCCCAAGAAAGCCATGACATAC	2469
OY	2416	TCGTGCTCACGCGAGAGAGGTGGAAAGCAGTAGAGCAAGCAGAGAGGAAGCGAAGCGGG	2475
Db	2470	TCGTGCTCACGCGAGAGAGGTGGAAAGCAGTAGAGCAAGCAGAGAGGAAGCGAAGCGGG	2529
OY	2476	CCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCGGACCGATGGGGATACAGACGCTC	2535
Db	2530	CCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCGGACCGATGGGGATACAGACGCTC	2589
OY	2536	AGCAGCAAGTGTGTCCAGACGTGAGAGAGATACCCGGGACCCAGCCCCCATAGGGGGCC	2595
Db	2590	AGCAGCAAGTGTGTCCAGACGTGAGAGAGATACCCGGGACCCAGCCCCCATAGGGGGCC	2649
OY	2596	GGCAGCATAGTGTGTCCAGCGCAACCCCTGAAGAGAGCGGAACCTGCTCATGCTGACAGC	2655
Db	2650	GGCAGCATAGTGTGTCCAGCGCAACCCCTGAAGAGAGCGGAACCTGCTGCACTGCTGACAGC	2709
OY	2656	AATGGGTACACAAACCTTGACGTGTTCAGCCCAAGCCACTCAACCCACCGAAGAACGC	2715
Db	2710	AATGGGTACACAAACCTTGACGTGTTCAGCCCAAGCCACTCAACCCACCGAAGAACGC	2769
OY	2716	AAAAGGCCAAACCCCACTCTCGAAGAGATGGGAGTGTGACTACAGTCTCGTGGGCTGGTA	2775
Db	2770	AAAAGGCCAAACCCCACTCTCGAAGAGATGGGAGTGTGACTACAGTCTCGTGGGCTGGTA	2829
OY	2776	AAGGCCCTTGCGCAAGAGCTCGTTCACAGATGTTTGATGATCTAGGGATCTACACCTGGA	2835
Db	2830	AAGGCCCTTGCGCAAGAGCTCGTTCACAGATGTTTGATGATCTAGGGATCTACACCTGGA	2889
OY	2836	GGCAGTGGGAGCAGCATCCCATCAACAGCCCTTAGTGGGTGAGAGGCACTCGGCTCGAC	2895
Db	2890	GGCAGTGGGAGCAGCATCCCATCAACAGCCCTTAGTGGGTGAGAGGCACTCGGCTCGAC	2949
OY	2896	CAGCTGCAGTACAGACGTGAGAGAGGTTCTGTGTGCACTGTGAATTCACCAACACCCGG	2955
Db	2950	CAGCTGCAGTACAGACGTGAGAGAGGTTCTGTGTGCACTGTGAATTCACCAACACCCGG	3009
OY	2956	GCCCAAGTGAAGACCCCTGAGATCCGGAAGTACAAAGAGCGATTCAACTCCGAGATCCTC	3015
Db	3010	GCCCAAGTGAAGACCCCTGAGATCCGGAAGTACAAAGAGCGATTCAACTCCGAGATCCTC	3069
OY	3016	TGTGAGGCTTTTGGGGGTCAACTGTCTGTGTGGCAGAGAAACGGGCTGATGTTCTG	3075
Db	3070	TGTGAGGCTTTTGGGGGTCAACTGTCTGTGTGGGCAAGAGAAACGGGCTGATGTTCTG	3129
OY	3076	GACCGAATGGGAGAGGCAAGGTGATGAGACTCATTTGGGCGGACGCTTCACAGCATGTG	3135

Db	3130	GACCGAAGTGGGCGAGGGCGAAGTGTATGACTCATTTGGGCGGCGAACCCCTTCAGACAGATG	3189
Qy	3136	GATGTGCTGGAGGGGCTCAACCTGCTCATCAACATCTCAAGGAAAAAGAACAACTGCGG	3195
Db	3190	GATGTGCTGGAGGGGCTCAACCTGCTCATCAACATCTCAAGGAAAAAGAACAACTGCGG	3249
Qy	3196	GTGTATTACCTGTCTCTGGCTCCCGGAACAAGATTCTGGACAAATGACCCAGAAAGTGGAGAG	3255
Db	3250	GTGTATTACCTGTCTCTGGCTCCCGGAACAAGATTCTGGACAAATGACCCAGAAAGTGGAGAG	3309
Qy	3256	AAGCAGGGCTTGGACCAACCGTGGGGGACATGGAGGGGCTGCGGGCACTACCGTGTGTGAAA	3315
Db	3310	AAGCAGGGCTTGGACCAACCGTGGGGGACATGGAGGGGCTGCGGGCACTACCGTGTGTGAAA	3369
Qy	3316	TACAGCGGATTAAAGTTCTTGCTATCGCCCTCAAGAGCTTCCTGGAGTGTATGCTGG	3375
Db	3370	TACAGCGGATTAAAGTTCTTGCTATCGCCCTCAAGAGCTTCCTGGAGTGTATGCTGG	3429
Qy	3376	GGCCCCCAACCCCTACACAAATTATAGGCTCTTAAGTCCCTTGGCCGACCTCCCCACCGC	3435
Db	3430	GGCCCCCAACCCCTACACAAATTATAGGCTCTTAAGTCCCTTGGCCGACCTCCCCACCGC	3489
Qy	3436	CCTCTGCTGGTGCAGCTGACAGTGAAGAGAGGGGCAAGGGCTCAAGGTCATCTATGCTCC	3495
Db	3490	CCTCTGCTGGTGCAGCTGACAGTGAAGAGAGGGGCAAGGGCTCAAGGTCATCTATGCTCC	3549
Qy	3496	AGTGTGGCTTCCATGCTGTGTGATGTGACTCGGGGAAACAGCTATGACATCTACATCCT	3555
Db	3550	AGTGTGGCTTCCATGCTGTGTGATGTGACTCGGGGAAACAGCTATGACATCTACATCCT	3609
Qy	3556	GTGCACATCCAGAGCCAGATCAAGCCCAATGCCATCATCTTCTCCGCCAACCCGAGGCG	3615
Db	3610	GTGCACATCCAGAGCCAGATCAAGCCCAATGCCATCATCTTCTCCGCCAACCCGAGGCG	3669
Qy	3616	ATGAGAGATGCTGCTGTGCTCAAGAGACAGAGGAGTGTACAGTCAACAGTACGGGCGCATC	3675
Db	3670	ATGAGAGATGCTGCTGTGCTCAAGAGACAGAGGAGTGTACAGTCAACAGTACGGGCGCATC	3729
Qy	3676	ATTAAAGATGTGTGTGCTGCAAGTGGGGGAGATGCTTCTTGTGGCTTACATCTGCTCC	3735
Db	3730	ATTAAAGATGTGTGTGCTGCAAGTGGGGGAGATGCTTCTTGTGGCTTACATCTGCTCC	3789
Qy	3736	AACCAAGTAAATGGGCTGGGGTGGAGAAAGCCATTGAGATCCGCTCTTGTGGAGACGGGCGAC	3795
Db	3790	AACCAAGTAAATGGGCTGGGGTGGAGAAAGCCATTGAGATCCGCTCTTGTGGAGACGGGCGAC	3849
Qy	3796	CTGCACGGGGCTTCAATGACCAACAGAGCTCAAGGCTCAAGTTCCTGTGTGACGGGAAT	3855
Db	3850	CTGCACGGGGCTTCAATGACCAACAGAGCTCAAGGCTCAAGTTCCTGTGTGACGGGAAT	3909
Qy	3856	GACAAAGTGTGTGTGCTCAAGTCCGCTCTTGGGGGACAGACCAGTTTACTTTCATGACT	3915
Db	3910	GACAAAGTGTGTGTGCTCAAGTCCGCTCTTGGGGGACAGACCAGTTTACTTTCATGACT	3969
Qy	3916	CTGAACCGTAACTGCATCATGAACTGGTGA	3945
Db	3970	CTGAACCGTAACTGCATCATGAACTGGTGA	3999
RESULT 10			
ADE34153			
ID ADE34153 standard; DNA; 4414 BP.			
XX ADE34153;			
XX 29-JAN-2004 (first entry)			
XX Human DNA encoding misshapen/NIKs-related kinase, Mink3b.			
XX Human; misshapen/NIKs-related kinase; Mink3b; ds; antiinflammatory;			
XX immunosuppressive; cytoskeletal, germinal centre kinase;			
XX G-UDN N-terminal kinase; JNK; extracellular signal response kinase; ERK;			



KM growth factor induced-ERK activation; proliferation;  
KM cell proliferation disorder; cell survival;  
KM intracellular signal transduction; apoptosis; morphological change;  
KM cell migration; gene therapy; inflammatory disease; autoimmune disease;  
KM immunodeficiency; cancer.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 209..2587  
FT /\*tag= a  
FT /product= "Mink3b"  
XX US2003077597-A1.  
XX 24-APR-2003.  
XX 19-OCT-2001; 2001US-00029115.  
XX 19-OCT-2001; 2001US-00029115.  
XX (LUOY/) LUO Y.  
XX (FUCA/) FU C A.  
XX (SHEN/) SHEN M.  
XX Luo Y, Fu CA, Shen M;  
XX WPI; 2003-635076/60.  
XX P-PSDB; ADE34152.  
PT New misshapen/NIKs-related kinase nucleic acid and proteins useful in  
PT gene therapy and for treating disorders, e.g. acute and chronic  
PT inflammatory diseases.  
PS Claim 3; SEQ ID NO 3; 53bp; English.  
XX The invention relates to a recombinant nucleic acid capable of  
CC hybridizing to a Human DNA encoding misshapen/NIKs-related kinase  
CC (Mink3a, 3b and 3c, germinal centre kinase proteins) appearing as  
CC ADE34151, ADE34153 and ADE34155, or at least 90% identity to them, or  
CC their complements. Also included are a recombinant polypeptide at least  
CC 95 % sequence identity to Mink3a, 3b or 3c (appearing as ADE34150,  
CC ADE34152 and ADE34154), screening for a candidate bioactive agent capable  
CC of modulating c-JUN N-terminal kinase (JNK) or extracellular signal  
CC response kinase (ERK) phosphorylation or activity, screening for a  
CC candidate bioactive agent capable of modulating growth factor induced-ERK  
CC activation in a mammalian cell, screening for a candidate bioactive agent  
CC capable of modulating proliferation in a mammalian cell, diagnosing a  
CC mammalian cell proliferation disorder, a medicament for treating a  
CC mammalian cell proliferation disorder and screening for a candidate agent  
CC capable of modulating cell survival. The MINK3 (misshapen/NIKs-related  
CC kinase) nucleic acids are useful in the modulation of intracellular  
CC signal transduction, cell proliferation, apoptosis, morphological change  
CC and migration of mammalian cells. MINK3 nucleic acids and proteins are  
CC specifically useful in gene therapy, and for treating, preventing or  
CC diagnosing acute and chronic inflammatory diseases, autoimmune diseases  
CC and diseases characterised by immunodeficiency. The compositions may also  
CC be used to treat MINK3 dysfunction related disorders, e.g. cancer. The  
CC nucleotide sequences may also be used as hybridisation probes, in  
CC chromosome and gene mapping, and in generating antisense RNA and DNA. The  
CC present sequence encodes Mink3b.  
XX  
SQ Sequence 4414 BP; 1010 A; 1339 C; 1317 G; 748 T; 0 U; 0 Other;  
Query Match 87.0%; Score 3437.2; DB 9; Length 4414;  
Best Local Similarity 90.1%; Pred. No. 0;  
Matches 3885; Conservative 0; Mismatches 3; Indels 426; Gaps 2;

DB 161 TACAAGGCTCGCATGTCACAGCGGCGAGCTGCTGCATCAAGTCAATGATGTACG 220  
QY 184 GAGGACGAGGAGGAGGATCAAA CAGAGATCAACATGCTGAAAAGTACTTCCACAC 243  
DB 221 GAGGACGAGGAGGAGGATCAAA CAGAGATCAACATGCTGAAAAGTACTTCCACAC 280  
QY 244 CGCAACATCGGACCTCTAGGAGCCCTTCATCAAGAAAGCCCCCGGAAAGATGAC 303  
DB 281 CGCAACATCGGACCTCTAGGAGCCCTTCATCAAGAAAGCCCCCGGAAAGATGAC 340  
QY 304 CAGCTCTGCTGATGATGAGATTCTGTGTCCTGTTCACTGATCACTGTTAAAGAAC 363  
DB 341 CAGCTCTGCTGATGATGAGATTCTGTGTCCTGTTCACTGATCACTGTTAAAGAAC 400  
QY 364 ACAAAAGGCAACGCTCTGAAAGAGAGCTATGCTATATCTGCAAGGAGATCTTCAG 423  
DB 401 ACAAAAGGCAACGCTCTGAAAGAGAGCTATGCTATATCTGCAAGGAGATCTTCAG 460  
QY 424 GGTCTGGCCCATCTCCATGCCCCCAAGGTATTCATGAGACATCAAGGGGAGAAATGTG 483  
DB 461 GGTCTGGCCCATCTCCATGCCCCCAAGGTATTCATGAGACATCAAGGGGAGAAATGTG 520  
QY 484 CTGCTGACAGAGAAATGCTGAGAGTCAAGTATTTTGGGGTGAAGTCTCAGCTGAC 543  
DB 521 CTGCTGACAGAGAAATGCTGAGAGTCAAGTATTTTGGGGTGAAGTCTCAGCTGAC 580  
QY 544 CGCACGCTGGGACAGACGGAACATCTTCAATGGGACTCCCTCATGATGCTCCAGAGTGC 603  
DB 581 CGCACGCTGGGACAGACGGAACATCTTCAATGGGACTCCCTCATGATGCTCCAGAGTGC 640  
QY 604 ATGCTCTGTGATGAGAACCTGATGCCCATATGATTAACAGAGATGATATTGGTCTTA 663  
DB 641 ATGCTCTGTGATGAGAACCTGATGCCCATATGATTAACAGAGATGATATTGGTCTTA 700  
QY 664 GGAATCAAGGCTATCGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 723  
DB 701 GGAATCAAGGCTATCGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 760  
QY 724 CGAGCCCTCTTCTCATTTCTCGGAAACCTTCGCGCAGAGGCTCAAGTCCAGAGTGTCT 783  
DB 761 CGAGCCCTCTTCTCATTTCTCGGAAACCTTCGCGCAGAGGCTCAAGTCCAGAGTGTCT 820  
QY 784 AAGAAGTTCATTGACTTCAATTGACACATGTTCTATCAAGACTTACCTGAGCCGCCACCC 843  
DB 821 AAGAAGTTCATTGACTTCAATTGACACATGTTCTATCAAGACTTACCTGAGCCGCCACCC 880  
QY 844 ACGGAGAGCTACGAGAGTTTCCCTCATCCGGGACGAGCCAGAGAGAGAGAGAGAGAG 903  
DB 881 ACGGAGAGCTACGAGAGTTTCCCTCATCCGGGACGAGCCAGAGAGAGAGAGAGAGAG 940  
QY 904 ATCCAGCTTAAAGACCACTTGAACCGATCCCGAAGAGAGCGGGGTGAAGAGAGAGACA 963  
DB 941 ATCCAGCTTAAAGACCACTTGAACCGATCCCGAAGAGAGCGGGGTGAAGAGAGAGACA 1000  
QY 964 GAATATGATGACAGCGGACGAGAGAGAGAGATGACAGCCATGAGAGAGAGAGAGAGCA 1023  
DB 1001 GAATATGATGACAGCGGACGAGAGAGAGAGATGACAGCCATGAGAGAGAGAGAGAGCA 1060  
QY 1024 AGCTCCATCATGAAACGAGGCTCGAGAGTCAAGCTTACGCGGGAGTTTCTCCGAGCTCAG 1083  
DB 1061 AGCTCCATCATGAAACGAGGCTCGAGAGTCAAGCTTACGCGGGAGTTTCTCCGAGCTCAG 1120  
QY 1084 CAGGAAATTAAGAGCACTGAGAGGCTTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAG 1143  
DB 1121 CAGGAAATTAAGAGCACTGAGAGGCTTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAG 1180  
QY 1144 CAGGAG 1203  
DB 1181 CAGGAG 1240  
QY 1204 GAGGAG 1263

D	b	1241	AAGCAGAAAGAGAGACCGCGCGCGGTGGAGAGCAACAGCGCGGAGACGGGAAACAAGCGG	1300
O	y	1264	AAGCTGCAGAGAAAGAGACACAGCGCGCTCGAGGACATTCAGAGCTCTCGCGCGGAG	1323
D	b	1301	AAGCTGCAGAGAAAGAGACAGACAGCGCGCTGAGAGGACATTCAGAGGCTCTCGCGCGGAG	1360
O	y	1324	GAGGACGGCGCGGACCGCGGAGCGTGGACAGGAATTCAAAGCGGAAAGCACTGGAGAGAG	1383
D	b	1361	GAGGACGGCGCGGACCGGAGCGTGGAGCAAGAAATTCAAAGCGGAAAGCACTGGAGAGAG	1420
O	y	1384	CGGCAGTGAGAACGTCTCCAGAGGACGCTGGAGAGAGCATGCGCTACCTCAAGTCCCTG	1443
D	b	1421	CGGCAGTGAGAACGTCTCCAGAGGAGCTGGAGAGAGCATGCTCAACTCAAGTCCCTG	1480
O	y	1444	CAGCAGCAACAACAGCAGCAGAGCTTCAGAAACAGCAGCAGCAGAGCTTCCTCGTGG	1503
D	b	1481	CAGCAGCAGCAACAGCAGCAGAGCTTCAGAAACAGCAGCAGCAGAGCTTCCTCGTGG	1540
O	y	1504	GACAGGAAGCCCTGTACCATTTAGTGTGGGGCAGTAAATCCCGTGACAAACAGAGCCGTG	1563
D	b	1541	GACAGGAAGCCCTGTGTACCATTTAGTGTGGGGCAGTAAATCCCGTGACAAACAGAGCCGTG	1600
O	y	1564	GCCGAGAGGTAGAAAGAGAGAAACAAGATGTAAACAAGCAGAGAACTCTCCCTTGCCAG	1623
D	b	1601	GCCGAGAGGTAGAAAGAGAGAAACAAGATGTAAACAAGCAGAGAACTCTCCCTTGCCAG	1660
O	y	1624	AGCAAGCCAGGACAGCAGCGGGGCTGAGGCCCTCATCCCGCAAGCTCTCCACAGGCCCCA	1683
D	b	1661	AGCAAGCCAGGACAGCAGCGGGGCTGAGGCCCTCATCCCGCAAGCTCTCCACAGGCCCCA	1720
O	y	1684	GGAACCCCTTTTCCAGATCTCTCTCTATGACAGGCGCGGTGGAGCCCCAGAGAGGACCCGAC	1743
D	b	1721	GGAACCCCTTTTCCAGATCTCTCTCTATGACAGGCGCGGTGGAGCCCCAGAGAGGACCCGAC	1780
O	y	1744	A-----	1744
D	b	1781	AAGAGCTGTGTGGACACCGGGGTCCCATGTAAAGCAATATGACAGCACTGTACCCCGATCC	1840
O	y	1745	-AGTCCCTGCAGAGACAGAGCCCAACCCGAAACTGTGTCTTCCTCCAGCTCTCCATGACCC	1803
D	b	1841	CAGTCCCTGCAGAGACAGAGCCCAACCCGAAACTGTGTGTCTTCCTCCAGCTCTCCATGACCC	1900
O	y	1804	GACCTGTGCATTCCTCCGACCCCATGTGCCACGCTCCGAGGAGCTGTATCTCGCCAG	1863
D	b	1901	GACCTGTGCATTCCTCCGACCCCATGTGCCACGCTCCGAGGAGCTGTATCTCGCCAG	1960
O	y	1864	AATTGAGACCCCACTCTGAGAGAACTGTGGCCCAAGCCGGAATCCCCAGCCTGGAGTCCGC	1923
D	b	1961	AATTGAGACCCCACTCTGAGAGAACTGTGGCCCAAGCCGGAATCCCCAGCCTGGAGTCCGC	2020
O	y	1924	CCAGATTAACAGAGCCCAACCAAGGTGCTCAGAGACCTCATCTATGTGCACTGCTT	1983
D	b	2021	CCAGATTAACAGAGCCCAACCAAGGTGCTCAGAGACCTCATCTATGTGCACTGCTT	2080
O	y	1984	AAACACAGTGGGGCTGAGAGGTCCTCGGCGCAGCCAGAGAGTTCGTGTCCAGACTTCGACGC	2043
D	b	2081	AAACACAGTGGGGCTGAGAGGTCCTCGGCGCAGCCAGAGAGTTCGTGTCCAGACTTCGACGC	2140
O	y	2044	AACTCCGCTGAGCAAACTATCTGTCAAAAGGCGGGCAGAGCGGGGACCCCAAGAGCTTCCA	2103
D	b	2141	AACTCCGCTGAGCAAACTATCTGTCAAAAGGCGGGCAGAGCGGGGACCCCAAGAGCTTCCA	2200
O	y	2104	GGGCGCCCTGTGACAGCCCTGTGGCCCGGCCCAACGCTCTAGTAAACCCGACCTCAGAGAG	2163
D	b	2201	GGGCGCCCTGTGACAGCCCTGTGGCCCGGCCCAACGCTCTAGTAAACCCGACCTCAGAGAG	2260
O	y	2164	AGCGACCTTGTGGGAAAGCTTCGAGCAGCGTCTTCCAGGCTCTCAACGGGACCTTCCC	2223
D	b	2261	AGCGACCTTGTGGGAAAGCTTCGAGCAGCGTCTTCCAGGCTCTCAACGGGACCTTCCC	2320
O	y	2224	CAGGCTGTCTCACTGGAGCGGAAACCGCGTGGAGAGCTCTCAAACTGGAGACAGCTCCCT	2283
D	b	2321	CAGGCTGTCTCACTGGAGCGGAAACCGCGTGGAGAGCTCTCTCAAACTGGAGACAGCTCCCT	2380

QY	2284	GTGCTCTCCCTGGGGAATTAAGCCAAAGCCAGACGACGACGCTCAGAGGCGAGGCGCC	2343
Db	2281	GTGCTCTCCCTGGGGAATTAAGCCAAAGCCAGACGACGACGCTCAGAGGCGAGGCGCC	2440
QY	2344	GCA-----	2346
Db	2441	GCAATGATGACCTGCTGGGAGAGGATGCGTGCTCATCTGATTGGGCTTAGCCTCA	2500
QY	2347	-----	2346
Db	2501	GGGTGCTGGGTGTCAGGGGTGGGTCTCCGCTGATCTAACGAGAAGGGCTGTGGGATGG	2560
QY	2347	-----	2346
Db	2561	AGGGACTGTGTCTTCATGTGTCTAACTTTCTTAACTTCTCTTAACCTCTCTCTTA	2620
QY	2347	-----	2346
Db	2621	ACCTCTCTCTTGCTGCTTTCTTCCCTCGGCCCCCTCCAGAGCTAATAAGCGACATTTG	2680
QY	2347	-----	2346
Db	2681	GTGAGGTTAAGTAGATGGGCGCTGTGTGGAGCCCTCTGTGCGCCCTGTGGGCGCTC	2740
QY	2347	-----	2346
Db	2741	CCGGCACCCTTTGTGTCTACCTCCACCAGGCCAGCTTCTCCGCCCTCAGCTGTGCTC	2800
QY	2347	-----GACCTTGTGTGTGTCTAAAGAGCGGACTCTGGACGAGGCCCTCGGCTCCC	2397
Db	2801	TCCTCTGACGAGCTTTGTGTGTCTTAAGAGCGGACTTGGACGAGGCCCTCGGCTCCC	2860
QY	2398	AAGAAGCCATGAGCTACTGTGTGTCTCAGCGAGGAGGTGGAAGACACTGTAGACGACGAG	2457
Db	2861	AAGAAGCGCATGAGCTACTGTGTGTCTCAGCGAGGAGGTGGAAGACACTGTAGACGACGAG	2920
QY	2458	GAGGAGGCGGAAGGCGGCGCCAGACGAGAGGGAGCAGAGATACCTCTGGGGGCCCGCAGAT	2517
Db	2921	GAGGAGGCGGAAGGCGGCGCCAGCAGAGAGGGAGCAGAGATACCTCTGGGGGCCCGCAGAT	2580
QY	2518	GGGATATCAGACAGCGTCAGACCATGTGTGTCCACGACGTGAGAGATCACCGGAGCC	2577
Db	2981	GGGATATCAGACAGCGTCAGACCATGTGTGTCCACGACGTGAGAGATCACCGGAGCC	3040
QY	2578	CAGCCCCCATTCAGGGGCGGCGCACCATGTGTGTCCAGCGCACCCCTGAAGAGAGCGGAGC	2637
Db	3041	CAGCCCCCATTCAGGGGCGGCGCACCATGTGTGTCCAGCGCACCCCTGAAGAGAGCGGAGC	3100
QY	2638	CTGCTGCATGTGTGACAGCAATGGGTACACAACTGTGCTGACTGTGTCTCAGGCCACGCAC	2697
Db	3101	CCGCTGCATGTGTGACAGCAATGGGTACACAACTGTGCTGACTGTGTCTCAGGCCACGCAC	3160
QY	2698	TCACCCACCCGAGAACACGACAAAGGCGCAAGGCCACCTCGAAGAGTGGGAGTGGATAC	2757
Db	3161	TCACCCACCCGAGAACACGACAAAGGCGCAAGGCCACCTCGAAGAGTGGGAGTGGATAC	3220
QY	2758	CAGTCTGATGGGTGTATAAGGCCCTCTGGAGAGAGCTGTTCACGATGTTGTGTGATCTTA	2817
Db	3221	CAGTCTGATGGGTGTATAAGGCCCTCTGGAGAGAGCTGTTCACGATGTTGTGTGATCTTA	3280
QY	2818	GGGATCTTACCAAGCCTGAGGAGGACGTGGGAGACGATCCCTCATCAGCCCTTAGTGAGGTGA	2877
Db	3281	GGGATCTTACCAAGCCTGAGGAGGACGTGGGAGACGATCCCTCATCAGCCCTTAGTGAGGTGA	3340
QY	2878	GAGGGACTCGGCTCTGACCACTGTCACTAACAAGTGAAGAGGTTCTGTGTGTCAAGTG	2937
Db	3341	GAGGGACTCGGCTCTGACCACTGTCACTAACAAGTGAAGAGGTTCTGTGTGTCAAGTG	3400
QY	2938	AATCCCAACCAACACCGGGCCCAAGTGAAGACCCCTAGATCCGGAAGTACAAGAACGA	2997
Db	3401	AATCCCAACCAACACCGGGCCCAAGTGAAGACCCCTAGATCCGGAAGTACAAGAACGA	3460

QY 2998 TTCACTCCGAGATCTCTGTCGACGCCCTTTGGGGGGTCAACCTGCTGTGGGACGAG 3057  
 DB 3461 TTCACTCCGAGATCTCTGTCGACGCCCTTTGGGGGGTCAACCTGCTGTGGGACGAG 3520  
 QY 3058 AACGGGCTGATGTTGCTGACCGAAGTGGGCGAGGAGTGTATGACTCATTTGGGGCG 3117  
 DB 3521 AACGGGCTGATGTTGCTGACCGAAGTGGGCGAGGAGTGTATGACTCATTTGGGGCG 3580  
 QY 3118 CGAGCTTCCAGAGATGATGTGTGAGAGGGGCTCAACCTGCTCATCACTCATGAGG 3177  
 DB 3581 CGAGCTTCCAGAGATGATGTGTGAGAGGGGCTCAACCTGCTCATCACTCATGAGG 3640  
 QY 3178 AAAAGGAACTGCGGGGTGATTAAGTTCCTGCTGCTCCGGAAGAAATCTGACAGAT 3237  
 DB 3641 AAAAGGAACTGCGGGGTGATTAAGTTCCTGCTGCTCCGGAAGAAATCTGACAGAT 3700  
 QY 3238 GACCCAGAGTGGAGAAAGACGAGGCTGACCACTGCGGGGACATGAGGCGCTGCGGG 3297  
 DB 3701 GACCCAGAGTGGAGAAAGACGAGGCTGACCACTGCGGGGACATGAGGCGCTGCGGG 3760  
 QY 3298 CACTACCGTGTGTAATAGAGCGGATTAAGTTCCTGCTCATGCTCCCTCAAGAGCTCC 3357  
 DB 3761 CACTACCGTGTGTAATAGAGCGGATTAAGTTCCTGCTCATGCTCCCTCAAGAGCTCC 3820  
 QY 3358 GTGAGAGTGTATGCTGCGGGCCCCCAACCTCAACCAATTCATGSCCTTGAAGCTCTT 3417  
 DB 3821 GTGAGAGTGTATGCTGCGGGCCCCCAACCTCAACCAATTCATGSCCTTGAAGCTCTT 3880  
 QY 3418 GCCGACCTCCGCCACCGGCTCTGCTGTGTCGACCTGACGATGAGAGAGGCGAGCGCTC 3477  
 DB 3881 GCCGACCTCCGCCACCGGCTCTGCTGTGTCGACCTGACGATGAGAGAGGCGAGCGCTC 3940  
 QY 3478 AAGGTCACTATGCTGCTGAGTGTGCTTCCAGTGTGATGATGCTGAGCTCGGGGAAACG 3537  
 DB 3941 AAGGTCACTATGCTGCTGAGTGTGCTTCCAGTGTGATGATGCTGAGCTCGGGGAAACG 4000  
 QY 3538 TATGACATCTATATCCCTGTGTCACATCCAGAGCCGATCAGGCCCATGCAATCTTC 3597  
 DB 4001 TATGACATCTATATCCCTGTGTCACATCCAGAGCCGATCAGGCCCATGCAATCTTC 4060  
 QY 3598 CTCGCCAACACCGAGCGGATGAGATGCTGCTGTGTCACAGAGAGAGGCTGTACGCTC 3657  
 DB 4061 CTCGCCAACACCGAGCGGATGAGATGCTGCTGTGTCACAGAGAGAGGCTGTACGCTC 4120  
 QY 3658 AACAGTACGGGCGCATATTAAAGATGTGTGCTGACGTGGGGGAGATGCTTACTTCT 3717  
 DB 4121 AACAGTACGGGCGCATATTAAAGATGTGTGCTGACGTGGGGGAGATGCTTACTTCT 4180  
 QY 3718 GTGGCTTACATCTGCTCAACCAAGTATGAGGCTGGGGTGAAGAACCATGATCCGC 3777  
 DB 4181 GTGGCTTACATCTGCTCAACCAAGTATGAGGCTGGGGTGAAGAACCATGATCCGC 4240  
 QY 3778 TCTGTGAGAGCGGGCCACTGCGAGGGGCTTTCATGCAAAACGAGCTCAGAGGCTCAG 3837  
 DB 4241 TCTGTGAGAGCGGGCCACTGCGAGGGGCTTTCATGCAAAACGAGCTCAGAGGCTCAG 4300  
 QY 3838 TTCTGTGTGAGCGGAATGACAAAGTGTGTTTTTGTGCTCAGTCCGCTCTGCGGGCGACGAGC 3897  
 DB 4301 TTCTGTGTGAGCGGAATGACAAAGTGTGTTTTTGTGCTCAGTCCGCTCTGCGGGCGACGAGC 4360  
 QY 3898 CAAAGTTTACTTACATGACTCTGACACGTTAATGTCATCATGAAGTGTGAAAAGGCG 3951  
 DB 4361 CAAAGTTTACTTACATGACTCTGACACGTTAATGTCATCATGAAGTGTGAAAAGGCG 4414

## RESULT 11

AA88207 standard; cDNA; 7132 BP.

AA88207;

13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #24011.  
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX Homo sapiens.  
 OS WO200175067-A2.  
 PN 11-OCT-2001.  
 PD 30-MAR-2001; 2001WO-US008631.  
 PF 31-MAR-2000; 2000US-00540217.  
 PR 23-AUG-2000; 2000US-00649167.  
 XX (HYSE-) HYSEQ INC.  
 PA Drmanac RT, Liu C, Tang YT;  
 PI WPI; 2001-639362/73.  
 DR P-PSDB; ABG24020.  
 XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX Claim 1; SEQ ID NO 24011; 103bp; English.  
 PS The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AA84197-AA84564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 7132 BP; 1569 A; 2123 C; 2159 G; 1280 T; 0 U; 1 Other;  
 Query Match 85.9%; Score 3392.8; DB 5; Length 7132;  
 Best Local Similarity 92.6%; Pred. No. 0;  
 Matches 3822; Conservative 0; Mismatches 12; Indels 292; Gaps 13;  
 QY 7 ATGGGACCAACCAAGCCCGCCGAGCCTGAGCAATGCACTGTCCGCTCGGGAGC 66  
 DB 158 ATGGGACCAACCAAGCCCGCCGAGCCTGAGCAATGCACTGTCCGCTCGGGAGC 217  
 QY 67 CTGCTGGGATCTTTAGCTTTGTGAGAGTGTGCGCAATGGAACCTTACGAGAGGTGAC 126  
 DB 218 CTGCTGGGATCTTTAGCTTTGTGAGAGTGTGCGCAATGGAACCTTACGAGAGGTGAC 277  
 QY 127 AAGGTGCGCATGTGCAAGAGCGGGCACTGCTGCCATCAAGTCATGATGATCAAGAG 186  
 DB 278 AAGGTGCGCATGTGCAAGAGCGGGCACTGCTGCCATCAAGTCATGATGATCAAGAG 337  
 QY 187 GACGAGAGGAAGAGATCAACAGAGATCAACATGCTGAAAGTACTCTCACCAACGCGC 246  
 DB 338 GACGAGAGGAAGAGATCAACAGAGATCAACATGCTGAAAGTACTCTCACCAACGCGC 397

OY	247	AAACATCGCACCTTACTACGAGCCTTACTCAAGAAAGCCCCCGGGAAAGATGACCA	306
Db	398	AAACATCGCACCTTACTACGAGCCTTACTCAAGAAAGCCCCCGGGAAAGATGACCA	457
OY	307	CTCTGGCTGGGAGATGGAGTTCTGGTGGTCTGTGGTTCAAGTACATGACCTGGTAAATACCA	366
Db	458	CTCTGGCTGGGAGATGGAGTTCTGGTGGTCTGTGGTTCAAGTACATGAGTGGTAAATACCA	517
OY	367	AAAGGCACGCGCTGGAAGAGAGACTGTATCGCTATATCTGCAGGAGATCCTCAGGGGT	426
Db	518	AAAGGCACGCGCTGGAAGAGAGACTGTATCGCTATATCTGCAGGAGATCCTCAGGGGT	577
OY	427	CTGGCCCATCTTCATGCCCCACAGGTGATTCATGTGAGACATCAAGGGCAGAAATGTCTG	486
Db	578	CTGGCCCATCTTCATGCCCCACAGGTGATTCATGTGAGACATCAAGGGCAGAAATGTCTG	637
OY	487	CTGACAGAGAAATGCTGAGGTCAAGCTATGTGATTTTGGGGTGAAGTGTCAAGCTGGAACGC	546
Db	638	CTGACAGAGAAATGCTGAGGTCAAGCTATGTGATTTTGGGGTGAAGTGTCAAGCTGGAACGC	697
OY	547	ACCGTGGACAGACGGAACACTTTCATTGGGACCTCCCTATCTGATATGGCTCCAGAGTATC	606
Db	698	ACCGTGGACAGACGGAACACTTTCATTGGGACCTCCCTATCTGATATGGCTCCAGAGTATC	757
OY	607	GCCCTGTGATGAAACCTGTATGCCACCTATGATTAACAGAGTGAATATTTGGTCTCTAGGA	666
Db	758	GCCCTGTGATGAAACCTGTATGCCACCTATGATTAACAGAGTGAATATTTGGTCTCTAGGA	817
OY	667	ATCAACGCCATTCGAGATGGCAGAGGGAGCCCCCTCTGTGTGACATGCAACCCCATCGGA	726
Db	818	ATCAACGCCATTCGAGATGGCAGAGGGAGCCCCCTCTGTGTGACATGCAACCCCATCGGA	877
OY	727	GCCCTCTTCATATTCCTCGGAACCTCGGCCAGAGCTCAAGTCCAAAGATGGTCTAAG	786
Db	878	GCCCTCTTCATATTCCTCGGAACCTCGGCCAGAGCTCAAGTCCAAAGATGGTCTAAG	937
OY	787	AAGTTCATTGACTTTCATTGACACATGTCTCAACAATTACTGAGCCGCCACCCACG	846
Db	938	AAGTTCATTGACTTTCATTGACACATGTCTCAACAATTACTGAGCCGCCACCCACG	997
OY	847	GAGCAGCTTACTGAAGTTTCCTTCAATCCGGGACAGGCCACGGAGCCGACAGTCCGATC	906
Db	998	GAGCAGCTTACTGAAGTTTCCTTCAATCCGGGACAGGCCACGGAGCCGACAGTCCGATC	1057
OY	907	CAGCTTAAGGACCAATTTGCCATTCGCGGAGCAAGGCGGGGTGAGAAAGAGAGACGAA	966
Db	1058	CAGCTTAAGGACCAATTTGCCATTCGCGGAGCAAGGCGGGGTGAGAAAGAGAGACGAA	1117
OY	967	TATGAGTACAGCGGACGAGGAGGAGGAGATGACAGCCATGTGAGAGAGAGAGAGCAAGC	1026
Db	1118	TATGAGTACAGCGGACGAGGAGGAGGAGGAGATGACAGCCATGTGAGAGAGAGAGAGCAAGC	1177
OY	1027	TCCATCATGAACGTGCTCGGAGAGTGCATCTTACGCCCGGAGATTCTTCGCGTCCAGCAG	1086
Db	1178	TCCATCATGAACGTGCTCGGAGAGTGCATCTTACGCCCGGAGATTCTTCGCGTCCAGCAG	1237
OY	1087	GAAAAATAAGACAACTCAGAGGCTTTAAAAACAGCAGCAGCAGCTGCAACAACAGCAGCAG	1146
Db	1238	GAAAAATAAGACAACTCAGAGGCTTTAAAAACAGCAGCAGCAGCTGCAACAACAGCAGCAG	1297
OY	1147	CGAGACCCCGAGGACACATCAACACCTGTCTGCACAGCGGACAGCGCGCATAGAGGAG	1206
Db	1298	CGAGACCCCGAGGACACATCAACACCTGTCTGCACAGCGGACAGCGCGCATAGAGGAG	1357
OY	1207	CAGAAAGAGAGACGGCGCCGCTGAGAGCAACAGCGGCGGGAGCGGGAGCAAGCAGGAA	1266
Db	1358	CAGAAAGAGAGACGGCGCCGCTGAGAGCAACAGCGGCGGGAGCGGGAGCAAGCAGGAA	1417
OY	1267	CTGCAGAGAGAGAGACAGACGCGCGGCTGAGAGCAATGCAAGCTCTCTCGCGCGGAGAG	1326
Db	1418	CTGCAGAGAGAGAGACAGACGCGCGGCTGAGAGCAATGCAAGCTCTCTCGCGCGGAGAG	1477

QY	1327	GAGCGCGCGGACGGGAGCCGTGAACA-----	1352
Db	1478	GAGCGCGCGGACGGGAGCCGAGCAAGAAATATATTCTCAACAGGCTAAGAGAGAGACAG	1537
QY	1353	-----GAAATAC	1359
Db	1538	CGACAGCTCGAGATCCTTACAGCAACAGCTGCTCCAGGAACAGGCCCTGCTGTGGAAATAC	1597
QY	1360	AAGCGGAAGACGTGAGAGAGACGGGCACTCAGAACTGTCTCCAGAGGACAGCTGACAG	1419
Db	1598	AAGCGGAAGACGTGAGAGAGACCGGCAAGTCAGAAAGTCTCCAGAGGACAGCTGACAG	1657
QY	1420	GAGCATGCGCTTCAAGTCCCTGACAGACAGCAACAGGACGACGCTTCAAGAAACAG	1479
Db	1658	GAGCATGCGCTTCAAGTCCCTGACAGACAGCAACAGGACGACGCTTCAAGAAACAG	1717
QY	1480	CAGCAGCAGCACTCTGCTGCGGAGCAGAAAGCCCTGTACATTATGTCGCGGCATG	1539
Db	1718	CAGCAGCAGCACTCTGCTGCGGAGCAGAAAGCCCTGTACATTATGTCGCGGCATG	1777
QY	1540	AATCCCGCTGACAAACCGAGCTGGGCCCCGAGAGGTAAAGAGAAACAAAGATGAACAG	1599
Db	1778	AATCCCGCTGACAAACCGAGCTGGGCCCCGAGAGGTAAAGAGAAACAAAGATGAACAG	1837
QY	1600	CAGCAGAACTCTCCCTTGGACCAAGAGCAAGGACGAGCAGCGGGGCTGAGACCCCATC	1659
Db	1838	CAGCAGAACTCTCCCTTGGACCAAGAGCAGGACGAGCAGCGGGGCTGAGACCCCATC	1897
QY	1660	CCCCAGGCTTCCCAAGGGCCCCCAGAGACCCCTTTCCAGACTCTCTATGACAGGCG	1719
Db	1898	CCCCAGGCTTCCCAAGGGCCCCCAGAGACCCCTTTCCAGACTCTCTATGACAGGCG	1957
QY	1720	GTGAGACCCCAAGAGGAGCCGCAACA-----	1744
Db	1958	GTGAGACCCCAAGAGGAGCCGCAACAAGCTGTGSCACACGGGATCCACTGAAAGCA	2017
QY	1745	-----AGTCCCTGAGAGACGAGCCCAACCCGAAACTTGGCT	1779
Db	2018	TATGAGACGACTGTAAACCCCAATCCCAAGTCCCTGAGAGACAGGCCCAACCGAAACTTGGCT	2077
QY	1780	GCTTTCAGAGCTTCCAGTAGACCCCGAGCCCTGECATTCCTCCGACCACTGCCAGGCCAGT	1839
Db	2078	GCTTTCAGAGCTTCCAGTAGACCCCGAGCCCTGECATTCCTCCGACCACTGCCAGGCCAGT	2137
QY	1840	GCCCCAGAGAGCTGTCAATCCGCAAGAAATTCAAGACCCCACTCTGAAGAGACCTGCGCCAGC	1899
Db	2138	GCCCCAGAGAGCTGTCAATCCGCAAGAAATTCAAGACCCCACTCTGAAGAGACCTGCGCCAGC	2197
QY	1900	CCGAATCCCCAGAGCTGTGGTCCGCGCAGATTAACAGAGGCCCAACCCAAAGTGCCTCAGAGG	1959
Db	2198	CCGAATCCCCAGAGCTGTGGTCCGCGCAGATTAACAGAGGCCCAACCCAAAGTGCCTCAGAGG	2257
QY	1960	ACTCATCTATGCGCACTGCCCCCTTAAACAAGTGGGGCCGAGAGGCTCCCGCCAGGCCAG	2019
Db	2258	ACTCATCTATGCGCACTGCCCCCTTAAACAAGTGGGGCCGAGAGGCTCCCGCCAGGCCAG	2317
QY	2020	GCAGTGCGGTGCGAAGACCTGCGAAGCACTCCGCTGGCAAACTATGTCAAAAGCGGGCA	2079
Db	2318	GCAGTGCGGTGCG-----	2329
QY	2080	GAGCGGGGCAACCCCAAGCTTCAAGGGCCCTGCTAGCCCCCTGAGCCGCGCCAAAGCC	2139
Db	2330	-----	2329
QY	2140	TCTAGTAACCCCGACCTTACAGAGAGAGCAACCTTGGCTGGAAACCTTGGACAGCTTCTT	2199
Db	2330	---AGTAACCCCGACCTTACAGAGAGAGCAACCTTGGCTGGAAACCTTGGACAGCTTCTT	2386
QY	2200	CCAGGCTCTCAAGGGCACTTCCCAAGGCTGGCTCACTGAGCGGAAACCGGCTGGAGCC	2259
Db	2387	CCAGGCTCTCAAGGGCACTTCCCAAGGCTGGCTCACTGAGCGGAAACCGGCTGGAGCTC	2446
QY	2260	TCTCTCAAACTGACAGCTCCCTGCTGCTCTCCCTGGGAATAAAGCCCAAGCAGAC	2319

Db 2447 TCCCTCCAAACCGGACGCTCCCTCTGTCTCTCCCTGGGATTAAGCCAGCCGAC 2506  
 Qy 2320 CACCGCTCACGGCCAGGCGGCGCCCA-----GACTTTGTG 2355  
 Db 2507 CACCGCTCACGGCCAGGCGGCGCCGACATTAAGCGAATTGGTGAATCTTTGTG 2566  
 Qy 2356 TTGCTGAAAAGCGGACTCTTGGAAGAGCCCTCGGCTCCCAAGAAAGGCATGACTAC 2415  
 Db 2567 TTGCTGAAAAGCGGACTCTTGGAAGAGCCCTCGGCTCCCAAGAAAGGCATGACTAC 2626  
 Qy 2416 TCGCTGTCAGCGAGAGGTGAAAGCAGTAGGAGCAGAGAGAAAGCGAGCGG 2475  
 Db 2627 TCGCTGTCAGCGAGAGGTGAAAGCAGTAGGAGCAGAGAGAAAGCGAGCGG 2686  
 Qy 2476 CCAGCAGAGGGAGCAGAGATACCTTGAGGGCGCGAGCGATGAGGATACAGACGCTC 2535  
 Db 2687 CCAGCAGAGGGAGCAGAGATACCTTGAGGGCGCGAGCGATGAGGATACAGACGCTC 2746  
 Qy 2536 AGCACCATTGGTGTCCAGAGTGAAGATCACCGGAAACCCAGCCCTTACGGGGGC 2595  
 Db 2747 AGCACCATTGGTGTCCAGAGTGAAGATCACCGGAAACCCAGCCCTTACGGGGGC 2806  
 Qy 2596 GGACCATGGTGTCCAGAGCAGCCCTGAAAGAGAGCGAACTGTGCACTGTACAGC 2655  
 Db 2807 GGACCATGGTGTCCAGAGCAGCCCTGAAAGAGAGCGAACTGTGCACTGTACAGC 2866  
 Qy 2656 AATGGGTACCAAACTGCTGAGTGTCCAGCCCAAGCCACTGACCCAGAGAACGC 2715  
 Db 2867 AATGGGTACCAAACTGCTGAGTGTCCAGCCCAAGCCACTGACCCAGAGAACGC 2926  
 Qy 2716 AAAGGCCAAAGCCACTCTGAAAGATGGAGTGTGATCTACAGTCTCTGGGCTGTA 2775  
 Db 2927 AAAGGCCAAAGCCACTCTGAAAGATGGAGTGTGATCTACAGTCTCTGGGCTGTA 2986  
 Qy 2776 AAAGCCCTGGCAAGAGCTGTTGATGATCTGAGGATCTACAGCTGTA 2835  
 Db 2987 AAAGCCCTGGCAAGAGCTGTTGATGATCTGAGGATCTACAGCTGTA 3046  
 Qy 2836 GGCAGTGGGGAACAGATCCCATCAAGCCCTAGTGGTGAAGAGGCACTCGCTGAC 2895  
 Db 3047 GGCAGTGGGGAACAGATCCCATCAAGCCCTAGTGGTGAAGAGGCACTCGCTGAC 3106  
 Qy 2896 CAGCTGACATCAAGCTGAGAGAGGTTCTGTGTCAGCTGAATCCCAACAACCCGG 2955  
 Db 3107 CAGCTGACATCAAGCTGAGAGAGGTTCTGTGTCAGCTGAATCCCAACAACCCGG 3166  
 Qy 2956 GCCCAGTGAACCCCTGAGATCCGGAAGTCAAGAAAGGCACTCCGAGATCCTC 3015  
 Db 3167 GCCCAGTGAACCCCTGAGATCCGGAAGTCAAGAAAGGCACTCCGAGATCCTC 3226  
 Qy 3016 TGTGCAACCTTTGGGGGTCGAACCTGTGTTGGGCAACGA- GAACGGGCTGATTTGCT 3074  
 Db 3227 TGTGCAACCTTTGGGGGTCGAACCTGTGTTGGGCAACGAAGAGCGGCTGATTTGCT 3286  
 Qy 3075 GGAACGAAGTGGGCAAGGAGGTGATGATCTATTGGGCGGCGCTTCCAGCAGAT 3134  
 Db 3287 GGAACGAAGTGGGCAAGGAGGTGATGATCTATTGGGCGGCGCTTCCAGCAGAT 3346  
 Qy 3135 GGAATGCTGAGAGGGGCTCAACCTGCTCATCAACATCTCAGGGAAAGAAACAATGCG 3194  
 Db 3347 GGAATGCTGAGAGGGGCTCAACCTGCTCATCAACATCTCAGGGAAAGAAACAATGCG 3406  
 Qy 3195 GGTGTATTACCTGTCTGTGCTCCGGAACAAGATTCTGCACAATGACCAAGATGAGAA 3254  
 Db 3407 GGTGTATTACCTGTCTGTGCTCCGGAACAAGATTCTGCACAATGACCAAGATGAGAA 3466  
 Qy 3255 GAAGCAGGGCTGGAACACCGTGGGGACATGAGGGCTCGGGCACTACCGTGTGTGAA 3314  
 Db 3467 GAAGCAGGGCTGGAACACCGTGGGGACATGAGGGCTCGGGCACTACCGTGTGTGAA 3526  
 Qy 3315 ATACGAGCGGATTAAAGTTCCGTGTCATCGCCCTAAGAGCTCGTGAAGGTGTGCTG 3374

Db 3527 ATACGAGCGGATTAAAGTTCCGTGTCATCGCCCTCAAGAGCTCCGTGAGGTGTATGCTG 3586  
 Qy 3375 GGCCCCCAACCTTACCAAAATTCAT- GGCTTCAAGTCTTTGGCCGACCTCCCCACC 3433  
 Db 3587 GGCCCCCAACCTTACCAAAATTCATGAGGCTTTCAAGTCTTTGGCCGACCTCCCCACC 3646  
 Qy 3434 GCCCTTGT- GGTGACCTGACAGTAGAGAGGGGAGGCGGCTCAAGTCACTATGAGC 3492  
 Db 3647 GCCCTTGTGAGTCACTGACAGTAGAGAGGGGAGGCGGCTCAAGTCACTATGAGC 3706  
 Qy 3493 TCCAGTGTGGCTTCCATGCTGTGATGTCATCTGGGAAACAAGTATGACATCTACATC 3552  
 Db 3707 TCCAGTGTGGCTTCCATGCTGTGATGTCATCTGGGAAACAAGTATGACATCTACATC 3766  
 Qy 3553 CTTGTGACATCCAGAGCCAGATCAG- CCCCATGCTATCTTCTCCCAACACCGA 3611  
 Db 3767 CTTGTGACATCCAGAGCCAGATCAGCCCCCATGCTATCTTCTCCCAACACCGA 3826  
 Qy 3612 C-GGATGAGATGCTGCTGCTAGC- AGGACGAGGGTGTACGTCACACGTAACG 3668  
 Db 3827 CGGCAATGAGATGCTGCTGCTAGCAGAGAGACAGAGTTGTCTACGTCACACGTAACG 3886  
 Qy 3669 GCGCATCATTA- GATGTGTGTGCTGAGTGGGGGAGATGCTACTTCTGTGGCTACA 3727  
 Db 3887 GCGCATCATTAAGGAGTGTGTGCTGAGTGGGGGAGATGCTACTTCTGTGGCTACA 3946  
 Qy 3728 TCTGCTCAACAGCA- TAATGGCTGGGTGAGAAAGCCATTGAGATCCGCTGTGGAG 3786  
 Db 3947 TCTGCTCAACAGCAATAATGGGCTGGGTGAGAAAGCCATTGAGATCCGCTGTGGAG 4006  
 Qy 3787 ACGGGCCACTCGACGGGGCTTCATGCAAAACGAGCTGAGAGGCTCAAGTTCTGTGT 3846  
 Db 4007 ACGGGCCACTCGACGGGGCTTCATGCAAAACGAGCTGAGAGGCTCAAGTTCTGTGT 4066  
 Qy 3847 GAGCGAATGACAGAGTGTGCTTCTCAGTCCGCTCTGGGGGACAGCC- AAGTTTA 3905  
 Db 4067 GAGCGAATGACAGAGTGTGCTTCTCAGTCCGCTCTGGGGGACAGCCCTAAGTTTA 4126  
 Qy 3906 CTTGATGACTGTGACCGTAACTGTCATCATGAAGTGTGAAAGGCG 3951  
 Db 4127 CTTGATGACTGTGACCGTAACTGTCATCATGAAGTGTGAAAGGCG 4172

RESULT 12  
 AAD17762  
 ID AAD17762 standard; DNA; 3735 BP.  
 AC AAD17762:  
 XX  
 DT 10-DEC-2001 (first entry)  
 XX  
 DE Human novel STE20-like protein, NOV-3d encoding DNA.  
 XX  
 KW Human: NOV-X protein; KIA1233-like protein; STE20-like protein; tumour;  
 KW tryptase inhibitor-like protein; gene therapy; haematopoietic; illness;  
 KW immunological disorder; neurodegenerative disorder; Alzheimer's disease;  
 KW Parkinson's disease; immunomodulatory; pharmacogenomic; haemostatic;  
 KW human immunodeficiency virus; HIV; fertility disorder; neuroprotective;  
 KW cytosolic; neotropic; anti-fertility; cancer; chromosome 17;  
 KW NOV-3d protein; de.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..3735  
 FT /\*tag= a  
 FT /product= "Human novel STE20-like protein, NOV-3d"  
 PN MO200162928-A2.  
 XX 30-AUG-2001.  
 PD 26-FEB-2001; 2001MO-US006151.  
 XX PF



XX 25-FEB-2000; 2000US-0184951P.  
PR 28-FEB-2000; 2000US-0185548P.  
PR 01-MAR-2000; 2000US-0185567P.  
PR 18-APR-2000; 2000US-0197723P.  
PR 27-APR-2000; 2000US-0199957P.  
PR 23-FEB-2001; 2001US-00789390.

XX (CURA-) CURAGEN CORP.

PA Vernet CAM, Fernandes E, Shinkets RA, Macdougall J, Spaderna SK;

XX WPI; 2001-582051/65.

XX P-PSDB; AAE10614.

PT New isolated KIAA1233-like, STE20-like, or trypsin inhibitor-like  
PT polypeptide for diagnosing and treating pathological disorders, such as  
PT Parkinson's disease and for use in pharmacogenomics.

XX Claim 9; Page 67-68; 189pp; English.

CC The invention relates to novel human polypeptides referred to as NOV-X and  
CC their corresponding nucleic acid sequences. NOV-X collectively include  
CC NOV-1, NOV-2a and NOV-2b which are novel KIAA1233-like polypeptides, NOV-  
CC 3a, NOV-3b, NOV-3c and NOV-3d which are novel STE20-like polypeptides and  
CC NOV-4a, NOV-4b, NOV-4c, NOV-4d and NOV-4e which are novel trypsin  
CC inhibitor-like polypeptides. NOV-X is used to identify a potential  
CC therapeutic agent that can modulate its activity and can be used for  
CC treating a pathology related to aberrant expression or aberrant  
CC physiological interactions of NOV-X. NOV-X or its DNA is used to  
CC determine the presence or predisposition to a disease associated with  
CC altered levels of NOV-X. NOV-X, its DNA and its antibody are used to  
CC treat or prevent a pathology associated with NOV-X. The pathological  
CC states that can be treated or prevented are haematopoietic, cancer,  
CC immunological, tumour, neurodegenerative (e.g. Alzheimer's and  
CC Parkinson's disease), human immunodeficiency virus (HIV) illness and  
CC fertility disorders. NOV-X and its DNA are used in pharmacogenomics for  
CC predictive medicine. NOV-X DNA is used in gene therapy. The present  
CC sequence is a DNA encoding human novel STE20-like protein, NOV-3d  
CC gene is located at chromosome 17

XX Sequence 3735 BP; 880 A; 1105 C; 1137 G; 613 T; 0 U; 0 Other;

XX Query Match 85.0%; Score 3358.2; DB 5; Length 3735;

XX Best Local Similarity 92.7%; Pred. No. 0;

XX Matches 3673; Conservative 0; Mismatches 38; Indels 252; Gaps 4;

QY 7 ATGGGCGACCAAGCCCGCCGCGAGCTGAGCAGATGACCTGTGCGCCCTGCGGAGC 66  
DB 1 ATGGGCGACCAAGCCCGCCGCGAGCTGAGCAGATGACCTGTGCGCCCTGCGGAGC 60  
QY 67 CTTGCTGGGATCTTTGAGAGCTTTGAGAGGTGTGCGGAATGGAACCTACGAGACAGGTATC 126  
DB 61 CTTGCTGGGATCTTTGAGAGCTTTGAGAGGTGTGCGGAATGGAACCTACGAGACAGGTATC 120  
QY 127 AAGGGTCGCGATGTCAAGACGCGGGCAGCTGCTGCCATCAAGTCAATGATGTCAGAG 186  
DB 121 AAGGGTCGCGATGTCAAGACGCGGGCAGCTGCTGCCATCAAGTCAATGATGTCAGAG 180  
QY 187 GACGAGAGGAAGAGATCAAAACAGAGATCAATGCTGAAAAAGTACTTCAACACCGC 246  
DB 181 GACGAGAGGAAGAGATCAAAACAGAGATCAATGCTGAAAAAGTACTTCAACACCGC 240  
QY 247 AACATTCGCACTTAACGAGAGCTTTCATCAAGAGAGAGCCCGGGAAACATGACGAG 306  
DB 241 AACATTCGCACTTAACGAGAGCTTTCATCAAGAGAGAGCCCGGGAAACATGACGAG 300  
QY 307 CTTGCTGGGATCTTTGAGAGCTTTGAGAGGTGTGCGGAATGGAACCTACGAGACAGGTATC 366  
DB 301 CTTGCTGGGATCTTTGAGAGCTTTGAGAGGTGTGCGGAATGGAACCTACGAGACAGGTATC 360  
QY 367 AAAGGCAACGCGCTGAAGAGGACTGTATGCTATATCTGACGGAGATCTTCAGGGGT 426  
DB 361 AAAGGCAACGCGCTGAAGAGGACTGTATGCTATATCTGACGGAGATCTTCAGGGGT 420

DB 361 AAAGGCAACGCGCTGAAGAGGACTGTATGCTATATCTGACGGAGATCTTCAGGGGT 420  
QY 427 CTTGCGCCATCTCATGTGCCCAAGAGTATCCATGAGACATCAAGGGGCAAGATGTGCTG 486  
DB 421 CTTGCGCCATCTCATGTGCCCAAGAGTATCCATGAGACATCAAGGGGCAAGATGTGCTG 480  
QY 487 CTGACAGAGAAATGCTAGAGTCAAGCTAGTGGATTTTGGGGTGAAGTCTCAGCTGAGCCG 546  
DB 481 CTGACAGAGAAATGCTAGAGTCAAGCTAGTGGATTTTGGGGTGAAGTCTCAGCTGAGCCG 540  
QY 547 ACCGTCGAGAGAGGAAACATTTTGGGATCTGCTGAGAGAGGCTCCAGAGGTATC 606  
DB 541 ACCGTCGAGAGAGGAAACATTTTGGGATCTGCTGAGAGAGGCTCCAGAGGTATC 600  
QY 607 GCTGTGATGAGAAACCTGATCCAGCTATGATTAAGAGATGATTTGGTCTCTAGGA 666  
DB 601 GCTGTGATGAGAAACCTGATCCAGCTATGATTAAGAGATGATTTGGTCTCTAGGA 660  
QY 667 ATCAAGCCATGAGATGAG 726  
DB 661 ATCAAGCCATGAGATGAG 720  
QY 727 GCCCTTCTCCATTCCTCGGAAACCTCGGCGAGAGCTCAAGTCCAGAGAGAGAGAGAGAGAG 786  
DB 721 GCCCTTCTCCATTCCTCGGAAACCTCGGCGAGAGCTCAAGTCCAGAGAGAGAGAGAGAGAG 780  
QY 787 AAGTTCATTGACTTCAATGACATGATCTCATCAAGACTTACCTGAGCGCCCAACCG 846  
DB 781 AAGTTCATTGACTTCAATGACATGATCTCATCAAGACTTACCTGAGCGCCCAACCG 840  
QY 847 GAGCAGTACTGAGATTTCCCTTCATCCGAGACAGCCAGAGCGGAGAGAGAGAGAGAGAGAG 906  
DB 841 GAGCAGTACTGAGATTTCCCTTCATCCGAGACAGCCAGAGCGGAGAGAGAGAGAGAGAGAG 900  
QY 907 CAGCTTAAGACCAATGACATGACATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 966  
DB 901 CAGCTTAAGACCAATGACATGACATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
QY 967 TATGAGTACACAGCGAG 1026  
DB 961 TATGAGTACACAGCGAG 1020  
QY 1027 TCCATCATGAAGTGTCTGAGAGTGAAGCTGAGCGGAGAGTTCCTCGGCTCCAGAGAG 1086  
DB 1021 TCCATCATGAAGTGTCTGAGAGTGAAGCTGAGCGGAGAGTTCCTCGGCTCCAGAGAG 1080  
QY 1087 GAAATTAAGACCAATGACAGAGCTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1146  
DB 1081 GAAATTAAGACCAATGACAGAGCTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
QY 1147 CGAGACCCCGAGAGCAATCAACCTGTGACAGAGCGGAGAGCGGAGAGAGAGAGAGAGAGAG 1206  
DB 1141 CGAGACCCCGAGAGCAATCAACCTGTGACAGAGCGGAGAGCGGAGAGAGAGAGAGAGAGAG 1200  
QY 1207 CAGAAAG 1266  
DB 1201 CAGAAAG 1260  
QY 1267 CTGACAG 1326  
DB 1261 CTGACAG 1320  
QY 1327 GAGCGCGAG 1386  
DB 1321 GAGCGCGAG 1380  
QY 1387 CAGTCAAG 1446  
DB 1381 CAGTCAAG 1440  
QY 1447 CAGCAGCAACAG 1506  
DB 1441 CAGCAGCAACAG 1500



QY 1507 AGGAAGCCCTGTACATTATATGTGGGGCATGAAATCCCGCTGACAAAACAGCCTGGGCC 1566  
DB 1501 AGGAAGCCCTGTACATTATATGTGGGGCATGAAATCCCGCTGACAAAACAGCCTGGGCC 1560  
QY 1567 CGAGAGTGAAGAAGAGAAACAAGATGAACAAGACAGAACTCTCCCTTGGCCAAAGAC 1626  
DB 1561 CGAGAGTGA----- 1570  
QY 1627 AAGCCAGGACAGACGGGGCTGAGGCCCCCAATCCCCAGGCTCTCCAGAGGCCCCACAGA 1686  
DB 1571 -----TGGCACACCGGGGTCCCACTGAAGCCATATGTACACACTGTGA 1611  
QY 1687 CCCCTTTCCCAAGCTCTCTCTATGACAGAGCCGGGTGAGACCCCAAGAGGACCCGACAG 1746  
DB 1612 CCCCGATCCC-----AG 1623  
QY 1747 TCCCTGACAGACACAGCCCAACCCGAAACCTGGCTGCTTCCAGCCTCCCATGACCCGAC 1806  
DB 1624 TCCCTGACAGACACAGCCCAACCCGAAACCTGGCTGCTTCCAGCCTCCCATGACCCGAC 1683  
QY 1807 CCTGCAATCCCCGACCCGACTGCAAGCCCAAGTCCCGAGAGAGCTGTCAATCCGACGAAAT 1866  
DB 1684 CCTGCAATCCCCGACCCGACTGCAAGCCCAAGTCCCGAGAGAGCTGTCAATCCGACGAAAT 1743  
QY 1867 TCAAGACCCCACTCTGAAAGAGACCTGGCCCCCAAGCCCAAGTCCCCAGCCTGGGTCCGCCA 1926  
DB 1744 TCAAGACCCCACTCTGAAAGAGACCTGGCCCCCAAGCCCAAGTCCCCAGCCTGGGTCCGCCA 1803  
QY 1927 GATAACAGAGGCCCAACCCCAAGGTGCTGACAGAGACCTCATATGAGCCCACTGCCCTTAAAC 1986  
DB 1804 GATAACAGAGGCCCAACCCCAAGGTGCTGACAGAGACCTCATATGAGCCCACTGCCCTTAAAC 1863  
QY 1987 ACCAGTGGAGGCGGAGGGTCCCGGACAGCCCAAGAGTCCGTGCGAGAAGCTTCGACAGAAC 2046  
DB 1864 ACCAGTGGAGGCGGAGGGTCCCGGACAGCCCAAGAGTCCGTGCG----- 1908  
QY 2047 TCCGCTTGGCAATCTATCTGCAAGAGCGGGGACAGCCGAGGACCCCAAGCCTTCAGAGG 2106  
DB 1909 ----- 1908  
QY 2107 CCCCTGTGACAGCCCTGGAGCCCGCCCAAGCCTCTAGTAACCCCGACCTGACAGAGAGC 2166  
DB 1909 -----AGTAACCCGACCTGACAGAGAGC 1932  
QY 2167 GACCTGTGCTGGGAACGCTCGGACAGCGTCTTTCAGGCTCTACAGGGGCACTTCCCGAG 2226  
DB 1993 GACCTGTGCTGGGAACGCTCGGACAGCGTCTTTCAGGCTCTACAGGGGCACTTCCCGAG 1992  
QY 2227 GCTGTGCTACATGAGAGCGGAACGCGGTGGAGGCTCTCTCCAACTGAGACAGTCCCTGTG 2286  
DB 1993 GCTGTGCTACATGAGAGCGGAACGCGGTGGAGGCTCTCTCCAACTGAGACAGTCCCTGTG 2052  
QY 2287 CTCTCCCTGGGAATTAAGCCCAAGCCCGACGACACCGCTCAAGGGCGAGGCCGCGGCA 2346  
DB 2053 CTCTCCCTGGGAATTAAGCCCAAGCCCGACGACACCGCTCAAGGGCGAGGCCGCGGCA 2112  
QY 2347 -----GACTTGTGTGCTGAAGAGACGGAATCTTGAACGAG 2382  
DB 2113 AGCTATAGCGAGCAATTGTGTAGAGACTTTGTGTGTGTAAGAGACGGAAGCTGTGAGAG 2172  
QY 2383 GCCCTGTGGGCTCCCAAGAGGCAATGGAATATCTGTGTGTCAAGAGAGAGGTGGAAGC 2442  
DB 2173 GCCCTGTGGGCTCCCAAGAGGCAATGGAATATCTGTGTGTCAAGAGAGAGGTGGAAGC 2232  
QY 2443 AGTGAAGACGACGAGAGAGAGGCGAAGCGGGCCAGACGAGAGGGAGGACGATACCCCT 2502  
DB 2293 AGTGAAGACGACGAGAGAGAGGCGAAGCGGGCCAGACGAGAGGGAGGACGATACCCCT 2292  
QY 2503 GGGGGCCGACGAGATGGGGATACAGACAGCGTCAAGACCATATGTGTGTCAAGAGCTGAG 2562  
DB 2293 GGGGGCCGACGAGATGGGGATACAGACAGCGTCAAGACCATATGTGTGTCAAGAGCTGAG 2352

QY 2563 GAGATCACGGGAGCCCAAGCCCAATACGGGGGCGGACCATATGTGTGTCAAGGACCCCT 2622  
DB 2353 GAGATCACGGGAGCCCAAGCCCAATACGGGGGCGGACCATATGTGTGTCAAGGACCCCT 2412  
QY 2623 GAAAGAGCGGAACTGTGCTGATGTGACAGCAATGGGTATACAAACTGTGCTGACGTG 2682  
DB 2413 GAAAGAGCGGAACTGTGCTGATGTGACAGCAATGGGTATACAAACTGTGCTGACGTG 2472  
QY 2683 GTTCAAGCCCAAGCACTCAACCCAGAGAAACAGCAAAAGGCCAAAGCCCTCCAGAGGAT 2742  
DB 2473 GTTCAAGCCCAAGCACTCAACCCAGAGAAACAGCAAAAGGCCAAAGCCCTCCAGAGGAT 2532  
QY 2743 GGGAGTGTGATCTACAGTCTGTGGGCTGGTAAAGGCCCTTGGCAAGAGCTGTTCAGG 2802  
DB 2553 GGGAGTGTGATCTACAGTCTGTGGGCTGGTAAAGGCCCTTGGCAAGAGCTGTTCAGG 2592  
QY 2803 ATGTTTGTGATCTTAGGATCTACAGCCTTGAAGGACAGTGGGACAGCATCCCATCA 2862  
DB 2593 ATGTTTGTGATCTTAGGATCTACAGCCTTGAAGGACAGTGGGACAGCATCCCATCA 2652  
QY 2863 GCCCTAGTGGTGAAGAGGGCACTCGGCTGCAACCAAGCTGCAATGACAGTGAAGAGGCT 2922  
DB 2653 GCCCTAGTGGTGAAGAGGGCACTCGGCTGCAACCAAGCTGCAATGACAGTGAAGAGGCT 2712  
QY 2923 TCTGTGTCAACGTGAATCCCAACCAACCCGGGGCCCAAGTGAAGACCCCTGAAGTCCGG 2982  
DB 2713 TCTGTGTCAACGTGAATCCCAACCAACCCGGGGCCCAAGTGAAGACCCCTGAAGTCCGG 2772  
QY 2983 AAGTACAAAGACGATTCACATCTCGAGATCTCTGTGACAGCCTTTGGGGGGTCAACCTG 3042  
DB 2773 AAGTACAAAGACGATTCACATCTCGAGATCTCTGTGACAGCCTTTGGGGGGTCAACCTG 2832  
QY 3043 CTGTGGGCACTGAGAAACGGGCTGATGTGCTGCAACCAAGTGGGACAGGCTGATAT 3102  
DB 2833 CTGTGGGCACTGAGAAACGGGCTGATGTGCTGCAACCAAGTGGGACAGGCTGATAT 2892  
QY 3103 GGAATCAATGGGCGGCGACGCTTCAAGCAGATGATGTGCTGAGAGGGGCTCAACCTGCTC 3162  
DB 2893 GGAATCAATGGGCGGCGACGCTTCAAGCAGATGATGTGCTGAGAGGGGCTCAACCTGCTC 2952  
QY 3163 ATCAACATCTCAGGGAAGAAAGAACAACTGGGGGTGATTAACCTGTCTCTGCTCGGAAC 3222  
DB 2953 ATCAACATCTCAGGGAAGAAAGAACAACTGGGGGTGATTAACCTGTCTCTGCTCGGAAC 3012  
QY 3223 AAGATTTGCACAATGACCCAGAAAGTGAAGAAAGAGGCTGACCAACGTTGGGGGAC 3282  
DB 3013 AAGATTTGCACAATGACCCAGAAAGTGAAGAAAGAGGCTGACCAACGTTGGGGGAC 3072  
QY 3283 ATGAGAGGCTGGGGGCACTACCGTGTGTGAATAACGAGCGGATTAAGTTCTGGTCAATC 3342  
DB 3073 ATGAGAGGCTGGGGGCACTACCGTGTGTGAATAACGAGCGGATTAAGTTCTGGTCAATC 3132  
QY 3343 GCCCTCAAGAGCTCCGTGAGAGGTATGCTGGGCCCCCAAAACCTTACCAAAATTCAATG 3402  
DB 3133 GCCCTCAAGAGCTCCGTGAGAGGTATGCTGGGCCCCCAAAACCTTACCAAAATTCAATG 3192  
QY 3403 GCTTTCAAGTCTTTTCCGACCTTCCCAACCGCCCTGTGTGTGACCTGACAGTGAAG 3462  
DB 3193 GCTTTCAAGTCTTTTCCGACCTTCCCAACCGCCCTGTGTGTGACCTGACAGTGAAG 3252  
QY 3463 GAGGGGAGCGGCTCAAGTCTCATATGAGCTCCAGTGTGCTTCAATGCTGTGGAATGTC 3522  
DB 3253 GAGGGGAGCGGCTCAAGTCTCATATGAGCTCCAGTGTGCTTCAATGCTGTGGAATGTC 3312  
QY 3523 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGACATTCAGAGGCAAGTACCGCC 3582  
DB 3313 GACTCGGGGAACAGCTATGACATCTACATCCCTGTGACATTCAGAGGCAAGTACCGCC 3372  
QY 3583 CATGCCATCATCTTCTCTCCCAACAACCGAGCGGACATGAGATGCTGTGTCTTACAGGAC 3642  
DB 3373 CATGCCATCATCTTCTCTCCCAACAACCGAGCGGACATGAGATGCTGTGTCTTACAGGAC 3432  
QY 3643 GAGGGTGTCTACGTTCACACGTAAGGGGACATCAATTAAGATGTGTGTCTGCAATGGGGG 3702

DB 3433 GAGGGGTCTAGCTAACAACGATACGGGCGCATCATTAAGAGATGTGTGCTGACGTGGGG 3492  
|||  
QY 3703 GAGATGCTTACTTCTGTGGCTTCACTCTGCTCCAAACCAATATAGGGCTGGGAGAA 3762  
|||  
DB 3493 GAGATGCTTACTTCTGTGGCTTCACTCTGCTCCAAACCAATATAGGGCTGGGAGAA 3552  
|||  
QY 3763 GGCATTGAGATCGCTCTGTGAGACGGGCACTCGACGGGGCTTTCATGCAAAACGA 3822  
|||  
DB 3553 GGCATTGAGATCGCTCTGTGAGACGGGCACTCGACGGGGCTTTCATGCAAAACGA 3612  
|||  
QY 3823 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAGGTGTTTTTCCCTCAGTCCG 3882  
|||  
DB 3613 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAGGTGTTTTTCCCTCAGTCCG 3672  
|||  
QY 3883 TCTGGGGGAGACGCCAAGTTTACTTCATGACCTTCAACCTGACCTGATGAACTGG 3942  
|||  
DB 3673 TCTGGGGGAGACGCCAAGTTTACTTCATGACCTTCAACCTGACCTGATGAACTGG 3732  
|||  
QY 3943 TGA 3945  
|||  
DB 3733 TGA 3735

## RESULT 13

AAD17761  
ID AAD17761 standard; DNA; 3822 BP.

AC AAD17761;

DT 10-DEC-2001 (first entry)

DE Human novel STE20-like protein, NOV-3c encoding DNA.

KM Human; NOV-X protein; KIAA1233-like protein; STE20-like protein; tumour;  
KM trypsin inhibitor-like protein; gene therapy; haematopoietic; illness;  
KM immunological disorder; neurodegenerative disorder; Alzheimer's disease;  
KM Parkinson's disease; immunomodulatory; pharmacogenomic; haemostatic;  
KM human immunodeficiency virus; HIV; fertility disorder; neuroprotective;  
KM cytosolic; neotropic; anti-fertility; cancer; chromosome 17;  
KM NOV-3c protein; de.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..3822

FT FT /product= "Human novel STE20-like protein, NOV-3c"

PN MO200162928-A2.

PD 30-AUG-2001.

PF 26-FEB-2001; 2001WO-US006151.

XX 25-FEB-2000; 2000US-0184951P.

PR 28-FEB-2000; 2000US-0185548P.

PR 01-MAR-2000; 2000US-0185967P.

PR 18-APR-2000; 2000US-0197723P.

PR 27-APR-2000; 2001US-0199579P.

PR 23-FEB-2001; 2001US-00789390.

PA (CURA-) CURAGEN CORP.

PI Vernet CAM, Fernandes E, Shinkets RA, Macdougall J, Spaderna SK;

DR MPI; 2001-582051/65.

DR P-PSDB; AAB10613.

XX New isolated KIAA1233-like, STE20-like, or trypsin inhibitor-like  
PT polypeptide for diagnosing and treating pathological disorders, such as  
PT Parkinson's disease and for use in pharmacogenomics.

XX

PS Claim 9; Page 58-59; 1899p; English.  
XX The invention relates to novel human polypeptides referred as NOV-X and  
CC their corresponding nucleic acid sequences NOV-X collectively include  
CC NOV-1, NOV-2a and NOV-2b which are novel KIAA1233-like polypeptides; NOV-  
CC 3a, NOV-3b, NOV-3c and NOV-3d which are novel STE20-like polypeptides and  
CC NOV-4a, NOV-4b, NOV-4c, NOV-4d and NOV-4e which are novel trypsin  
CC inhibitor-like polypeptides. NOV-X is used to identify a potential  
CC therapeutic agent that can modulate its activity and can be used for  
CC treating a pathology related to aberrant expression or aberrant  
CC physiological interactions of NOV-X. NOV-X or its DNA is used to  
CC determine the presence or predisposition to a disease associated with  
CC altered levels of NOV-X. NOV-X, its DNA and its antibody are used to  
CC treat or prevent a pathology associated with NOV-X. The pathological  
CC states that can be treated or prevented are haematopoietic, cancer,  
CC immunological, tumour, neurodegenerative (e.g. Alzheimer's and  
CC Parkinson's disease), human immunodeficiency virus (HIV) illness and  
CC fertility disorders. NOV-X and its DNA are used in pharmacogenomics for  
CC predictive medicine. NOV-X DNA is used in gene therapy. The present  
CC sequence is a DNA encoding human novel STE20-like protein, NOV-3c.  
CC gene is located at chromosome 17

SQ Sequence 3822 BP; 904 A; 1129 C; 1165 G; 624 T; 0 U; 0 Other;

Query Match 82.9%; Score 3275.6; DB 5; Length 3822;  
Best Local Similarity 90.9%; Pred. No. 0;  
Matches 3682; Conservative 0; Mismatches 29; Indels 339; Gaps 5;

QY 7 ATGGGCGAACCAGCCCGCCGCTGAGACGACATGACCTTCCGCTGGGGAG 66  
|||  
DB 1 ATGGGCGAACCAGCCCGCCGCTGAGACGACATGACCTTCCGCTGGGGAG 60  
|||  
QY 67 CCTGCTGGGATTTTGTAGCTTGTGAGGAGTGTGAGCAATGAACTTCAAGAGGTATC 126  
|||  
DB 61 CTTGCTGGGATTTTGTAGCTTGTGAGGAGTGTGAGCAATGAACTTCAAGAGGTATC 120  
|||  
QY 127 AAGGCTGCGCATGTGACAGCGGGAGCTGTGCTGACATCAAGGTGATGATGACGAG 186  
|||  
DB 121 AAGGCTGCGCATGTGACAGCGGGAGCTGTGCTGACATCAAGGTGATGATGACGAG 180  
|||  
QY 187 GACGAGGAGGAAAGATCAACAGAGATCAACATGCTGAAAAGTACTTCAACACCGC 246  
|||  
DB 181 GACGAGGAGGAAAGATCAACAGAGATCAACATGCTGAAAAGTACTTCAACACCGC 240  
|||  
QY 247 AACATCGCACCTACTACGAGAGCTTTCATCAAGAGAGCCCGGAAACGATGACCG 306  
|||  
DB 241 AACATCGCACCTACTACGAGAGCTTTCATCAAGAGAGCCCGGAAACGATGACCG 300  
|||  
QY 307 CTCTGGCTGTGATGAGAGTTCTGTGTGCTGTGCTGATGACTGACCTGTAAGAACCA 366  
|||  
DB 301 CTCTGGCTGTGATGAGAGTTCTGTGTGCTGTGCTGATGACTGACCTGTAAGAACCA 360  
|||  
QY 367 AAAGCAAGCCCTTGAAGAGAGCTGTATCCCTTATCTGAGGAGATCTCAGGGGT 426  
|||  
DB 361 AAAGCAAGCCCTTGAAGAGAGCTGTATCCCTTATCTGAGGAGATCTCAGGGGT 420  
|||  
QY 427 CTGGCCATCTTCATGAGCCCAAGAGGTGATTCATGAGACATCAAGGGGAGATGTGCTG 486  
|||  
DB 421 CTGGCCATCTTCATGAGCCCAAGAGGTGATTCATGAGACATCAAGGGGAGATGTGCTG 480  
|||  
QY 487 CTGACAGAGATGCTGAGGTCAAGCTAGTGAATTTTGGGGTGAAGTCTCAGCTGACCGC 546  
|||  
DB 481 CTGACAGAGATGCTGAGGTCAAGCTAGTGAATTTTGGGGTGAAGTCTCAGCTGACCGC 540  
|||  
QY 547 ACCGTGGGAGAGCAACCTTTTCAATGAGATCTCCCTACTGATGCTCAGAGGTCAATC 606  
|||  
DB 541 ACCGTGGGAGAGCAACCTTTTCAATGAGATCTCCCTACTGATGCTCAGAGGTCAATC 600  
|||  
QY 607 GCGTGTGATGAGAACCTTGATGCCACTATGATTCAGAGAGATATTGGTCTCAGAGA 666  
|||  
DB 601 GCGTGTGATGAGAACCTTGATGCCACTATGATTCAGAGAGATATTGGTCTCAGAGA 660  
|||  
QY 667 ATCAGAGCATGAGATGGCAGAGGAGAGCCCTCTGTGTGATGACATGCCATGCGA 726  
|||

Db	661	ATCAACAGCCATGAGATGGCAGAGGGAGGCCCCCTCTGTGTGACATGCACCCCATGGCA	720
Oy	727	GCCCTCTTCTCATTTCTCTGGAAACCTTCGGCCAGGCTCAAGTCCAGAAAGTGTCTAAG	786
Db	721	GCCCTTCTCTCATTTCTCTGGAAACCTTCGGCCAGGCTCAAGTCCAGAAAGTGTCTAAG	780
Oy	787	AAGTTCATTGACTTCAATGACACATGTCTCATCAAGACTTACCTGAGCCGCCACCCACG	846
Db	781	AAGTTCATTGACTTCAATGACACATGTCTCATCAAGACTTACCTGAGCCGCCACCCACG	840
Oy	847	GAGCAGCTACTGAAAGTTTCCCTTCAATCCGGGACACAGCCACCGAGCCGAGCTCCGCAATC	906
Db	841	GAGCAGCTACTGAAAGTTTCCCTTCAATCCGGGACACAGCCACCGAGCCGAGCTCCGCAATC	900
Oy	907	CAGCTTAAAGAACCAATTGACCGATCCCGGAAAGACGGGGGTGAGAAAGAGAGACAGAA	966
Db	901	CAGCTTAAAGAACCAATTGACCGATCCCGGAAAGACGGGGGTGAGAAAGAGAGACAGAA	960
Oy	967	TATGAGTACAGCGGACGCGAGGAGGAAAGATGACAGCCATGAGAGAGAAAGAGACCAAGC	1022
Db	961	TATGAGTACAGCGGACGCGAGGAGGAAAGATGACAGCCATGAGAGAGAAAGAGACCAAGC	1022
Oy	1027	TCCATCATGAAAGTTCCTGTGAGAGTTCGACTCTACGCGCGGGAATTTCTCCGGCTCCAGCAG	1088
Db	1021	TCCATCATGAAAGTTCCTGTGAGAGTTCGACTCTACGCGCGGGAATTTCTCCGGCTCCAGCAG	1080
Oy	1087	GAAATTAAGAGCACTCAGAGGCTTTAAACACAGACAGCAGACTGACAGCAGCAGCAGCAG	1144
Db	1081	GAAATTAAGAGCACTCAGAGGCTTTAAACACAGACAGCAGACTGACAGCAGCAGCAGCAGCAG	1144
Oy	1147	CGAGACCCCGAGGCAACATCAAAACACTTGTGCACACAGCGGACAGCGCGCATAGAGAG	1206
Db	1141	CGAGACCCCGAGGCAACATCAAAACACTTGTGCACACAGCGGACAGCGCGCATAGAGAG	1200
Oy	1207	CAGAAAGAGAGAGCGGCGCGCTGTGAGAGCAACAGCGCGGAGAGCGGAGCGAGAG	1266
Db	1201	CAGAAAGAGAGAGCGGCGCGCTGTGAGAGCAACAGCGCGGAGAGCGGAGCGAGAG	1260
Oy	1267	CTGCAAGAGAAAGGACAGCAGCGGGGGGCTGAGAGCAATGCAGGCTCTGCGCGGGAGAGAG	1322
Db	1261	CTGCAAGAGAAAGGACAGCAGCGGGGGGCTGAGAGCAATGCAGGCTCTGCGCGGGAGAGAG	1322
Oy	1327	GAGCGGCGGACAGGCGGAGCGTGAACA-----	1352
Db	1321	GAGCGGCGGACAGGCGGAGCGGAGCGAATATATTCTGCACAGGCTAGAGGAGGACAG	1380
Oy	1353	-----GGAATAC	1355
Db	1381	CGACAGCTCGAGATCTTTCAGCAACAGCTGCTCCAGAAACAGGCCCTGCTGCGAATATAC	1440
Oy	1386	AAGCGGAAGACGCTGAGAGGAGGAGGCGGAGTCAAGAACGCTCCAGAGGAGCTGACAGCAG	1411
Db	1441	AAGCGGAAGACGCTGAGAGGAGGAGGCGGAGTCAAGAACGCTCCAGAGGAGCTGACAGCAG	1500
Oy	1420	GAGCATGCGCTACTCAAGTCCCTGACAGCAGCAACAGCAGCAGCAGCTTTCAGAAACAG	1479
Db	1501	GAGCATGCGCTACTCAAGTCCCTGACAGCAGCAACAGCAGCAGCAGCAGCAGCTTTCAGAAACAG	1566
Oy	1480	CAGCAGCAGCAGCTCTCTGCTGGGAGCAGGAAGCCCTGTACATTTAGTGGGGCANTG	1533
Db	1561	CAGCAGCAGCAGCTCTCTGCTGGGAGCAGGAAGCCCTGTACATTTAGTGGGGCANTG	1622
Oy	1540	AATCCCGCTGACAAACCAAGCCTGGGCGCGAGAGGTAGAAAGAGAAACAAGATGAAACAAG	1599
Db	1621	AATCCCGCTGACAAACCAAGCCTGGGCGCGAGAGGTAGAAAGAGAAACAAGATGAAACAAG	1657
Oy	1600	CAGCAGAACTCTCCCTTGGCCAAAGAGCAAGCCAGGACAGCAGGGGCTGAGCCGCCCATTC	1655
Db	1658	-----TGGCAACCGGGTC	1671
Oy	1660	CCCCAGGCTCTCCCAAGGGCCCCCAGAGACCTCTTTCCCAAGCTCTCTCATGACAGGCGCG	1715

[illegible]

QY 2776 AAGGCCCTGGCAAGAGCTCGTTCAAGATGTTGTGATCTAGGGATCTAACAGCCTGGA 2835  
 DB 2653 AAGGCCCTGGCAAGAGCTCGTTCAAGATGTTGTGATCTAGGGATCTAACAGCCTGGA 2712  
 QY 2836 GGCAGTGGGGACAGCATCCCATCAAGCCTAGTGGGTGAGAGGGCCTCGCTCGAC 2895  
 DB 2713 GGCAGTGGGGACAGCATCCCATCAAGCCTAGTGGGTGAGAGGGCCTCGCTCGAC 2772  
 QY 2896 CAGCTGAGTACGAGAGTGAAGAGGGTCTGTGTGTCACAGTGAATCCCAACCAACCCGG 2955  
 DB 2773 CAGCTGAGTACGAGAGTGAAGAGGGTCTGTGTGTCACAGTGAATCCCAACCAACCCGG 2832  
 QY 2956 GCCCAGTGAAGACCCCTGAGATCCGAGATCAAGAAAGCGATTCACTCCGAGATCTTC 3015  
 DB 2833 GCCCAGTGAAGACCCCTGAGATCCGAGATCAAGAAAGCGATTCACTCCGAGATCTTC 2892  
 QY 3016 TGTGACGCCCTTTGGGGGGTCAACTGCTGTGGGACGAGAGACGGGCTGATGTTGCTG 3075  
 DB 2893 TGTGACGCCCTTTGGGGGGTCAACTGCTGTGGGACGAGAGACGGGCTGATGTTGCTG 2952  
 QY 3076 GACCGAAGTGGGACAGGGGCAAGGTGATGACATTTGGGGGGGCGACGCTTCAGAGATG 3135  
 DB 2953 GACCGAAGTGGGACAGGGGCAAGGTGATGACATTTGGGGGGGCGACGCTTCAGAGATG 3012  
 QY 3136 GATGTGCTGAGAGGGCTCAACCTGCTCATCAACATCTCAGGGAAAGAAAGAACTGCGG 3195  
 DB 3013 GATGTGCTGAGAGGGCTCAACCTGCTCATCAACATCTCAGGGAAAGAAAGAACTGCGG 3072  
 QY 3196 GTGTATTAACCTGTCTCGGCTCCGGAAACAAGATTCTGACATAGACCAGAGTGAAG 3255  
 DB 3073 GTGTATTAACCTGTCTCGGCTCCGGAAACAAGATTCTGACATAGACCAGAGTGAAG 3132  
 QY 3256 AAGCAGGGCTGAGCAACCGTGGGGGACATGAGAGGGCTGGGGGACATACCGTGTGGA 3315  
 DB 3133 AAGCAGGGCTGAGCAACCGTGGGGGACATGAGAGGGCTGGGGGACATACCGTGTGGA 3192  
 QY 3316 TACGAGCGGATTAAAGTCTGTGTCATCGCCCTCAAGAGCTCCGTGAGGTGATGCTTG 3375  
 DB 3193 TACGAGCGGATTAAAGTCTGTGTCATCGCCCTCAAGAGCTCCGTGAGGTGATGCTTG 3252  
 QY 3376 GCGCCCAAAACCTTACCAAAATTCATGAGCTTCTTCCGCAACCTCCCAACCGC 3435  
 DB 3253 GCGCCCAAAACCTTACCAAAATTCATGAGCTTCTTCCGCAACCTCCCAACCGC 3312  
 QY 3436 CCTTCTGCTGTGACCTGACATGATGAGAGGGGCGCGCTCAAGTCACTATGCTTCC 3495  
 DB 3313 CCTTCTGCTGTGACCTGACATGATGAGAGGGGCGCGCTCAAGTCACTATGCTTCC 3372  
 QY 3496 AGTGTGCTTCCATGCTGTGATGTCAGCTCGGGGACAGCTATGACATCTTACCTCT 3555  
 DB 3373 AGTGTGCTTCCATGCTGTGATGTCAGCTCGGGGACAGCTATGACATCTTACCTCT 3432  
 QY 3556 GTGCAATTCAGAGCCAGATCAAGCCCATGCGCATCATTTCTTCCCAACCGCAGCGC 3615  
 DB 3433 GTGCAATTCAGAGCCAGATCAAGCCCATGCGCATCATTTCTTCCCAACCGCAGCGC 3492  
 QY 3616 ATGGAGTCTCTGTGCTACAGAGACGAGGGGTCTAGTCAACAAGACGGGGCGCATC 3675  
 DB 3493 ATGGAGTCTCTGTGCTACAGAGACGAGGGGTCTAGTCAACAAGACGGGGCGCATC 3552  
 QY 3676 ATTTAAGATGTGATGTGCTGAGTGGGGGAGATGCTTCTGTGCTCAATCTTCTCC 3735  
 DB 3553 ATTTAAGATGTGATGTGCTGAGTGGGGGAGATGCTTCTGTGCTCAATCTTCTCC 3612  
 QY 3736 AACCAATTAATGGGCTGGGGGTGAAGAAAGCATTTAGATCCGCTGTGAGAGACGGGCAC 3795  
 DB 3613 AACCAATTAATGGGCTGGGGGTGAAGAAAGCATTTAGATCCGCTGTGAGAGACGGGCAC 3672  
 QY 3796 CTTCAGAGGGGTCTTCAATGCAAAAGAGCTCAGAGGCTCAAGTCTCTGTGAGCGGAT 3855  
 DB 3673 CTTCAGAGGGGTCTTCAATGCAAAAGAGCTCAGAGGCTCAAGTCTCTGTGAGCGGAT 3732

QY 3856 GACAAGTGTGTTTTTCCCTCACTCCGCTCTGGGGGACAGCAGCAAGTTACTTCACTACT 3915  
 DB 3733 GACAAGTGTGTTTTTCCCTCACTCCGCTCTGGGGGACAGCAGCAAGTTACTTCACTACT 3792  
 QY 3916 CTGAACCGTAACCTGATCAGTAAGCTGGA 3945  
 DB 3793 CTGAACCGTAACCTGATCAGTAAGCTGGA 3822

RESULT 14  
 AAC98909  
 ID AAC98909 standard; cDNA, 2345 BP.  
 XX  
 AAC98909;  
 XX  
 09-MAR-2001 (first entry)  
 XX  
 DE Human pancreatic cancer antigen nucleotide sequence SRQ ID NO:137.  
 XX  
 KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection;  
 KW diagnosis; identification; cytostatic; neuroprotective; neurotropic;  
 KW immunomodulatory; relaxant; contraceptive; gynaecological;  
 KW antiinflammatory; cardiant; gene therapy; chromosome mapping;  
 KW linkage analysis; tissue identification; tissue typing; forensic; neural;  
 KW immune system; muscular; reproductive; gastrointestinal; pulmonary;  
 KW cardiovascular; renal; proliferative; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055320-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000MO-US005989.  
 XX  
 PR 12-MAR-1999; 99US-0124270P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM;  
 DR WPI, 2000-579444/54.  
 DR P-PSDB; AAB54144.  
 XX  
 PT New nucleic acid that is a pancreatic cancer antigen for preventing,  
 PT treating, or ameliorating a medical condition, particular pancreatic  
 PT cancer, or for use in assays for diagnosing a pathological condition.  
 XX  
 PS Claim 1; Page 596-597; 1379pp; English.  
 XX  
 CC AAC98773 to AAC99231 encode the human pancreatic cancer associated  
 CC proteins, called pancreatic cancer antigens, given in AAB54008 to  
 CC AAB54466. The human pancreatic cancer antigens have cytostatic,  
 CC neuroprotective, neurotropic, immunomodulatory, relaxant, contraceptive,  
 CC gynaecological, cardiant and antiinflammatory activities, and can be used  
 CC in gene therapy. The polynucleotide and proteins can be used for  
 CC preventing, treating, or ameliorating a medical condition or in assays  
 CC for diagnosing a pathological condition or a susceptibility to one in a  
 CC subject. Binding partners to the proteins and the activity of the  
 CC proteins can be identified. The pancreatic cancer antigens can be used to  
 CC detect, treat or prevent pancreatic disorders, especially cancer.  
 CC Agonists and antagonists to the antigens can be screened for. The  
 CC pancreatic cancer antigen polynucleotides can be used to design nucleic  
 CC acid hybridisation probes that can be used in chromosome mapping, linkage  
 CC analysis, tissue identification and/or typing and a variety of forensic  
 CC and diagnostic methods. The proteins can be used to generate antibodies  
 CC which are used to purify, detect and target the polypeptides. Including  
 CC both in vivo and in vitro diagnostic and therapeutic methods. The  
 CC proteins can be used to treat or prevent neural, immune system, muscular,  
 CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or  
 CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent  
 CC sequences used in the exemplification of the present invention  
 XX

SQ Sequence 2345 BP; 499 A; 693 C; 671 G; 467 T; 0 U; 15 Other;  
 Query Match 38.0%; Score 1502.6; DB 3; Length 2345;  
 Best Local Similarity 99.2%; Pred. No. 6.9e-278;  
 Matches 1527; Conservative 3; Mismatches 8; Indels 2; Gaps 2;

```

QY 2413 TACTGTGTGTCAGAGAGAGAGTGGAAAAGCAGTAGAGAGACGAGAGAGAGAGAGAGG 2472
DB 1 TATTGTGTCAGAGAGAGAGTGGAAAAGCAGTAGAGAGACGAGAGAGAGAGAGAGG 60
QY 2473 GGGCCAGAGAGAGAGAGAGATACCCCTGGGGGCGGACGATGGGATACAGACAGC 2532
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RESULT 15  
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 ID AAF84940 standard; DNA; 3996 BP.

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XX AC AAF84940;
XX AC
XX 09-JUN-2001 (first entry)
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DE Nucleotide sequence of cell cycle protein Tnik isoform 2.
XX
KM Cell cycle protein; Tnik; germinal center kinase; Nck; Traf2; cell cycle;
XX tumour necrosis factor receptor associated factor 2; gene therapy; ss.
XX Homo sapiens.
XX OS
XX FH
XX Key Location/Qualifiers
XX CDS 1..3996
XX FT /*tag=
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FT "Tnik
  
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MO200129197-A2.  
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 23-OCT-2000; 2000MO-US041455.  
 21-OCT-1999; 99US-00425324.  
 (RIGF-) RIGEL PHARM INC.  
 Luo Y, Fu CA, Shen M;  
 WPI; 2001-30033/31.  
 P-PSDB; AAB68217.



XX Novel germinal center kinase cell cycle polypeptide useful for screening  
 PT modulators of cell cycle and for use in diagnostics and therapeutics.  
 XX Claim 1; Fig 22; 96p; English.  
 XX The present sequence encodes an isoform of a human cell cycle protein  
 CC designated Tnk1. Tnk1 is a member of the germinal center kinase family.  
 CC Tnk1 binds to tumour necrosis factor (TNF) receptor associated factor 2  
 CC (Traf2) or the adapter protein Nck. Tnk1 polypeptides and polynucleotides  
 CC are useful for screening for compounds that are modulators of cell cycle,  
 CC and in therapeutics. The Tnk1 polynucleotide is also useful in gene  
 CC therapy.  
 XX  
 SQ Sequence 3996 BP; 1203 A; 911 C; 1064 G; 818 T; 0 U; 0 Other;  
 Query Match 35.6%; Score 1407.2; DB 4; Length 3996;  
 Best Local Similarity 62.5%; Pred. No. 1.4e-259;  
 Matches 2528; Conservative 0; Mismatches 1363; Indels 153; Gaps 15;

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Wed Mar 3 08:13:26 2004

us-10-029-115-1.rng

Page 36

Search completed: March 2, 2004, 10:12:35  
Job time : 1049 secs

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GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 12:59:16 ; Search time 70 Seconds  
(without alignments)  
9508.433 Million cell updates/sec

Title: US-10-029-115-1

Perfect score: 3951  
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Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 164199 seqs, 84230614 residues

Total number of hits satisfying chosen parameters: 328398

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents NA New:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3601	91.1	4863	6	US-10-764-503-30
2	818.6	20.7	3786	5	US-09-744-794C-46
3	214.2	5.4	1975	6	PCT-US04-03417-41
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5	141	3.6	2778	5	US-09-744-794C-33
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7	134.8	3.4	12242	1	PCT-US03-31219-6
8	115	2.9	445	6	US-10-767-701-920
9	112.4	2.8	2838	6	US-10-770-726-27
10	92.2	2.3	484	6	US-10-767-701-28242
11	86	2.2	11409	6	US-10-767-471-603
12	86	2.2	11409	6	US-10-767-471-195
13	83.4	2.1	14321	6	US-10-767-471-191
14	83.4	2.1	14641	6	US-10-767-471-193
15	83.4	2.1	14760	6	US-10-767-471-192
16	83.4	2.1	24841	6	US-10-767-471-10753
17	83.4	2.1	72779	6	US-10-767-471-10639
18	79.6	2.0	2309	6	US-10-767-471-482
19	79.4	2.0	14859	6	US-10-767-471-10846
20	79.4	2.0	67163	6	US-10-767-471-10712
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22	77.8	2.0	679	6	US-10-767-701-4740
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	28	66.2	1.7	111469	6	US-10-767-471-10820	Sequence 10820, A
	29	66	1.7	2213	6	US-10-770-726-31	Sequence 31, Appl
C	30	65.6	1.7	1021	6	US-10-767-701-11316	Sequence 11316, A
	31	64.2	1.6	201	6	US-10-767-471-10130	Sequence 10130, A
	32	64.2	1.6	201	6	US-10-767-471-10130	Sequence 38286, A
C	33	62.2	1.6	803755	6	US-10-767-471-10700	Sequence 10700, A
	34	61.6	1.6	6900	6	PCT-US04-02188-13	Sequence 13, Appl
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C	36	61.6	1.6	106707	1	PCT-US03-34223-8	Sequence 8, Appl
C	37	60.6	1.5	520	6	US-10-767-701-1270	Sequence 1270, Ap
	38	60.2	1.5	583	6	US-10-767-701-4088	Sequence 4088, Ap
C	39	60	1.5	1139	6	US-10-767-701-2898	Sequence 2898, Ap
	40	59.2	1.5	713	6	US-10-767-701-1473	Sequence 1473, Ap
	41	59.2	1.5	1578	6	US-10-417-884A-1441	Sequence 1441, Ap
	42	58.6	1.5	201	6	US-10-767-471-3749	Sequence 3749, Ap
	43	58.6	1.5	201	6	US-10-767-471-3826	Sequence 3826, Ap
	44	58.6	1.5	201	6	US-10-767-471-3904	Sequence 3904, Ap
	45	58.6	1.5	201	6	US-10-767-471-3994	Sequence 3994, Ap

## ALIGNMENTS

RESULT 1  
US-10-764-503-30  
Sequence 30, Application US/10764503  
GENERAL INFORMATION:  
APPLICANT: Levanon Erez, et al.  
TITLE OF INVENTION: METHODS AND SYSTEMS FOR IDENTIFYING NATURALLY OCCURRING ANTISENSE  
TITLE OR INVENTION: TRANSCRIPTS AND METHODS, KITS AND ARRAYS UTILIZING SAME  
FILE REFERENCE: 26946  
CURRENT FILING DATE: US/10/764,503  
PRIOR APPLICATION NUMBER: 2004-01-27  
PRIOR FILING DATE: 2004-01-27  
PRIOR APPLICATION NUMBER: US 09/718,407  
PRIOR FILING DATE: 2000-11-24  
PRIOR APPLICATION NUMBER: US 09/732,938  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/785,439  
PRIOR FILING DATE: 2001-02-20  
PRIOR APPLICATION NUMBER: US 09/907,923  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: US 09/993,398  
PRIOR FILING DATE: 2001-11-26  
PRIOR APPLICATION NUMBER: US 10/201,605  
PRIOR FILING DATE: 2002-7-24  
PRIOR APPLICATION NUMBER: PCT/IL02/00904  
PRIOR FILING DATE: 2002-11-11  
PRIOR APPLICATION NUMBER: US 10/441,281  
PRIOR FILING DATE: 2003-5-20  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 30  
LENGTH: 4863  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-764-503-30

Query Match 91.1%; Score 3601; DB 6; Length 4863;  
Best Local Similarity 95.0%; Pred. No. 0;  
Matches 3829; Conservative 0; Mismatches 5; Indels 195; Gaps 3;

QY 7 ATGGGACACCCAGCCCGCCGAGCTGGACGATCGACTGTCCGCTCGGAGC 66  
DB 185 ATGGGACACCCAGCCCGCCGAGCTGGACGATCGACTGTCCGCTCGGAGC 244  
QY 67 CTTGCTGGATCTTGGACTTGTGAGAGTGTGCGGATGGAACCTACGACAGTGTAC 126  
DB 245 CTTGCTGGATCTTGGACTTGTGAGAGTGTGCGGATGGAACCTACGACAGTGTAC 304  
QY 127 AAGGATGGCATGTCACAGCGGAGCTGGCTCCATCAAGTTCATGATGTCACGAG 186  
DB 305 AAGGATGGCATGTCACAGCGGAGCTGGCTCCATCAAGTTCATGATGTCACGAG 364

OY	187	GACGAGGAGGAAGAGATCTAAACAGAGAGATCAACAATGCTGAAAAAAGTACTTCCACCACCGC	246
Db	365	GACGAGGAGGAAGAGATCAAAACAGAGATCAACAATGCTGAAAAAAGTACTTCCACCACCGC	424
OY	247	AACATCGCACTTACTGACGAGCTTCAATCAAGAAGACCCCGGGAAGAGATGACCG	306
Db	425	AACATCGCACTTACTGAGGCTTCAATCAAGAAGACCCCGGGAAGAGATGACCG	484
OY	307	CTCTGGCTGTGTAGTGAAGTTCTGTGTGCTGGTTCAATGACTGACCTGTGTAAGAACACA	366
Db	485	CTCTGGCTGTGTAGTGAAGTTCTGTGTGCTGGTTCAATGACTGACCTGTGTAAGAACACA	544
OY	367	AAAGGCAACGGCCCTGAAGGAGGACGTATCGCTATATCTGACGGGAGATCCTCAGGGGT	426
Db	545	AAAGGCAACGGCCCTGAAGGAGGACGTATATCGCTATATCTGACGGGAGATCCTCAGGGGT	604
OY	427	CTGGCCATCTTCATGATCCCAACAGGTGATCCATCGAGACATCAAGGGGACAGATGTGTG	486
Db	605	CTGGCCATCTTCATGATCCCAACAGGTGATCCATCGAGACATCAAGGGGACAGATGTGTG	664
OY	487	CTGACAGAGAAATGCTGAGGTCAAGCTAATGGAATTTTGGGGTGAAGTCTCACTTGAACGC	546
Db	665	CTGACAGAGAAATGCTGAGGTCAAGCTAATGGAATTTTGGGGTGAAGTCTCACTTGAACGC	724
OY	547	ACCGTGGGACAGACGGACACTTTCATTTGGGACCTCCCTACCTGGATGTGCTCAGAGGTATC	606
Db	725	ACCGTGGGACAGACGGACACTTTCATTTGGGACCTCCCTACCTGGATGTGCTCAGAGGTATC	784
OY	607	GCTGTGATGAGAACCTCTGATGCCACTATGATTAAGAGAGTGAATTTTGGTCTCTAGGA	666
Db	785	GCTGTGATGAGAACCTCTGATGCCACTATGATTAAGAGAGTGAATTTTGGTCTCTAGGA	844
OY	667	ATCAGAGCATTCAGATGAGAGAGGAGACCCGCCCTGTGTGATGATGACACCCCATGGA	726
Db	845	ATCAGAGCATTCAGATGAGAGAGGAGACCCGCCCTGTGTGATGATGACACCCCATGGA	904
OY	727	GCCCTCTTCTCATTTCTCTGGAACCCCTCGCCAGAGCTCAAGTCCAAAGATGTGTTAAG	786
Db	905	GCCCTCTTCTCATTTCTCTGGAACCCCTCGCCAGAGCTCAAGTCCAAAGATGTGTTAAG	964
OY	787	AAGTTCATTTGACTTCATTTGACACATGTCTCATCAAGACTTTCAGAGCCCGCCACCG	846
Db	965	AAGTTCATTTGACTTCATTTGACACATGTCTCATCAAGACTTTCAGAGCCCGCCACCG	1024
OY	847	GAGCAGCTACTGAAGTTTCCCTCATTCGCGGACCAAGCCACGAGCGGCAAGTCCGATC	906
Db	1025	GAGCAGCTACTGAAGTTTCCCTCATTCGCGGACCAAGCCACGAGCGGCAAGTCCGATC	1084
OY	907	CAGCTTAAAGACCACTTGAACCGATCCCGGAAGAACGGGGTGAAGAAAGAGAGACAGA	966
Db	1085	CAGCTTAAAGACCACTTGAACCGATCCCGGAAGAACGGGGTGAAGAAAGAGAGACAGA	1144
OY	967	TATGAGTACAGCGGACGCGAGGAGGAATGACAGCCATGAGAGAGGAAGAGGCAAGC	1026
Db	1145	TATGAGTACAGCGGACGCGAGGAGGAATGACAGCCATGAGAGAGGAAGAGGCAAGC	1204
OY	1027	TCCATCATGAACGTGCTGAGAGTCACTTACGCGCGGAGATTTCCTCGGCTCCAGCAG	1086
Db	1205	TCCATCATGAACGTGCTGAGAGTCACTTACGCGCGGAGATTTCCTCGGCTCCAGCAG	1264
OY	1087	GAAAAATAGACCACTCAGAGGCTTTAAACAGCAGCAGCAGCTGACAGACAGAGCAG	1146
Db	1265	GAAAAATAGACCACTCAGAGGCTTTAAACAGCAGCAGCAGCTGACAGACAGAGCAG	1324
OY	1147	CGAGACCCCGAGGCAACATCAAAACCTGTGCAACAGCGGACGCGCGATAGAGAG	1206
Db	1325	CGAGACCCCGAGGCAACATCAAAACCTGTGCAACAGCGGACGCGCGATAGAGAG	1384
OY	1207	CAGAAAGAGAGCGGCGCGCGTGGAGAGCAACAGCGGCGGAGCGGAGACAGCGAG	1266
Db	1385	CAGAAAGAGAGCGGCGCGCGTGGAGAGCAACAGCGGCGGAGCGGAGACAGCGAG	1444

QY	1287	CTGCAGAGAAAGAGACGACAGCGCGGCTGAGAGACATGACAGGCTCTGCGCGGGAAGAG	1326
Db	1445	CTGCAGAGAAAGAGACGACAGCGCGGCTGAGAGACATGACAGGCTCTGCGCGGGAAGAG	1504
QY	1327	GAGCGGCGGCGGAGGCGGAGCTGTGACAGAAATACAGCGGAAGCAGCTGAGAGACAGCG	1386
Db	1505	GAGCGGCGGCGGAGGCGGAGCGGAGCAGAAATACAGCGGAAGCAGCTGAGAGACAGCG	1564
QY	1387	CAGTCAGAACGTCTCCAGAGGCAAGCTTGACAGAGAGCATGCTTCAAGTCCCTGCAG	1446
Db	1565	CAGTCAGAACGTCTCCAGAGGCAAGCTTGACAGAGAGCATGCTTCAAGTCCCTGCAG	1624
QY	1447	CAGCAGACAAACGACGACGACGCTTCAGAAACAGCAGACGACGACGCTCTGCGGGGAC	1506
Db	1625	CAGCAGACAAACGACGACGACGCTTCAGAAACAGCAGACGACGACGCTCTGCGGGGAC	1684
QY	1507	AGGAAGCCCTGTATCAATTATGATCGGGGACATGAATCCGCTGACAAACAGCTTGAGCC	1566
Db	1685	AGGAAGCCCTGTATCAATTATGATCGGGGACATGAATCCGCTGACAAACAGCTTGAGCC	1744
QY	1567	CGAGAGGTAGAAAGAGAAACAAAGATGAAACAGCAGACGAATCTCTCCCTTGCCAGAGC	1626
Db	1745	CGAGAGGTAGAAAGAGAAACAAAGATGAAACAGCAGACGAATCTCTCCCTTGCCAGAGC	1804
QY	1627	AAAGCAGGACGACAGGGGCTGTAGCCCCCATCTCCCCAGGCTCTCCAGGGCCCCCAGGA	1686
Db	1805	AAAGCAGGACGACAGGGGCTGTAGCCCCCATCTCCCCAGGCTCTCCAGGGCCCCCAGGA	1864
QY	1687	CCCCCTTCCGACGCTCCCTCTATGACAGAGCGGGTGGAGCCCCAGAGGGACCGCACAA--	1744
Db	1865	CCCCCTTCCGACGCTCTCTCTATGACAGAGCGGGTGGAGCCCCAGAGGGACCGCACAAAG	1924
QY	1745	-----AG 1746	
Db	1925	AGCGGTGGGACACCGGGTCCCATGAGGCATATGACAGACCTGTATACCCCGATCCCAG	1984
QY	1747	TCCCTGACGACCAAGCCCACTGGCTGCTTCCAGGCTCCCATGACCCCGAC	1806
Db	1985	TCCCTGACGACCAAGCCCACTGGCTGCTTCCAGGCTCCCATGACCCCGAC	2044
QY	1807	CCCTCCATCCCCGACCACTGCCACGCGCCAGTGGCGGAGAGTGTTCATCCGCAAAAT	1866
Db	2045	CCCTCCATCCCCGACCACTGCCACGCGCCAGTGGCGGAGAGTGTTCATCCGCAAAAT	2104
QY	1867	TCAGACCCCACTCTGAAAGACCTGAGCCCAAGCCGATCCCCAGGCTGGGTCCGCCA	1926
Db	2105	TCAGACCCCACTCTGAAAGACCTGAGCCCAAGCCGATCCCCAGGCTGGGTCCGCCA	2164
QY	1927	GATTAACGAGGCCCAACCCAGGTGCTTCAGAGACCTCATCTATCGCATGCTGCCCTTAAC	1986
Db	2165	GATTAACGAGGCCCAACCCAGGTGCTTCAGAGACCTCATCTATCGCATGCTGCCCTTAAC	2224
QY	1987	ACCAATGGGGCGGAGAGGTCCCGGCGAGCCAGGCAATCCGTGCAACAACCTCGAGCAAC	2046
Db	2225	ACCAATGGGGCGGAGAGGTCCCGGCGAGCCAGGCAATCCGTGCG-----	2269
QY	2047	TCGCGCTGGCAATCTATCTGCAAAAGCGGAGAGGCGGACCCCAAAAGCTTCAGAGG	2106
Db	2270	-----	2269
QY	2107	CCCCCTGTACGCCCTCGGCGGCGCAAGCCTCTAGTAAACCCCGACCTTCAGAGAGAC	2166
Db	2270	-----AGTAAACCCCGACCTTCAGAGAGAGC	2293
QY	2167	GACCTGTGCTGGGAAAGCTGTGGAACAAGGTCTTTCACACCTTCACCGGCAACCTCCCCAG	2226
Db	2294	GACCTGTGCTGGGAAAGCTGTGGAACAAGGTCTTTCACACCTTCACCGGCAACCTCCCCAG	2353
QY	2227	GCTGGCTCACCTGAGCGGGAACCGGCTGGAGACCTCTCCAAACTGGAACAGCTCCCTGTG	2286
Db	2354	GCTGGCTCACCTGAGCGGGAACCGGCTGGAGTCTCTCTCAAAACCGGACAGTCTCCCTGTG	2413
QY	2287	CTCTCCCTGGGAATAAAGCCCAAGCCGACGACCAACGCTTCACGGCAAGCGCGGCCGCA	2346

Db	2414	CTCTCCCTGGGGAATAAAGCCAAAGCCCAAGCAACCGCTCACGGCCAGGCCGGCCGCA	2473
Oy	2347	-----GACTTGTTGTTGCTGAAAGCCGAACTCTGACGAG	2385
Db	2474	AGCTATAAGCGAGCAATTGCTGAGGACTTTGTGTTGCTGAAGAAGCCGACTCTGGACGAG	2533
Oy	2383	GCCCTCGGCTCTCCGAAAGGCCATGAGCTACTGTGTGTCACGAGGAAGGTGGAAAGC	2442
Db	2534	GCCCCCTGGCTCCCAAGAGGCCATGAGCTACTGTGTGTCACGAGGAAGGTGGAAAGC	2593
Oy	2443	AGTAGAGAGCAACGAGGAGGAAGCGAAGCGGGCCAGGACGAGGGGACAGATACCCCT	2502
Db	2584	AGTAGAGAGCAACGAGGAGGAAGCGAAGCGGGCCAGGAGGAGGAGAGATACCCCT	2652
Oy	2503	GGGGGCCGACGAGTAGGGGATACAGACAGCGTCACACCATGTTGTTCCACGACGTGAG	2562
Db	2654	GGGGGCCGACGAGTAGGGGATACAGACAGCGTCACACCATGTTGTTCCACGACGTGAG	2713
Oy	2563	GAGATCACCGGGAGCCGAGCCCCCATACGCGGGCGCCACATGTTGTTCCAGCCCT	2622
Db	2714	GAGATCACCGGGAGCCGAGCCCCCATACGCGGGCGCCACATGTTGTTCCAGCCCT	2772
Oy	2623	GAAAGGAGCGGGAACCTGCTGATGCTCTACAGCATATGGGTACAAACCTGCTGACGTG	2688
Db	2774	GAAAGGAGCGGGAACCTGCTGATGCTCTACAGCATATGGGTACAAACCTGCTGACGTG	2833
Oy	2683	GTCCAGCCGACGACTCACCCACCGAGAACAGCAAGGCCCAAGCCCACTCGAAGGAT	2742
Db	2834	GTCCAGCCGACGACTCACCCACCGAGAACAGCAAGGCCCAAGCCCACTCGAAGGAT	2893
Oy	2743	GGGAGTGTGACTACCAAGCTCTGTGGGCTGTAAAGCCCTGGCAAGACTGTTCAAG	2802
Db	2894	GGGAGTGTGACTACCAAGCTCTGTGGGCTGTAAAGCCCTGGCAAGACTGTTCAAG	2953
Oy	2803	ATGTTTTGTGAGATCTAAGGATCTACACAGCTGGAGGCAATGGGGACAGATCCCACTCA	2866
Db	2954	ATGTTTTGTGAGATCTAAGGATCTACACAGCTGGAGGCAATGGGGACAGATCCCACTCA	3013
Oy	2863	GCCCTAAGTGGGTTGAGAGGGGCACTGGCTCGACCAAGCTTGAGTAAGAGTGAAGAGGT	2922
Db	3014	GCCCTAAGTGGGTTGAGAGGGGCACTGGCTCGACCAAGCTTGAGTAAGAGTGAAGAGGT	3073
Oy	2923	TCTGTGTCAACGTGAATCCCAACCAACCCGGGGCCCAAGTAGAACCTCTGATATCCGG	2988
Db	3074	TCTGTGTCAACGTGAATCCCAACCAACCCGGGGCCCAAGTAGAACCTCTGATATCCGG	3133
Oy	2983	AAAGTCAAGAAAGCGATTCAACTCCGAGATCCTCTGTGAGCCCTTTGGGGGGTCAACTG	3193
Db	3134	AAAGTCAAGAAAGCGATTCAACTCCGAGATCCTCTGTGAGCCCTTTGGGGGGTCAACTG	3243
Oy	3043	CTGGTGGGCAAGGAAAGGGGTGATGTTGCTGACCGAATGGGGCAGGGGCAAGGTGAT	3102
Db	3194	CTGGTGGGCAAGGAAAGGGGTGATGTTGCTGACCGAATGGGGCAGGGGCAAGGTGAT	3253
Oy	3103	GGACTCATTTGGGCGGCGAGCGCTTCCAGCAGATGATGTGTCTGAGAGGGCTCAACTGTCTC	3162
Db	3254	GGACTCATTTGGGCGGCGAGCGCTTCCAGCAGATGATGTGTCTGAGAGGGCTCAACTGTCTC	3313
Oy	3163	ATCACCATCTCAAGGAAAAGGAAACAACTGGGGGTATTAACCTGTCTGTCCGGAAC	3222
Db	3314	ATCACCATCTCAAGGAAAAGGAAACAACTGGGGGTATTAACCTGTCTGTCCGGAAC	3373
Oy	3223	AAAGATTCTGCAACATGACCCGAAATGTGAGAAAGAAAGGAGGTGAGCAACCGTGGGGGAC	3288
Db	3374	AAAGATTCTGCAACATGACCCGAAATGTGAGAAAGAAAGGAGGTGAGCAACCGTGGGGGAC	3433
Oy	3283	ATGAGAGGCTGGGAGCACTACCGTGTGTAATACGAGCGGATTAAGTTCTGTGCTATC	3342
Db	3434	ATGAGAGGCTGGGAGCACTACCGTGTGTAATACGAGCGGATTAAGTTCTGTGCTATC	3493
Oy	3343	GCCCTCAAGAGCTCCGTGAGGTGATATGCTGGGCCCCCAACCTTAACAATAATTCATG	3402

Db	3494	GCCCTCAAGAGCTCCGTGAGAGTGTATGCTGTGGGCCCCCAACCTTACCAAAATTCTATG	3553
Qy	3403	GCCTTCAAAGTCTCTTTCGCCAGCCTTCCCAACCGCCCTCTGTGTGTGACTGACGTAAAG	3468
Db	3554	GCCTTCAAAGTCTCTTTCGCCAGCCTTCCCAACCGCCCTCTGTGTGTGACTGACGTAAAG	3613
Qy	3463	GAGGGGGCAGGGGCTCAAGAGTCAATGATGGCTTCAAGTGTGGCTTTCATGCTGTGATGTC	3522
Db	3614	GAGGGGGCAGGGGCTCAAGAGTCAATGATGGCTTCAAGTGTGGCTTTCATGCTGTGATGTC	3673
Qy	3523	GACTCGGGGAAACAGTTATGACATCTACATCCCTGTGCAATCCAGAGCAGATCAACGCC	3582
Db	3674	GACTCGGGGAAACAGTTATGACATCTACATCCCTGTGCAATCCAGAGCAGATCAACGCC	3733
Qy	3563	CATGCCATCATCTTCTCTTCCCAACACCGGACGTGAGATGCTGTGCTTACGAGGAC	3642
Db	3734	CATGCCATCATCTTCTCTTCCCAACACCGGACGTGAGATGCTGTGCTTACGAGGAC	3793
Qy	3643	GAGGGTGTCTACGTCAACAGTACGGGGGACATCATTAAGATGTGGTCTGACGTGGGG	3702
Db	3794	GAGGGTGTCTACGTCAACAGTACGGGGGACATCATTAAGATGTGGTCTGACGTGGGG	3855
Qy	3703	GAGATGCTTACTTCTGTGGGCTTACATCTGCTCCAACAGATTAATGGCTGTGGGTGAGAA	3766
Db	3854	GAGATGCTTACTTCTGTGGGCTTACATCTGCTCCAACAGATTAATGGCTGTGGGTGAGAA	3913
Qy	3763	GCCATTGAGATCCGCTCTGTGGAGACGGGGCACTCGACGGGGTCTTTCATGCAAAACGA	3822
Db	3914	GCCATTGAGATCCGCTCTGTGGAGACGGGGCACTCGACGGGGTCTTTCATGCAAAACGA	3973
Qy	3823	GCTCAGAGGCTTCAAGTTTCTGTGTGAGGGGAAATGACAAAGTGTTTTTTGCTCAGTCCG	3888
Db	3974	GCTCAGAGGCTTCAAGTTTCTGTGTGAGGGGAAATGACAAAGTGTTTTTTGCTCAGTCCG	4033
Qy	3883	TCGTGGGGGACAGACCAAGTTTACTTCACTGCACTGTGAACCGTTAACTGATCATGACTGG	3942
Db	4034	TCGTGGGGGACAGACCAAGTTTACTTCACTGCACTGTGAACCGTTAACTGATCATGACTGG	4093
Qy	3943	TGAAAGGGC 3951	
Db	4094	TGACGGGCG 4102	
RESULT 2			
US-09-744-794C-46			
; Sequence 46, Application US/09744794C			
; GENERAL INFORMATION:			
; APPLICANT: INCYTE CORPORATION; HILLMAN, Jennifer L.;			
; APPLICANT: LAU, Preeti G.; TANG, Y. Tom;			
; APPLICANT: CORLEY, Neil C.; GUEGLER, Karl J.;			
; APPLICANT: BAUGHN, Mariah R.; PATTERSON, Chandra S.;			
; APPLICANT: BANDMAN, Olga; AU-YOUNG, Janice K.;			
; APPLICANT: GORGONE, Gina A.; YUE, Henry;			
; APPLICANT: AZIMZAI, Yalda; REDDY, Roopa M.;			
; APPLICANT: LU, Dying Aina M.; SHIH, Leo L.			
; TITLE OF INVENTION: HUMAN CELL SURFACE RECEPTORS			
; FILE REFERENCE: PF-0565 USN			
; CURRENT APPLICATION NUMBER: US/09/744,794C			
; CURRENT FILING DATE: 2001-10-05			
; NUMBER OF SEQ ID NOS: 60			
; SOFTWARE: PERL Program			
; SEQ ID NO 46			
; LENGTH: 3786			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc feature			
; OTHER INFORMATION: Incyte ID No: 2299715CB1			
US-09-744-794C-46			
Query Match	20.7%;	Score 818.6;	DB 5;
Best Local Similarity	56.2%;	Prod. No. 4.1e-168;	
Matches 2219;	Conservative	0;	Mismatches 1189;
		Indels 537;	Gaps 15;

QY 7 ATGGGGAACCCAGCCCCCGCCGACGCTTGGAGCAGATGACCTTGGCCGCTTGGCGGAGC 66  
Db 140 ATGGGGAACGACTCCCCCTGCAAAAAGTCTGGTGGACATGACTCTCTCCCTCGGGGAT 199  
QY 67 CCTGTGGGATCTTTGAGCTTGTGGAGGTGTGTGGCAATGAACTTACGGAAGGTGTAC 126  
Db 200 CTTGCTGGGATTTTGTAGCTGGTGGAAAGTGTGGAAATGGCACTATGACAAAGCTAT 259  
QY 127 AAGGCTGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGTCAATGATGTCAAGAG 186  
Db 260 AAGGCTGGCATGTCAAGACGGGGCAGCTGGCAAGGATCAAGATTAAGATGTCACTGAG 319  
QY 187 GACGAGGAGGAGAGATCAACAGAGAGATCAATCTGTAAGAAAGTACTCTACACGCGC 246  
Db 320 GATGAAGAGGAGGAGGATCAACAGAGATTAATGTCTAAGAAATCTCTATCAACAGA 379  
QY 247 AACATCGCACTACTACGAGAGCTTTCATCAAGAAAGGCCCCCGGAAACGATGACGAG 306  
Db 380 AACATTTGCAACATTAATATGATGTCTTTCATCAAAAAGAGCCCTCCAGGACATGATGACAA 439  
QY 307 CTCTGGCTGTGATGAGATTTCTGTGTGTCTGGTTCACTGATCTGACTGTGTAAGAACACA 366  
Db 440 CTCTGGCTGTGATGAGATTTCTGTGTGTCTGGGCTGGGCTCCATTACAGACCTTGTGAAAGAACCC 499  
QY 367 AAAGGCAAGCCCTGAAGAGAGAGCTGTATGCTATATCTGACAGGAGATCTCCAGGGGT 426  
Db 500 AAAGGCAACACTCAAGAAAGAGCTGATGCTTACATCTCCAGAGAAATCTTGAGGGGA 559  
QY 427 CTGGCCCATCTCCATGCCCCCAAGGTGATCATGAGACATCAAGGGGAGATGTCTG 486  
Db 560 CTGGCAACATCTTCACTATCATATGATTTCAACGGGATATCAAGGGGCGAGATGTGTG 619  
QY 487 CTGACAGAGAAATGCTGAGGTCAAGCTAGTGAATTTTGGGTGAGTCTCACTGAGACCGC 546  
Db 620 CTGACAGAAATGCAAGGGGTGAACCTTGTGACTTGTGAGTGTGCTCACTGAGACAGG 679  
QY 547 ACCGTGGGAGAGCGAAACATTTGATGAGACTCCCTACCTGATGGCTCCAGAGGTATC 606  
Db 680 ACTGTGGGGCGAGAAATGCTTTCATGAGCACTCCCTACCTGATGGCTCTTGAAGTCACTC 739  
QY 607 GCTGTGATGAGAAACCTGTATGCTCCACCTTATGATTAAGAGATGATATTTGTCTTGA 666  
Db 740 GCTGTGATGAGAAACCTGTATGCTCCACCTTATGATTAAGAGATGATCTTGTGTGAC 799  
QY 667 ATCAAGCCCATGAGATGAG 726  
Db 800 ATTAAGCCCATGAGATGAG 859  
QY 727 GCCCTCTTCTCATTTCTGAGAAACCTTCGCGCCAGGCTCAAGTCCAAAGAGGTCTAAG 786  
Db 860 GCACTGTTCTCATTTCTGAGAAACCTTCCTCCCGGCTGAGTCAAAAATATGTGTAGAG 919  
QY 787 AAGTTCAATGACTTCAATGACATGTCTCATCAAGACTTACCTGAGCCGCAACCCAG 846  
Db 920 AAGTTTATTAAGTTTATTAAGAGGTGCTGTGAAAGATTAATATGACAGGGCCCTCTACA 979  
QY 847 GAGCAGCTACTGAAGTTTCCCTTTCATCCGGGACCAAGCCCAAGAGGGGAGGTCCGATC 906  
Db 980 GAGCAGCTTTTAAACATCTTTTATTAAGGATCAAGCCAAATGAAAGGCAAGTTAATATC 1039  
QY 907 CAGCTTAAGAGCAACATTAAGAGATCCCGAAGAAAGCGGGGTGAGAAAGAGAGAGAGAG 966  
Db 1040 CAGCTTAAGAGATCAATTAAGATGTGTACAGAAAGAGAGAGAGAGAGAGAGAGAGAG 1099  
QY 967 TATGAGTACAGCGCAGCAG 1023  
Db 1100 TATGAGTACAGCGGAGGTGAG 1159  
QY 1024 AGCTCATATGAAGCTGCTGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1083  
Db 1160 AGTTCATATGTAAGCTGCTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1219

QY 1084 CAGGAAATTAAGAGCACTCAGAGGCTTTAAACAGCAGCAGCAGCTCAGCAGCAGCAG 1143  
Db 1220 CAGGAAATTAAGAGCACTCAGAGGCTTTAAACAGCAGCAGCAGCTCAGCAGCAGCAG 1279  
QY 1144 CAGCAGAGCCCCGAGGCAACATCAAAACCTGCTGCAACAGCCGACAGCGGCTGATAG 1203  
Db 1280 CTCCGGGAGCAGGAAATTAAGAGCACTGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1339  
QY 1204 GAGCAG 1263  
Db 1340 CAGCAGAAAG 1399  
QY 1264 AAGCTCAG 1323  
Db 1400 AGCAG 1459  
QY 1324 GAGAGCGCGGAG 1383  
Db 1460 TTGGAG 1492  
QY 1384 CGGCACTGAGAAAGCTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1443  
Db 1493 AGAGCGGAG 1549  
QY 1444 CAGCAG 1503  
Db 1550 CAGCTTAAG 1609  
QY 1504 CAG 1563  
Db 1610 GGCATGTATCTGATGAG 1653  
QY 1564 GCCGAG 1623  
Db 1654 -----GACAG 1684  
QY 1624 AGCAG 1683  
Db 1685 AGCAG 1744  
QY 1684 GAG 1743  
Db 1745 CAG 1788  
QY 1744 AAGTCCCTGAG 1803  
Db 1789 -----CCGTGAG 1844  
QY 1804 GACCTGACATCTCCGAG 1863  
Db 1845 GAAAC-----TCCAGCAG 1857  
QY 1864 AATTGAG 1923  
Db 1858 TATTAG 1880  
QY 1924 CAGAGTAAAG 1983  
Db 1881 -----1880  
QY 1984 AACACAGTGGGAG 2043  
Db 1881 -----AAGAGTGAAG 1915  
QY 2044 AACTCCGCTGGCAATCTATCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2103  
Db 1916 -----GACAGCTCTCAG 1928  
QY 2104 GGGCCCGTGTGAG 2163  
Db 1929 GGTTCAG 1988  
QY 2164 AGCAG 2223



Db 1989 AACGTTAGAGTGA-----TCATCATCCAAAGTGTGAAGGCTCTCCATCTCAGGCTG 2044  
 Qy 2224 CAGGCTGCTCACTGAGCGGAAACCGCTGGAGCTCTCTCCAACTGGAACAGCTCCCT 2283  
 Db 2045 GAAATGAGTGAAGAACTGGAAGTAAAGAAAGAAAGTCTTCAAGCTCCCTCAGCTCT 2104  
 Qy 2284 GTGCTCTCCCTGGGAATTAAGCCCAAGCCCAAGCTCCCTCAGCTCCCTCAGCTCCCT 2343  
 Db 2105 GATGACCTGAGCACTGGCCAAAGAGCTTGAAGAGTGAAGTGAAGGCTC----- 2154  
 Qy 2344 GACAGCTTGTGTGTTCTGAAAGAGCGGACTCTGAGCAAGGCTCCGCTCTCCCAAGAG 2403  
 Db 2155 -----ACCTCAAAAGTAAAGGACTACTCTCTCATCTCAGTGAAG 2192  
 Qy 2404 GCCATGAGCTACTGCTGCTCCAGCGAGAGGTGGAAGCACTGAGAGCAAGAGAGAA 2463  
 Db 2193 AGTGGG-----GAGGACGAGTGAAGAGGAGCAAGTGTGAGAGAAAGGGCTGAGCAG 2248  
 Qy 2464 GGGGAGGCGGCGGAGAGAGGAGAGAGATACCTCTGGGGGCGGAGAGAGAGAGAT 2523  
 Db 2249 TCCACCTCAGAGCAAGAGAGCAAGAGAGAGCTCTGAAATTTGAGCAATGAGTAA 2308  
 Qy 2524 ACAGACAGCTCAGAGCAAGAGAGTCCAGAGCTGAGAGATCAGCGGAGCCAGGCGC 2583  
 Db 2309 AGGGAATTTGGAAGAACTATGTTTCAATGATGTAAGAAAGTGAAGCGGCGCACTGAC 2368  
 Qy 2584 CCATACAGGAGGCGGAGCACTGATGCTGAGAGCAAGCTGGAAGAGAGAGAGAGCTGCTG 2643  
 Db 2369 CCATACAGAGAGGAGCACTGATGCTGAGAGCAAGCTGAGAGAGAGAGAGAGAGAG 2428  
 Qy 2644 CATGCTGACAGCAATGAGTGAACAACTGCTGAGAGTGCAGGCGGAGAGAGAGAG 2703  
 Db 2429 AA-----ACAGAAATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2470  
 Qy 2704 ACCGGAACAGAGAAAGCGCAAGCGCAGCTGAGAGAGAGAGAGAGAGAGAGAGAG 2763  
 Db 2471 -----AGATTTACTCAGATTTT 2486  
 Qy 2764 CGTGGCTGTAAGAGCCCTGAGCAAGAGCTGTTCAAGATGTTTGTGAGATCTAGAGATC 2823  
 Db 2487 CTCATCTAGAGGGAACAAGTGAATCTGATGAGATTTTCTGATGAGAGATGAGAG 2546  
 Qy 2824 TACAGAGCTGAGAGAGAGAGAGAGATCCCATCAGAGCTGATGAGAGAGAGAGAG 2883  
 Db 2547 CAGAAAGCCATAAG----- 2559  
 Qy 2884 ACTGGCTGAGCAAGCTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2943  
 Db 2560 -----GAAAGATCTTACCGGAAAGGCTCAGAGTGAATGATCTT 2602  
 Qy 2944 ACCAACAACCGGAGCCAGAGTGAAGAGCCCTGAGATCCGGAAGTACAGAGAGAGATCAAC 3003  
 Db 2603 ACCAACAACCTAGCCAGAGTGAAGAGCCCGGAGATCTTAAATACAGAGAGAGATTTAAC 2662  
 Qy 3004 TCCGAGATCTCTGAGAGCCCTTTGGGGGCTCAACTGCTGAGAGAGAGAGAGAGAGAG 3063  
 Db 2663 TCTGAGATCTCTGAGAGCCCTTTGGGGGCTCAACTGCTGAGAGAGAGAGAGAGAGAG 2722  
 Qy 3064 CTGAGATCTCTGAGAGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3123  
 Db 2723 CTGAGATCTCTGAG 2782  
 Qy 3124 TCCAGAGAGATGATGCTGAG 3183  
 Db 2783 TTTTCAACAAATGAG 2842  
 Qy 3184 AACAAATGAG 3243  
 Db 2843 GATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 2902  
 Qy 3244 GAAATGAG 3303

Db 2903 GAAATGAG 2962  
 Qy 3304 CGTGTGTAAGTACAGAGAGATTAAGTCTGCTGATCGGCTTCAAGAGCTCCGTGAG 3363  
 Db 2963 AAGATGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 3022  
 Qy 3364 GTGATGCTGGGCGGCGGAG 3423  
 Db 3023 GTTATGAG 3080  
 Qy 3424 CTCCCGAG 3483  
 Db 3081 -----AATG 3085  
 Qy 3484 ATCTATGCTCTCATGCTGCTTCCATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 3543  
 Db 3086 GTATATGATCTCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 3145  
 Qy 3544 ATCTATGCTCTCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 3603  
 Db 3146 ATTTATCTTCAACATATCTCATGATGATGATGATGATGATGATGATGATGATGATGAT 3205  
 Qy 3604 AACACGAG 3663  
 Db 3206 AATACAGATGAG 3265  
 Qy 3664 TACGAG 3723  
 Db 3266 TATGAG 3325  
 Qy 3724 TACATGCTCTTCAACAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3783  
 Db 3266 TATATGATCTTCAACAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3385  
 Qy 3784 GAG 3843  
 Db 3386 GAAATGATCTTGAAG 3445  
 Qy 3844 TGTAG 3903  
 Db 3446 TGTAG 3505  
 Qy 3904 TACTTATGATCTGAG 3948  
 Db 3506 TATTTATGATCTTGAAG 3550

RESULT 3  
 PCT-US04-03417-41  
 Sequence 41, Application PC/TUS0403417  
 GENERAL INFORMATION:  
 APPLICANT: Kelly, Louise M.  
 APPLICANT: Carlow, Joseph M.  
 APPLICANT: Farlow, Deborah  
 APPLICANT: Healy, Aileen  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
 TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,  
 TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,  
 TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,  
 TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,  
 TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR  
 TITLE OF INVENTION: 5014  
 FILE REFERENCE: MP103-015  
 CURRENT APPLICATION NUMBER: PCT/US04/03417  
 CURRENT FILING DATE: 2004-02-05  
 PRIOR APPLICATION NUMBER: US 60/445,241  
 PRIOR FILING DATE: 2003-02-05  
 PRIOR APPLICATION NUMBER: US 60/448,389  
 PRIOR FILING DATE: 2003-02-18  
 PRIOR APPLICATION NUMBER: US 60/456,320  
 PRIOR FILING DATE: 2003-03-20  
 PRIOR APPLICATION NUMBER: US 60/460,279  
 PRIOR FILING DATE: 2003-04-03

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; PRIOR APPLICATION NUMBER: US 60/465,924
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/470,052
; PRIOR FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: US 60/498,106
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/500,179
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/502,909
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/510,351
; PRIOR FILING DATE: 2003-10-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 1975
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (127)...(1407)
; PCT-US04-03417-41

Query Match      5.4%; Score 214.2; DB 1; Length 1975;
Best Local Similarity 55.5%; Pred. No. 1.2e-37;
Matches 576; Conservative 0; Mismatches 398; Indels 63; Gaps 6;

QY      10  GCGGACCCAGCCCGCCGAGCTTGACGACATGACCTGCGCCCTGCGGAGCCCT 69
DB      115  GCGGCGCGGCGCATGCTGCTACCTCGGGGATTGGAAACAGCACTCTGAGTGAGCCCT 174
QY      70  GCTGGAGTCTTTGAGCTTGTGAGAGTGTGCGGCATGAACTTAAGAGAGTGAAG 129
DB      175  GAGGAGCTCTTCAACAGCTGACCGCATGGCCAAAGGCTCTTTGGGAGGCTTACAG 234
QY      130  GGTGCGCATGTCAAGACGGGAGCGTGTGCTGCATCAAGTATGATGTCAAGAGAGC 189
DB      235  GGCATCGATACCAACAAAGAGGTGTGCGGCATCAATGATGACCTGAGAGAGGCG 294
QY      190  GAGAGAGA---AGAGATCAACAGAGATCAACATGCTGAAAAAGTACTCTACCAAGCG 246
DB      295  GAGGATGAGATCGAGGACATCCAGCAGAGATCACTGCTCATGTCAGTGCAGAGCCCG 354
QY      247  AACATGCGCACTTACGAGACCTTTCATCAAGAAAGAGCCCGGAAACGATGACCG 306
DB      355  TACATCAACCGGCTACTTGGCTCTTAAAGAGCA-----CCAG 396
QY      307  CTCTGCTGTGATGAGAGTTCTGTGGTGTGCTTCACTGATGACCTGTAAAGACACA 366
DB      397  CTATGATCATCATGAGATGATCTGGGCGGCGCTCAGCATGAGCTTGTCT-----T 447
QY      367  AAAAGCAAGCCCTGAAGAGAGCTGTATGCTTATCTGACGAGAGATCTCAGGGGT 426
DB      448  AAAACAGGCTCCCTGAGAGAGACATTCATTGACGATCTCGGAGAGATTCGAAAGGC 507
QY      427  CTGGCCCATCTTCAGAGCCCAAGAGATCCATCAGAGATATTAAGGGGAGAGATGCG 486
DB      508  CTGGATTATCTGACATCCGACGCAAGATCCACGAGATCAATAAGCTGCCAAGCGTCA 567
QY      487  CTGACAGAGAAATGCTGAGGTCAAGCTAGTGAATTTTGGGGTGAAGTCTCAGTGA 546
DB      568  CTCTGGAGAGAGGTGACTGTAAGCTGGGAGCTTTGGGGTGAAGGAGCTCAGACAGC 627
QY      547  ACCGTGGGAGACGAAACATTTCAATGGAGCTCCCTACTGATGAGGCTCAGAGGTATC 606
DB      628  AGCAGATTAAGAGAGACATTCGTGGGACACCCCTTCTGATGAGCAGTGAAGGTATC 687
QY      607  GCCTGTGATGAAGAACCTGTATGCTTATGATTAAGAGAGTATTTTGTCTCTAAGA 666
DB      688  AAGC-----AGTCGGGCTTACGACTTCAAGCTGACATCTGTGCTCCCTGGGC 732
QY      667  ATCAGAGCATGAGATGGCAGAGGAGCCCGCCCTCTGTGTGATGACATGACCCCATG 726
```

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DB      733  ATCAGAGCATGAGATGGCCCAAGGGGAGCTTCAAACTTGACTTCAACCCCATGCGC 792
QY      727  GCCCTCTTCCATTTCCCGGAACCTTCGCGCCAGAGCTCAAGTCAAGAAATGCTTAAG 786
DB      793  GTCTGTCTGATTTCCCAAGAACAGCCCACTCACTGAGGGCCAGCAG---CAG 849
QY      787  AAGTTCAATGACTTCATTTGACATGATGCTCATCAAGATTACTGAGCCGCCACCAAG 846
DB      850  CCTTCAAGAGATTTGTGAGAGCCTGCTCAAAAGACCCCGATTCGGCCACAGGCC 909
QY      847  GAGAGCTACTGAAGTTTCCCTTATCCGGGACCAAGCCAGGAGCGGAGAGTCCGATC 906
DB      910  AAGAGGCTCTGAAGACCAAGTTTATCAACAGTCAACCAAGAAAGACTCTTCTTCAAG 969
QY      907  CAGCTTAAGGACCAATTGACCGATCCCGAAGAGCGGGTGAAGAAAGAGACAGAA 966
DB      970  GAGCTCATCGA-----CCGCTATTAAGGCTGGAAGTCAAGAGGGGATGCG 1014
QY      967  TATGATACAGCGGACGAGAGAGAGATGACAGCCATGAGAGAGAGAGAGCAAGC 1026
DB      1015  GAGAGTCCAGCTCTGAGAGCTCTGACATTTATGATGCGGAGCGGAGAGCGGAGAGG 1074
QY      1027  TCATCATGAACGTGCC 1043
DB      1075  CCATCTGAGAGTTCCC 1091

RESULT 4
US-10-772-636-41
; Sequence 41, Application US/10772636
; GENERAL INFORMATION:
; APPLICANT: Kelly, Louise M.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Fallow, Deborah
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,
; TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 20611, 5891,
; TITLE OF INVENTION: 91307, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
; TITLE OF INVENTION: 5014
; FILE REFERENCE: MP103-015P1RMONIM
; CURRENT APPLICATION NUMBER: US/10/772,636
; PRIOR FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,241
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,389
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/456,320
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/460,279
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/465,924
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/470,052
; PRIOR FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: US 60/498,106
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/500,179
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/502,909
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/510,351
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 1975
; TYPE: DNA
; ORGANISM: Homo sapiens
```

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (127) ... (1407)
US-10-772-636-41

```

Query Match	5.4%;	Score 214.2;	DB 6;	Length 1975;
Best Local Similarity	55.5%;	Pred. No. 1.2e-37;		
Matches 576;	Conservative	0;	Mismatches 398;	Indels 63;
				Gaps 6;

QY	10	GGCACCAGGACCCCGCCCGAGCTGGACACATCGACTCTGCGCCCTGGGGACCTT	69
Db	115	GGCGGCGGGCCATGCTCACTCCGGGGATTGGAAACGACACTCTGATGGACCTT	174
QY	70	GCTGGGATCTTTGAGCTTTGGAGTGGTCCGCAATGGAACTTACGACAGGTGTACAAG	129
Db	175	GAGAGGCTCTTACCAAGCTCGACCGCATTTGGCAAGGGCTCGTTTGGGAGGTCTACAAG	234
QY	130	GGTGGCATGTCCAAAGCGGGCACTGGCTGCCATCAAGGTCTATGGATGTCAACGGAGAC	189
Db	235	GGCATCGATTAACCAACAAAGAGGTGGTGGCCATCAAGATCTATGACCTTGAAGGAGGCC	294
QY	190	GAGGAGGA---AGAGATCAAAAGAGATTCAAATGTCTGAAAAAGTACTTCACCAAGCCG	246
Db	295	GAGGATGATGATCGAGACATTCAGACGAGATGATCTGTCTCACTGACGTGGACAGGCC	354
QY	247	AACATGCGCACTTACTACGAGCCTTCATCAAGAGAGAGCCCCCGGGAAACGATGACCG	306
Db	355	TACATTCACCGGCTACTTTGGCTCTTAATAAGAGCA-----CCAAG	396
QY	307	CTCTGCGTGGATGGAATTTCTGTGTGTCTGGTTCACTGATCTGACTGTGTAAAGACACA	366
Db	397	CTATGATTCATCAATGAGGTACTGGGCGGCGGCTCAGACATGGAATTTCT-----T	447
QY	367	AAAGGCAACGCCCTGAAGGAGACCTGTATGCTTATCTGACGAGGAGATCCTCAGGGT	426
Db	448	AAACCAAGTCCCTCGAGGAGACATCACTTGTCCAGATCTCTGCGGAGATTTGAAGGCG	507
QY	427	CTGGCCCATCTCATGCCCCACAGGATGATTCATCGAGACATCAAGGGCAGATGTGTG	486
Db	508	CTGGATTAATCTGCACTCCGAACGCAAGATTCACCGAGCATCAAGAGTGGCCACGTGCTA	567
QY	487	CTGACAGAGAACTCTGAGGTCAAGCTAGTGAATTTTGGGGTGAAGTCTCAGCTGAGCCG	546
Db	568	CTCTCGGAGGAGGGGTGACGTGMACTGGCGGACTTTGGGGTATGACGAGGCACTCAACAG	627
QY	547	ACCGTGGGCAAGCGGACACTTTGATTTGGGACCTCCCTATCTGGATGGCTCCAGAGGTATC	606
Db	628	ACGCAAGTTAAGAGGAACACTTGTGGGACCCCTTCTGATGTGGACCTGAGGTCTATC	687
QY	607	GCCGTGTATGAGAACCTGTATGCCACTATATTACAGAGATGTAATATTGGTCTCTAGGA	666
Db	688	AAGC-----AGTCGGCTTACGACTTCAAGGCTGACATCTGGTCCCTGGGCG	732
QY	667	ATCAGCCCATCGAGATGGCAGAGGAGGCCCCCTCTGTGTGACATGACATCCCATGCGA	726
Db	733	ATCAGACCCATCGAGCTGGCCAAAGGGGAGGCTCCAAACTGCACTCAACCCCATGCGC	792
QY	727	GCCCTTCTCCCATCTTCCTCGGAACCTTCGCGCCGAGGCTCAAGTCCAAAGATGTCTTAAG	786
Db	793	GTCCTGTTCTGATTTCCCAAAACAGGCCACCCACATGAGAGGGCACAACAG---CAAG	849
QY	787	AAGTTCAATTGACTCATTTGACACATGTCTCATCAAGACTTACCTTGAAGCGGCCACCG	846
Db	850	CCCTTCAAGAGAGTTGTGGAGGCGCTGCTTCAACAAAGACCCCGGATTCGGGCCACGGCC	909
QY	847	GAGCAGCTACTGAAGTTCCCTTCAATCCGGGACCAAGCCCAAGAGCGGAGGTCCGCAATC	906
Db	910	AAGGAGCTCCCGAAGCAACAGTTATATCAACGCTACACCAAGAGACCTCTCTCTCAAG	969
QY	907	CAGCTTAAGACCAATTTGACCGATCCCGGAGAAAGCGGGGTGAGAAAGAGAGACAGAA	966
Db	970	GAGCTATTCGA-----CCGCTATTAAGCGCTGAATGTCAGAGGGAGATGCG	1014

Oy	TATAGTATACGCGGCACGGAGGAGAATGACGCCATGGAGGAAGGAGACCACAGC	1026
Dd	GAGGAGTCGAGCTCTGAGGACTGTGACATTGATGGCCAGGCGGAGGAGCGGGGACCAAGGC	1074
Oy	967 TATAGTATACGCGGCACGGAGGAGAATGACGCCATGGAGGAAGGAGACCACAGC	1026
Oy	1027 TCCTCATGTAACGTGCC	1043
Dd	1075 CCCTCTCGAACGTTCCC	1091

RESULT 5  
US-09-744-794C-33  
; Sequence 33, Application US/09744794C

```

1  APPLICANT: INCYTE CORPORATION; HILLMAN, Jennifer
2  APPLICANT: LAL, Preeti G.; TANG, Y. Tom;
3  APPLICANT: CORLEY, Neil C.; GUEGLER, Karl J.;
4  APPLICANT: BAUGHN, Mariah R.; PATTERSON, Chandan
5  APPLICANT: BANDMAN, Olga; AU-YOUNG, Janice K.;
6  APPLICANT: GORGONE, Gina A.; YUE, Henry;
7  APPLICANT: AZIMZAI, Yalda; REDDY, Roopa M.;
8  APPLICANT: LU, Dung Anna M.; SHIH, Leo L.
9  TITLE OF INVENTION: HUMAN CELL SURFACE RECEPTORS
10 FILE REFERENCE: pr-0565 USN
11 CURRENT APPLICATION NUMBER: US/09/744,794C
12 CURRENT FILING DATE: 2001-10-05
13 NUMBER OF SEQ ID NOS: 60.
14 SOFTWARE: PERL Program
15 SEQ ID NO 33
16 LENGTH: 2778
17 TYPE: DNA
18 ORGANISM: Homo sapiens
19 FEATURES:
20 NAME/KEY: misc feature
21 OTHER INFORMATION: Incyte ID No: 2197671CBI
22 FEATURE:
23 NAME/KEY: unsure
24 LOCATION: (1) ... (2778)
25 OTHER INFORMATION: a, t, c, g, or other
26 US-09-744-794C-33

```

Query Match	3.6%;	Score 141;	DB 5;	Length 2778;
Best Local Similarity	51.8%;	Pred. No. 9e-22;		
Matches 476;	Conservative	0;	Mismatches 395;	Indels 48;
			Gaps	5;

Qy	64	GACCTCTGCGAATCTTTGAGCTTGTGAGAGTGGTGGCATGGAACTTCGAGCAGGTG	123
Db	110	GACCCAAAGACGTTTTTACAAAACTAGAGAAAATGGGAAGCGCTCTTTGGAGAGGTG	169
Qy	124	TACAAAGGTGGGCACTGTCAAGACGGGGCAGCTGGCTGCCATCAAGTCAATGATGTCAAG	183
Db	170	TTCAAAAGGCATTGGCAATCGGACTCAGAAAAGTGTTGCCATTAAGATCAATTGAATCTGAA	229
Qy	184	GAGAACAGAGAGCA--AGAGATCAAAACAGAGATCAACATGCTGAAAAGTACTCTCAC	240
Db	230	GAAGCTGAAGATGATGATGAGGACATTCAACAAGAAATCAACAGCTGAGTCACTGTGAC	289
Qy	241	CACCGCAACATCGGCACCTTACTACGAGACCTTTCATCAAGAGAGCCGCCCGGAAACGAT	300
Db	290	AGTGCATATGTATACCAATATTTATGATCTCTATCTGAAG-----GAT	331
Qy	301	GACCACTCTGGCTGTGATGAGAGTTCTGTGTGTCTGTTCAATGTAAGTCACTGATGTAAG	360
Db	332	ACAAAATTATGATTAATAATGAGAAATCTTGTGTGAGGCTCCGACATGATCTATTT-----	387
Qy	361	AAACAAGAGCAACGCCCTGAAGAGAGACGTATGCTCTATATCTGACAGAGATCCTC	420
Db	388	-----AGAACCTGGCCGATTTAGTGAAGACCAAGTGCCTACTATTTAAGAGAAATCTG	442
Qy	421	AGGGGTCTGGCCCATCTCCATGCCCCAAGATGATTCATCGAGACATCAAGGGGCAAGT	480
Db	443	AAAGGATCTGATTTATCTCCATTTGGAGAGAAAGAAATCCACAGAGACATTAAGGGCCAAC	502
Qy	481	GTCTGCTGACAGAGAAATGCTGAGGTCAAGCTACTGTGATTTTGGGTGAGTCTCAAGCTG	540

Db 503 GTCTCGTGTGACCATGGCGAGGGTGAAGCTGGCCGACTTTGGCGTGGCTGGCCACTTG 562

Qy 541 GACCCGACCGTGGGGAGACGGAACACTTTCATTTGGACTCCCTACTGATGTGCTCGAG 600

Db 563 ACAGACACCCAGATCAAAAAGAACACTTCGTGGGACCCCACTTTGGATGGCACCCGAG 622

Qy 601 GTCATCGCTGTGATGAGAACCTCTATGACCACCTATGATTTACAGAGTGTATTTGTCT 660

Db 623 GTTCATCAAAAC-----AGTGGGCTTATGACTTCGAAGGACAGACATCTGTCTC 667

Qy 661 CTAGGAATCACAGCCATCGAGATGGGAGAGGGAGCCCCCTGTGTGTGATCATGCACCC 720

Db 668 CTGGGCATTAACGCTATTGAACCTTGCAGAGGGGAACACCTCATTCGAGCTGCACCC 727

Qy 721 ATGCAGGCCCTTCTCTCAATTCCTCGAAACCTCGGCCAGGCTCAAGTCCAAAGAAAGTGG 780

Db 728 ATGAAAGTTTATTCTCTCATTCGAAAGAACCAACCCAGCGCTGGAGGAACCTACAG- 786

Qy 781 TCTAAGAAAGTTCAATGACTTTCATTTGACACATGCTCTATCAAGCTTAACCTGAGCCGCCA 840

Db 787 --TAAACCCCTCAAGAGAGTTTGTGGAGGCTGTATTGAATTAAGAGCGAGCCTTTAAACCC 844

Qy 841 CCCAGGAGCAGCTACTGAAGTTTCCCTCATCCGGGACGAGGCCAGCGGCGAGTCC 900

Db 845 ACTGCTAAGAGATTATTGAAGCACAAAGTTTATCTACGCAATGCAAGAAAAGAACTTCTTAC 904

Qy 901 CGCATCCAGCTTAAGGACCAATTGACGATCCCGGAAGAAAGCGGSGTGAAGAAAGAGAG 960

Db 905 TTGACCGAGCTCATGCACAGGTACAGAGATGGAGGCGAGCAGAGAGCCATGACGACTCG 964

Qy 961 ACAGAAATGAGTACACCG 979

Db 965 AGCTCCGAGAGTTCGAGC 983

```

RESULT 6
PCT-US03-31219-7
; Sequence 7, Application PC/TUS0331219
; GENERAL INFORMATION:
; APPLICANT: Schering Aktiengesellschaft
; APPLICANT: Parry, Gordon
; APPLICANT: Vogel, David
; APPLICANT: Whitlow, Marc
; APPLICANT: Wu, Qingsyu
; TITLE OF INVENTION: Modified Hepsin Molecules Having a Substitue Activation Sequence
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 53038A0M01
; CURRENT APPLICATION NUMBER: PCT/US03/31219
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/416,038
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 11924
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid 3
PCT-US03-31219-7

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Query Match	3.4%	Score 134.8	DB 1	Length 11924
Best Local Similarity	52.1%	Pred. NO. 3.1e-20		
Matches 301	Conservative	0	Mismatches 277	Indels 0
			Gaps	0
QY	935	GGAAGAACCGGGGTAGAAAGGACACAGATATGATACAGCGGCAGGAGGAGAG	994	
DB	6773	GGCAGAGACGAGGAGGAGGGGCGAGGAGGGGCGAGAGGGGCGAGGACGAGGAG	68322	
QY	995	ATGACAGCATTGGAAGAGAGAGCCAGCTCATATGTAAGTGGCTGTGAGAGTGA	1054	
DB	6833	AAGGCGACGAGACGAGGAGGGGCGAGGCGGCAGAGGGGCGAGGAGGAGGAGGCG	68922	

QY	1055	CTTACCGCGGAGCTTTCTCCGECTCCAGCAGAAATTAAGAGCACTCAGAGGCTTTAA	1114
Db	6893	AGGAGCAGGAGGAGGGGCGCAGAGGGGCGAGGCGAGGAGGGGCGAGAGGG	6952
QY	1115	AACAGCAGCAGCAGCTGCGAGCAGCAGCAGCAGCAGCCCGAGGCAACATCAAAACC	1174
Db	6993	GGCAGAGCAGAGAGAGAGGGGCGAGAGCAGAGAGAGGGGCGAGAGGGGCGAGAGCAGAGG	7012
QY	1175	TGCTGCACCAAGCGGCGAGCGCGCTAAGAGAGCAAGAGAGAGCGGCGCCGCTGGAGG	1234
Db	7013	AGGGGCGAGGAGGGGCGAGGAGGGGCGAGAGCGAGGAGGGGCGAGGACGAGAGGGGCGAGG	7072
QY	1235	AGCAACAGCGCGCGGAGCGCGGAGCAGGCGGAAGCTTCAGAGAAAGACAGCAGCGCGGCG	1294
Db	7073	AGGGGCGAGAGGGGCGAGGACAGAGAGGGGCGAGAGCAGAGAGAGGGGCGAGAGGGGCGAGG	7132
QY	1295	TGAGAGCATTCAGAGCTTCGCGCGGAGAGAGAGCGGCGAGCGGAGCGGAGCGTGAAGCAGG	1354
Db	7133	AGGGGCGAGGACAGAGAGGGGCGAGGAGCAGGAGGGGCGAGGACAGAGAGGGGCGAGGAGG	7192
QY	1355	AATACAGCGGAACGACTGGAGGAGCAGCGCGGCTCAGAACGTCCTCAGAGGGGAGCGTCG	1414
Db	7193	AGGGGCGAGAGGGGCGAGGAGCAGGAGGGGCGAGAGGGGCGAGAGCGGAGGGGCGAGAGG	7252
QY	1415	AGCAGGAGCATGTCTCACTCAAGTCCCTGCGAGCAGCAGCAACAGCAGCAGCTTCAGA	1474
Db	7253	GGCAGAGCAGAGAGAGAGGGGCGAGGAGGGGCGAGAGCAGAGAGAGGGGCGAGGAGGGGCGAGG	7312
QY	1475	AACAGCAGCAGCAGCACTCTCTGCTGGGGACAGGAAG	1512
Db	7313	AGCAGGAGGGGCGAGAGGGGCGAGGAGCAGAGAGGGGCGAG	7350

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RESULT 7
PCT-US03-31219-6
/ Sequence 6, Application PC/TUS0331219
/ GENERAL INFORMATION:
/ APPLICANT: Schering Aktiengesellschaft
/ APPLICANT: Parry, Gordon
/ APPLICANT: Vogel, David
/ APPLICANT: Whitlow, Marc
/ APPLICANT: Wu, Qingyu
/ TITLE OF INVENTION: Modified Hepsin Molecules Having a Substitue Activation Sequence
/ TITLE OF INVENTION: and Uses Thereof
/ FILE REFERENCE: 53038AOWM1
/ CURRENT APPLICATION NUMBER: PCT/US03/31219
/ CURRENT FILING DATE: 2003-10-02
/ PRIOR APPLICATION NUMBER: US 60/416,038
/ PRIOR FILING DATE: 2002-10-04
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 6
/ LENGTH: 12242
/ TYPE: DNA
/ ORGANISM: artificial sequence
/ FEATURE:
/ OTHER INFORMATION: plasmid 2
PCT-US03-31219-6

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Query Match	3.4%	Score 134.8	DB 1	Length 12242
Best Local Similarity	52.1%	Pred. No. 3.2e-20		
Matches 301	Conservative	0	Matches 277	Indels 0
			Gaps	0
Qy	935 GGAAGAGCGGGCTAGAAAGAGGAGACAGATATGATTAACAGCGGCACGCGAGGAG	994		
Db	7091 GGCAGAGCAGAGAGAGAGGGGCGAGAGGGGCGAGAGGGCGCAGAGGGGACAGAGAG	715		
Qy	995 ATGACAGCCATGAGAGGAGAGAGGCCAAGCTCCATCATGAACGTGCTTGGAGATCGA	105		
Db	7151 AGGGGCAAGAGCAGAGAGGGGCGCAGAGGGGCAAGAGGGGCGCAGAGAGGAGAGGGGCGC	7210		
Qy	1055 CTCCTAGCGCGGAGTTTCTCCGCGCTCAGCAGAGAAATTAAGACAACTCAGAGGCTTTAA	111		

Db	7211	AGGAGCAGAGAGGGGGCGAGAGGGGGCAGAGCAGAGAGGGGGCAGAGGGGGCAGGAGG	721707
Oy	1115	AACACGACGACGAGCTGCGACGACGACGACGACGACGACCCCGGCGACACATCAACACC	11747
Db	7271	GGCAGGACGACGAGAGGAGGGGGCGAGGACGAGAGAGGGGCGAGAGGGGGCGAGAGCAGAGG	73330
Oy	1175	TGCTGCACGACGGCGGCGCGCATATAGAGAGCAGAGAGAGAGCGCGCGCCGCTGAGAG	12344
Db	7331	AGGGGCGAGAGGGGGCAGGAGGGGGCGAGAGCAGAGAGAGGGGGCAGAGCAGAGGGGGCAGG	73908
Oy	1235	AGCAACAGCGGCGGGAGCGGGGACGACCGGAAGCTTCAGAGAGAGAGCAGACGCGGCGCG	129458
Db	7391	AGGGGCGAGAGGGGGCAGAGCAGGAGGGGGCAGAGACAGAGAGAGGGGGCAGAGGGGGCAGG	74508
Oy	1295	TGAGGACATGCAAGGCTCTGCGCGGGGAGAGAGCGCGCGCAGCGGAGCGTGAAGAG	13544
Db	7451	AGGGGCGAGAGCGAGAGGGGGCGAGGCGAGAGGGGGCGAGAGCGAGAGGGGGCGAGGACAGG	75108
Oy	1355	AATACAGCGGAAAGCAGCTGAGGAGGACGCGCAGTCAAGAACTGTCTCAGAGGCGAGCTCC	14144
Db	7511	AGGGGCGAGAGGGGGCGAGGAGCGAGAGGGGGCGAGAGGGGCGAGAGCGAGAGGGGGCGAGGAG	75707
Oy	1415	AGCAGGAGCATGCTTAAGTCCATGTCAGACGACGACGACGACGACGACGACGACGACGACGACG	14744
Db	7571	GCGAGGACAGAGAGGAGGGGGCGAGAGGGGGCGAGAGCAGAGAGAGGGGGCAGAGGGGGCAGG	76308
Oy	1475	AACAGCAGCAGCAGCAGCTCTCTCTGCGGGGACAGGAAG	1512
Db	7631	AGCAGGAGGGCGAGAGGGGGCGAGAGCGAGAGGGGGCAG	7668

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 US-10-767-701-920  
 : Sequence 920 Application US/10767701  
 : GENERAL INFORMATION:  
 : APPLICANT: Kovalic, David K.  
 : APPLICANT: Zhou, Yihua  
 : APPLICANT: Cao, Yongwei  
 : TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 : TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 : FILE REFERENCE: 38-21(53535)B  
 : CURRENT APPLICATION NUMBER: US/10/767,701  
 : CURRENT FILING DATE: 2004-01-29  
 : NUMBER OF SEQ ID NOS: 63128  
 : SEQ ID NO 920  
 : LENGTH: 445  
 : TYPE: DNA  
 : ORGANISM: Sorghum bicolor  
 : FEATURE:  
 : OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS1326\_1  
 US-10-767-701-920

Query Match	2.9%	Score 115	DB 6	Length 445
Best Local Similarity	60.0%	Pred. No. 2,1e-16		
Matches 237	Conservative 0	Mismatches 140	Indels 18	Gaps 2
QY	298	GATGACCAAGCTCTGGCTGGTGATGAGATTCTGTGGTGTCTGTTCAAGTACGTACCTGGTA	357	
Db	64	GAGGACTACTATGATGATGATTATGAGACTGTGGTGAGAGATGTTCTGATTTTGATA	123	
QY	358	AAGAACACAAAGAAGGACACGCCCTGAAGAGACATGTATGCGCTATATCTGCAGGGAGATC	417	
Db	124	GGCATCACAGAGG---AGCCTTTGATGATATCCAAATAGCTTATATATGTAGAGAGCA	180	
QY	418	CTCAGGGCTGGGCCCATCTCCAGTCCCAAGAGTGATCCATGAGACATCAAGGGGCGAG	477	
Db	181	CTAAAGGCGCTTGCTTACCTGCACATTTTAAAGTTCATAGATATTTAAGGTGGC	240	
QY	478	AATGTGCTGTGACAGAGATGCTGAGGTCAAGCTAAGTGGATTTTGGGGTGAAGTGTCCAG	537	
Db	241	AACATTTCTTAACTGAGCAGAGGCGAGGAGATGGGTGATTTTGGTGTACTCCCGCAG	300	

QY	538	CTGAGACCGCACCCTGGGAGAGAGGAACTTTTCATTGGGACATCCCACTGGATGGCTCCA	597
Db	301	CTGACAGAAACCATGTCTCAAAAGGCAACAGTTCATTGGTACTCCACATTGGATGGACCA	360
QY	598	GAGGTGATCGCCTGTGATGAGAAACCTGATGCGCACTATGATTTACGAGATGATATTGG	655
Db	361	GAGGTGAT-----TGAAGAACTCGTTATGATGAGAAAGGTAGATGTTGG	405
QY	658	TCTTAGGAATACAGACCATCGAGATGGGAGAGGG	692
Db	406	GCATTACGTGATCTGCAATTGAGATGGGACAGGG	440

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RESULT 9
US-10-770-726-27
; Sequence 27, Application US/10770726
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: CANCERS
; TITLE OF INVENTION: CONCENTRATES
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770.726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 27
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-27

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Query Match	2.8%	Score 112.4	DB 6	Length 2838
Best Local Similarity	51.8%	Pred. No. 1.4e-15		
Matches 322	Conservative 0	Mismatches 276	Indels 24	Gaps 2
QY	301	GACCAAGCTCTGGCTGTGTATGGAAGTTCTGTGATGCTGTGATGACATGACTACCTGTGTAAG	360	
DB	1375	GACGAGCTCTGGGTGTGTATGATGAGAGTTCTGTGAAGGAGGCGCCCTTCACCGGATCATGTCAC	1434	
QY	361	AACACAAAGGCAACGCCCTGAAGAGGACTGTATTCGCTTATTCGTGAGGAGATCTCT	420	
DB	1435	CACAC-----CAGATGTAAGAGAGCAGATCGGCGCCGTGTCTTTCAGTGTCTG	1485	
QY	421	AGGGGTCTGGCCATCTTCATGCCCAAGGTGATTCATGTGAGCATCAAGGGGCAAGAT	480	
DB	1486	CAGGCGCTGTGGTGTCTCACGCCAAGGCGCTTCATCCCGGACATCAAGGACCTCG	1545	
QY	481	GTGCTGTGACAGAGAAATGCTGAGGTCAAGCTAGATGTGATTTTGTGGGGTGAATGTCTACCTG	540	
DB	1546	ATCTGTGTGACCCATGATGCGAGGGTGAAGTGTCTCAAGCTTTTGGGTTCTGGGCCAAGGTG	1605	
QY	541	GACCGCACCGTGGGCAAGCGGACACTTTCATTGGGACTCCCTACCTGATGGCTTCAGAG	600	
DB	1606	AGCAAGGAGTGGCCCCCAAGGAATCGCTGTGCGGACGCGCTTACTGATGTGCCCCAGAG	1665	
QY	601	GTCAATCGCTGTATGAGGAACCTCGATGACCACTATGATTTACAGAGTGAATTTTGTCT	660	
DB	1666	CTCATCTTCGCCCTT-----CCCTACGGGCGCAAGGTGATGATCTTGGTCTG	1710	
QY	661	CTAGAAGATCACAGCGCATTCGAGATGGGAGAGGAGACCCCTCTGTGTGATCATCACCCC	720	
DB	1711	CTGGGGATTAATGGTGTGATTTGAGATGTGTGACGGAAGCCCCCTTACTTCAACGAGCACCC	1770	
QY	721	ATGCGAGCGCTCTTCTCTCATTCCTCGGAACCTTCGCGCCAGGCTCAAGTCCAGAAAGTGG	780	
DB	1771	CTCAAGGCGATGAGATGATTCGGGACAACTCGGCCACCCCGCATGGAAGACTCTCACAG	1830	
QY	781	TCTAAGAAAGTTCAATTGACTTCAATGACACATGTCTCATCAAGACTTACCTGAGCGGCCCA	840	
DB	1831	GTGTGCGCATCTCCGAAAGGGCTTCTCGGACCGCTGTGTGTGTGCGAGACCTTGCCCTCAGG	1890	

Qy	841	CCCAACGGAGACGCTACTGAAGTTTCCCTTCATCCGGACACAGCCACAGAGGCGCAGGTC	900
Db	1891	GCCACGGAGACGCCACTGCTGTAAGACCCCATTCCTCGCCAGAGGAGGGCGCCCTGCCAGC	195
Qy	901	CGCATCCAGCTTAAAGACACCA	922
Db	1951	ATCGAGCCCCCTCATGCGCCAGA	1972

RESULT 10  
US-10-767-701-28242

Query Match	2.3%	Score 92.2	DB 6	Length 484
Best Local Similarity	53.0%	Pred. No. 1.8e-11		
Matches 258, Conservative	0	Mismatches 208	Indels 21	Gaps 2

RESULT 11  
US-10-767-471-603

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: Sequence 603, Application US/10767471
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele et al.
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001505
: CURRENT APPLICATION NUMBER: US/10/767,471
: CURRENT FILING DATE: 2004-01-30
: NUMBER OF SEQ. ID NOS: 50231
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 603
: LENGTH: 11409
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-767-471-603

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Query Match 2.2%; Score 86; DB 6; Length 11409;  
Best Local Similarity 51.7%; Pred. No. 1.1e-09;  
Matches 246; Conservative 1; Mismatches 220; Indels 9; Gaps 2

RESULT 12  
US-10-767-471-195

Query Match	2.2%;	Score 86;	DB 6;	Length 14800;
Best Local Similarity	51.7%;	Pred. No. 1.2e-09;		



Matches 246; Conservative 1; Mismatches 220; Indels 9; Gaps 2;

Qy 1039 GTGCTGAGAGTGTACTCTACGCCGGAGTTTCTCCGGCTTCAGCAGAGAAATAGAC 1098  
Db 7498 GAGCGTGAAGAGAGAACTCCACAGAGAGGCAAACTGTCTGCAAGCTCTGAGAG 7557  
Qy 1099 AACTCAGAGGCTTTAAACACAGAGAGAGCTGACAGCAGCAGCAGCAGCAGCAGCAG 1158  
Db 7558 ATGCAAGCGTGTGACAG 7617  
Qy 1159 GCACACATCAAAACACTCTGCTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1218  
Db 7618 CTCTGTAAAG 7677  
Qy 1219 CG---CGCCCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1275  
Db 7678 CTGAGCAGCTCTTCCAG 7737  
Qy 1276 AAG 1329  
Db 7738 CGGAG 7797  
Qy 1330 CGGCGAG 1389  
Db 7798 CGGCGAG 7857  
Qy 1390 TCAGAGAGCTTCCAG 1449  
Db 7858 YTGAG 7917  
Qy 1450 CAG 1505  
Db 7918 GAG 7973

RESULT 13  
US-10-767-471-191  
; Sequence 191, Application US/10767471  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C0001505  
; CURRENT APPLICATION NUMBER: US/10/767,471  
; NUMBER OF SEQ ID NOS: 50231  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 191  
; LENGTH: 14321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-767-471-191

Query Match 2.1%; Score 83.4; DB 6; Length 14321;  
Best Local Similarity 51.0%; Pred. No. 4.2e-09;  
Matches 196; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

Qy 1115 AACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1174  
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Qy 1175 TGCTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1234  
Db 7442 TACAGCGGAG 7501  
Qy 1235 AGCAACAGCGCGGAG 1294  
Db 7502 AGGTGGCCAG 7561  
Qy 1295 TGGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1354  
Db 7562 AGGAAGCGAG 7621

Qy 1355 AATACAGCGGAG 1414  
Db 7622 AGGAGGCGCTCGGCGCAAG 7681  
Qy 1415 AGCAG 1474  
Db 7682 AGGAG 7741  
Qy 1475 AACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1498  
Db 7742 AGCAGACCGGCGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7765

RESULT 14  
US-10-767-471-193  
; Sequence 193, Application US/10767471  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C0001505  
; CURRENT APPLICATION NUMBER: US/10/767,471  
; NUMBER OF SEQ ID NOS: 50231  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 193  
; LENGTH: 14641  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-767-471-193

Query Match 2.1%; Score 83.4; DB 6; Length 14641;  
Best Local Similarity 51.0%; Pred. No. 4.3e-09;  
Matches 196; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

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Qy 1175 TGCTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1234  
Db 7762 TACAGCGGAG 7821  
Qy 1235 AGCAACAGCGCGGAG 1294  
Db 7822 AGGTGGCCAG 7881  
Qy 1295 TGGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1354  
Db 7882 AGGAAGCGAG 7941  
Qy 1355 AATACAGCGGAG 1414  
Db 7942 AGGAGGCGGTGCGGCGCAAG 8001  
Qy 1415 AGCAG 1474  
Db 8002 AGGAG 1534  
Qy 1475 AACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1498  
Db 8062 AGCAGACCGGCGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 8065

RESULT 15  
US-10-767-471-192  
; Sequence 192, Application US/10767471  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C0001505  
; CURRENT APPLICATION NUMBER: US/10/767,471



GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: March 2, 2004, 17:17:09 ; Search time 8003 Seconds  
(without alignments)  
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Searched: 37577330 seqs, 17593059518 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3951	100.0	3951	43	US-10-029-115-1	Sequence 1, Appl1
2	3288	83.2	3951	1	PCT-US02-33845-2	Sequence 2, Appl1
3	2201	55.7	5014	1	PCT-US03-37730-22	Sequence 22, Appl1
4	2099	53.1	4989	1	PCT-US03-37730-26	Sequence 26, Appl1
5	2048	51.8	5191	89	US-60-324-185-5555	Sequence 5555, Ap
6	1907	48.3	4033	43	US-10-029-115-5	Sequence 5, Appl1
7	1787	45.2	4133	54	US-10-725-121-11	Sequence 11, Appl1
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11	1714	43.4	4032	1	PCT-US02-33845-6	Sequence 6, Appl1
12	1701	43.1	3888	1	PCT-US02-01048-37	Sequence 37, Appl1
13	1701	43.1	3888	1	PCT-US03-37730-21	Sequence 21, Appl1
14	1701	43.1	3888	52	US-10-466-162-37	Sequence 37, Appl1
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17	1701	43.1	4557	32	US-09-770-174-3346	Sequence 3346, Ap
18	1701	43.1	4557	32	US-09-770-175-7824	Sequence 7824, Ap
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200	279	7.1	422	21	US-09-524-038-3162	Sequence 3162, App	273	224	5.7	467	35	US-09-948-128-55	Sequence 221, App
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202	278	7.0	278	23	US-09-540-212A-60488	Sequence 60488, A	275	224	5.7	467	35	US-09-948-128-55	Sequence 221, App
203	276	7.0	352	5	US-08-103-744B-25	Sequence 25, App	276	224	5.7	467	35	US-09-948-128-55	Sequence 221, App
204	276	7.0	352	5	US-08-103-744B-25	Sequence 25, App	277	224	5.7	467	35	US-09-948-128-55	Sequence 221, App
205	276	7.0	352	5	US-08-103-744B-25	Sequence 25, App	278	224	5.7	467	35	US-09-948-128-55	Sequence 221, App
206	276	7.0	352	6	US-08-249-651-25	Sequence 25, App	279	224	5.7	467	35	US-09-948-128-55	Sequence 221, App
207	276	7.0	352	16	US-09-249-651-25	Sequence 25, App	280	224	5.7	467	35	US-09-948-128-55	Sequence 221, App
208	276	7.0	352	16	US-09-249-651-25	Sequence 25, App	281	224	5.7	467	35	US-09-948-128-55	Sequence 221, App
209	275	7.0	421	21	US-09-912-293-98850	Sequence 98850, A	282	224	5.7	467	35	US-09-948-128-55	Sequence 221, App
210	275	7.0	421	21	US-09-528-409-5477	Sequence 5477, App	283	223	5.6	1009	16	US-09-203-136-55	Sequence 55, App
211	275	7.0	421	38	US-09-933-524-5477	Sequence 5477, App	284	223	5.6	1009	16	US-09-203-136-55	Sequence 55, App
212	275	7.0	425	29	US-09-933-524A-5477	Sequence 5477, App	285	223	5.6	1009	16	US-09-203-136-55	Sequence 55, App
213	264	6.7	264	12	US-09-699-999-1529	Sequence 1529, App	286	223	5.6	1009	16	US-09-203-136-55	Sequence 55, App
214	264	6.7	264	12	US-08-879-863-5237	Sequence 5237, App	287	222	5.6	257	1	US-09-898-888A-5575	Sequence 5575, App
215	264	6.7	264	12	US-08-879-863A-5237	Sequence 5237, App	288	222	5.6	257	1	US-09-898-888A-5575	Sequence 5575, App
					US-09-534-843-15184	Sequence 15184, A							

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C 291	222	5.6	257	46	US-10-182-997-9351	Sequence 9351, Ap	C 364	172	4.4	12400	1	PCT-US01-19835-1	Sequence 91, Appl1
C 292	222	5.6	257	46	US-10-182-998-5134	Sequence 5134, Ap	C 365	172	4.4	12917	107	US-60-500-337-19764	Sequence 19764, A
C 293	222	5.6	257	47	US-10-203-134-1174	Sequence 13174, A	C 366	171	4.3	481	1	PCT-US01-00663-54	Sequence 54, Appl
C 294	222	5.6	257	47	US-10-203-135-12675	Sequence 12675, A	C 367	171	4.3	481	35	US-09-864-761-47	Sequence 47, Appl
C 295	222	5.6	257	47	US-10-203-136-11772	Sequence 13172, A	C 368	171	4.3	481	46	US-10-182-995-47	Sequence 52, Appl
C 296	222	5.6	257	47	US-10-203-137-11292	Sequence 13292, A	C 369	171	4.3	481	46	US-10-182-995-47	Sequence 47, Appl
C 297	222	5.6	257	47	US-10-203-138-5263	Sequence 5263, Ap	C 370	171	4.3	481	46	US-10-182-997-55	Sequence 55, Appl
C 298	222	5.6	257	47	US-10-203-138A-5263	Sequence 5263, Ap	C 371	171	4.3	481	46	US-10-182-998-54	Sequence 54, Appl
C 299	222	5.6	257	47	US-10-203-139-12736	Sequence 12736, Ap	C 372	171	4.3	481	47	US-10-203-134-55	Sequence 55, Appl
C 300	222	5.6	257	80	US-60-236-359-7468	Sequence 7468, Ap	C 373	171	4.3	481	47	US-10-203-135-55	Sequence 55, Appl
C 301	221	5.6	249	22	US-09-534-843-15163	Sequence 15163, A	C 374	171	4.3	481	47	US-10-203-136-56	Sequence 56, Appl
C 302	220	5.6	445	28	US-09-666-024-135	Sequence 135, App	C 375	171	4.3	481	47	US-10-203-137-54	Sequence 54, Appl
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C 304	212	5.4	274	13	US-08-936-937-811	Sequence 811, App	C 377	171	4.3	481	47	US-10-203-138A-52	Sequence 52, Appl
C 305	212	5.4	274	22	US-09-534-843-15155	Sequence 15155, A	C 378	171	4.3	481	47	US-10-203-139-57	Sequence 57, Appl
C 306	212	5.4	274	56	US-60-008-131-811	Sequence 811, App	C 379	171	4.3	481	80	US-60-236-359-58	Sequence 58, Appl
C 307	208	5.3	532	20	US-09-496-911-12911	Sequence 12911, A	C 380	171	4.3	496	31	US-09-758-472-1729	Sequence 1729, Ap
C 308	208	5.3	532	41	US-09-975-673A-12911	Sequence 12911, A	C 381	171	4.3	549	47	US-10-235-926-1729	Sequence 1729, Ap
C 309	207	5.2	428	1	PCT-US01-08631-24005	Sequence 24005, A	C 382	168	4.3	549	27	US-09-649-164-1424	Sequence 7424, Ap
C 310	205	5.2	258	14	US-09-075-075-113	Sequence 11313, Ap	C 383	168	4.3	1784	1	PCT-US02-27777-76	Sequence 76, Appl
C 311	205	5.2	258	22	US-09-534-843-15147	Sequence 15147, A	C 384	168	4.3	1784	1	PCT-US02-27777A-76	Sequence 76, Appl
C 312	205	5.2	302	43	US-10-029-386-17518	Sequence 17518, A	C 385	165	4.2	185	27	US-09-652-125A-189	Sequence 189, App
C 313	205	5.2	500	16	US-09-234-611-17745	Sequence 17745, A	C 386	165	4.2	273	27	US-09-652-109-2944	Sequence 2944, Ap
C 314	205	5.2	500	16	US-09-235-076-32315	Sequence 32315, A	C 387	163	4.1	244	23	US-09-540-766-56311	Sequence 56331, A
C 315	205	5.2	500	17	US-09-289-766-36800	Sequence 36800, A	C 388	160	4.0	189	43	US-10-029-386-26488	Sequence 26488, A
C 316	205	5.2	500	18	US-09-332-782-32315	Sequence 32315, A	C 389	160	4.0	281	27	US-09-644-870-12780	Sequence 5780, Ap
C 317	205	5.2	500	31	US-09-737-223-33315	Sequence 33215, A	C 390	160	4.0	507	43	US-10-029-386-12728	Sequence 12798, A
C 318	205	5.2	500	37	US-09-904-809-17745	Sequence 17745, A	C 391	160	4.0	565	73	US-60-171-994-508	Sequence 508, App
C 319	205	5.2	500	37	US-09-918-995-32315	Sequence 32315, A	C 392	160	4.0	9301	81	US-60-245-225-113	Sequence 113, Appl
C 320	205	5.2	500	38	US-09-939-397-36800	Sequence 36800, A	C 393	160	4.0	3301	82	US-60-258-250-53	Sequence 33, Appl
C 321	205	5.2	507	43	US-10-029-386-3818	Sequence 3818, Ap	C 394	158	4.0	327	8	US-08-440-817-312	Sequence 312, App
C 322	205	5.2	769	20	US-09-471-275-5411	Sequence 5411, Ap	C 395	158	4.0	327	22	US-09-534-843-15157	Sequence 15157, A
C 323	205	5.2	769	20	US-09-488-725B-4672	Sequence 4672, Ap	C 396	155	3.9	310	23	US-09-540-229-108724	Sequence 108724, A
C 324	205	5.2	17701	107	US-60-500-337-19385	Sequence 19385, A	C 397	154	3.9	346	14	US-09-021-095-600	Sequence 600, App
C 325	204	5.2	224	13	US-08-979-854A-4087	Sequence 4087, A	C 398	154	3.9	411	28	US-09-534-843-15178	Sequence 15178, A
C 326	204	5.2	224	22	US-09-534-843-15165	Sequence 15165, A	C 399	154	3.9	411	28	US-09-699-998-1040	Sequence 3040, Ap
C 327	204	5.2	224	59	US-60-031-834-1053	Sequence 1053, Ap	C 400	154	3.9	3700	78	US-09-629-998-1040	Sequence 618, App
C 328	202	5.1	258	23	US-09-540-766-58603	Sequence 58603, A	C 401	153	3.9	236	14	US-09-035-173-64	Sequence 64, Appl
C 329	198	5.0	218	27	US-09-652-126-2628	Sequence 2628, Ap	C 402	153	3.9	236	14	US-09-081-109-134	Sequence 134, App
C 330	195	4.9	418	20	US-09-428-151A-3950	Sequence 3950, Ap	C 403	153	3.9	236	22	US-09-534-843-15150	Sequence 15150, A
C 331	195	4.9	418	25	US-09-614-387-5709	Sequence 5709, Ap	C 404	153	3.9	236	23	US-09-540-764-88168	Sequence 38168, A
C 332	194	4.9	307	14	US-09-076-667-2312	Sequence 2312, Ap	C 405	153	3.9	236	49	US-10-349-781-88168	Sequence 38168, A
C 333	194	4.9	307	22	US-09-534-843-15140	Sequence 15140, A	C 406	153	3.9	236	60	US-60-048-127-134	Sequence 134, App
C 334	194	4.9	307	60	US-60-048-002-2312	Sequence 2312, Ap	C 407	151	3.8	399	5	US-08-103-744B-24	Sequence 24, Appl
C 335	194	4.9	403	1	PCT-US99-24206-669	Sequence 669, App	C 408	151	3.8	399	5	US-08-103-744B-24	Sequence 24, Appl
C 336	194	4.9	403	33	US-09-807-521-669	Sequence 669, App	C 409	151	3.8	399	5	US-08-103-744-24	Sequence 24, Appl
C 337	190	4.8	410	21	US-09-528-409-34499	Sequence 34499, A	C 410	151	3.8	399	6	US-08-249-651-24	Sequence 24, Appl
C 338	190	4.8	410	38	US-09-933-524-34499	Sequence 34499, A	C 411	151	3.8	399	16	US-09-912-293-18849	Sequence 24, Appl
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C 341	185	4.7	349	13	US-08-993-774-2729	Sequence 2729, Ap	C 414	150	3.8	201	107	US-60-500-337-15873	Sequence 15873, A
C 342	185	4.7	349	22	US-08-993-774-2729	Sequence 2729, Ap	C 415	150	3.8	201	107	US-60-500-337-15875	Sequence 15875, A
C 343	185	4.7	349	59	US-60-034-975-2729	Sequence 15142, A	C 416	150	3.8	201	107	US-60-500-337-15891	Sequence 15891, A
C 344	184	4.7	397	17	US-09-277-214A-104	Sequence 104, App	C 417	150	3.8	201	107	US-60-500-337-15882	Sequence 15882, A
C 345	184	4.7	397	36	US-09-891-825-104	Sequence 104, App	C 418	150	3.8	201	107	US-60-500-337-15883	Sequence 15883, A
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C 348	180	4.6	422	37	US-09-915-738-1241	Sequence 1241, Ap	C 421	150	3.8	201	107	US-60-500-337-15890	Sequence 15890, A
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C 350	180	4.6	589	25	US-09-606-776-2928	Sequence 2928, Ap	C 423	150	3.8	201	107	US-60-500-337-15892	Sequence 15892, A
C 351	180	4.6	589	27	US-09-644-867-4254	Sequence 4254, Ap	C 424	150	3.8	201	107	US-60-500-337-15894	Sequence 15894, A
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C 353	178	4.5	226	22	US-09-534-843-15107	Sequence 15107, A	C 426	150	3.8	201	107	US-60-500-337-15900	Sequence 15900, A
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C 355	178	4.5	226	74	US-60-184-797-487	Sequence 487, App	C 428	150	3.8	201	107	US-60-500-337-15904	Sequence 15904, A
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C 358	174	4.4	174	22	US-09-534-843-15167	Sequence 15167, A	C 431	150	3.8	770	29	US-09-658-014-4887	Sequence 4887, Ap
C 359	174	4.4	174	58	US-60-023-378-2578	Sequence 2578, Ap	C 432	148	3.7	231	13	US-08-961-525-406	Sequence 406, App
C 360	173	4.4	511	23	US-09-540-229-108511	Sequence 108511, A	C 433	148	3.7	231	58	US-60-029-957-406	Sequence 406, App
C 361	172	4.4	5158	32	US-09-760-475-3946	Sequence 3946, Ap	C 434	146	3.7	178	43	US-10-029-386-17507	Sequence 17507, A



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437	144	3.6	254	17	US-09-293-655-852	Sequence 852, App
438	144	3.6	254	22	US-09-534-843-15122	Sequence 15122, App
439	144	3.6	254	64	US-60-082-030-852	Sequence 852, App
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C 443	142	3.6	179	46	US-10-182-995-10035	Sequence 10035, A
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C 446	142	3.6	179	47	US-10-203-134-12676	Sequence 12676, A
C 447	142	3.6	179	47	US-10-203-135-12737	Sequence 12737, A
C 448	142	3.6	179	47	US-10-203-136-13173	Sequence 13173, A
C 449	142	3.6	179	47	US-10-203-137-13293	Sequence 13293, A
C 450	142	3.6	179	47	US-10-203-138-5264	Sequence 5264, App
C 451	142	3.6	179	47	US-10-203-138A-5264	Sequence 5264, App
C 452	142	3.6	179	47	US-10-203-139-12737	Sequence 12737, A
C 453	142	3.6	179	80	US-60-236-359-7469	Sequence 7469, App
C 454	142	3.6	179	80	US-09-076-667-4069	Sequence 4069, App
C 455	140	3.5	378	20	US-09-469-036-12839	Sequence 12839, App
C 456	140	3.5	378	39	US-09-943-143-32839	Sequence 32839, A
C 457	140	3.5	612	73	US-60-171-494-386	Sequence 439, App
C 458	137	3.5	258	74	US-60-184-774-439	Sequence 4069, App
C 459	136	3.4	240	14	US-09-076-667-4069	Sequence 15106, A
C 460	136	3.4	240	22	US-09-534-843-15106	Sequence 4069, App
C 461	136	3.4	240	60	US-60-048-002-4069	Sequence 15106, A
C 462	134	3.4	829	77	US-60-213-359-3624	Sequence 3624, App
C 463	132	3.3	272	23	US-09-540-229-112313	Sequence 112313, A
C 464	130	3.3	201	107	US-60-500-337-83306	Sequence 83206, A
C 465	130	3.3	201	107	US-60-500-337-833229	Sequence 83229, A
C 466	130	3.3	387	1	PCT-US01-01239-531	Sequence 531, App
C 467	130	3.3	387	1	PCT-US01-08631-24007	Sequence 24007, A
C 468	130	3.3	387	32	US-09-764-902-531	Sequence 531, App
C 469	128	3.2	140	1	PCT-US01-00663-13291	Sequence 13291, A
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C 472	128	3.2	140	46	US-10-182-995-10033	Sequence 10033, A
C 473	128	3.2	140	46	US-10-182-997-9350	Sequence 9350, App
C 474	128	3.2	140	46	US-10-182-998-5133	Sequence 5133, App
C 475	128	3.2	140	47	US-10-203-134-13173	Sequence 13173, A
C 476	128	3.2	140	47	US-10-203-135-12674	Sequence 12674, A
C 477	128	3.2	140	47	US-10-203-136-13171	Sequence 13171, A
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C 503	127	3.2	287	22	US-09-534-843-15111	Sequence 15111, A
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C 506	126	3.2	250	13	US-08-992-868-3739	Sequence 15116, A
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510	122	3.1	258	22	US-09-539-800B-10390	Sequence 10390, A
511	122	3.1	258	22	US-09-539-800C-10390	Sequence 10390, A
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513	120	3.0	190	12	US-09-534-843-15171	Sequence 15171, A
514	119	3.0	258	22	US-09-534-843-15175	Sequence 15175, A
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516	118	3.0	245	22	US-09-534-843-15143	Sequence 15143, A
517	118	3.0	245	58	US-60-023-378-2566	Sequence 2566, App
518	117	3.0	266	14	US-09-032-771-114	Sequence 114, App
519	117	3.0	266	22	US-09-534-843-15123	Sequence 15123, A
520	117	3.0	266	59	US-60-038-885-114	Sequence 114, App
521	116	2.9	205	22	US-09-539-806B-42094	Sequence 42094, A
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526	115	2.9	620	74	US-60-187-387-668	Sequence 668, App
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529	113	2.9	504	19	US-09-396-885-1640	Sequence 1640, App
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531	112	2.8	539	20	US-09-474-436-239	Sequence 239, App
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535	109	2.8	570	1	PCT-US01-08631-30154	Sequence 30154, A
536	109	2.8	1954	1	PCT-US01-08631-27553	Sequence 27553, A
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540	104	2.6	437	18	US-09-342-216-360	Sequence 360, App
541	104	2.6	457	18	US-09-342-216A-360	Sequence 360, App
542	104	2.6	457	37	US-09-908-601-360	Sequence 360, App
543	104	2.6	457	37	US-09-912-292-9825	Sequence 9825, A
544	103	2.6	177	23	US-09-540-229-10198	Sequence 10198, A
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547	100	2.5	201	107	US-60-500-337-15874	Sequence 15874, A
548	100	2.5	201	107	US-60-500-337-15876	Sequence 15876, A
549	100	2.5	201	107	US-60-500-337-15884	Sequence 15884, A
550	100	2.5	201	107	US-60-500-337-15886	Sequence 15886, A
551	100	2.5	201	107	US-60-500-337-15888	Sequence 15888, A
552	100	2.5	201	107	US-60-500-337-15893	Sequence 15893, A
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563	98	2.5	385	72	US-60-162-245-1899	Sequence 1899, App
564	98	2.5	386	72	US-60-169-868-3184	Sequence 3184, App
565	96	2.4	269	13	US-08-962-919-1800	Sequence 1800, App
566	96	2.4	269	22	US-09-534-843-15183	Sequence 15183, A
567	95	2.4	201	107	US-60-500-337-183183	Sequence 183183, A
568	95	2.4	466	16	US-09-335-076-15062	Sequence 15062, A
569	94	2.4	466	16	US-09-348-797-37344	Sequence 37344, A
570	94	2.4	466	31	US-09-332-782-15062	Sequence 15062, A
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572	94	2.4	466	37	US-09-918-995-15062	Sequence 15062, A
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574	92	2.3	201	107	US-60-500-337-183239	Sequence 183239, A
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586	90	2.3	465	38	US-09-925-564-33743	Sequence 33743, A	659	72	1.8	304	37	US-09-912-293-10700	Sequence 70700, App
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588	89	2.3	89	22	US-09-534-843-15176	Sequence 15176, A	661	70	1.8	201	107	US-60-500-337-83274	Sequence 83274, A
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591	88	2.2	201	107	US-60-500-337-15870	Sequence 15870, A	664	69	1.7	283	21	US-09-533-999C-33195	Sequence 33195, A
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593	88	2.2	201	107	US-60-500-337-15889	Sequence 15889, A	666	69	1.7	285	23	US-09-547-599C-781	Sequence 781, App
594	88	2.2	201	107	US-60-500-337-15898	Sequence 15898, A	667	69	1.7	285	53	US-10-631-402-781	Sequence 781, App
595	88	2.2	201	107	US-60-500-337-15901	Sequence 15901, A	668	69	1.7	285	53	US-10-631-441-781	Sequence 781, App
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597	88	2.2	221	15	US-09-107-910-2740	Sequence 2740, App	670	68	1.7	87	1	PCT-US03-18714-18462	Sequence 18462, A
598	88	2.2	221	22	US-09-534-843-15109	Sequence 15109, A	671	68	1.7	87	1	PCT-US03-18714-18462	Sequence 18462, A
599	87	2.2	201	107	US-60-500-337-83284	Sequence 83284, A	672	68	1.7	201	107	US-60-500-337-83232	Sequence 83232, A
600	87	2.2	278	14	US-09-061-835-1419	Sequence 1419, App	673	68	1.7	252	14	US-09-010-765-55	Sequence 55, App
601	87	2.2	278	22	US-09-534-843-15105	Sequence 15105, A	674	68	1.7	252	23	US-09-540-766-37767	Sequence 37767, A
602	87	2.2	289	74	US-60-184-797-645	Sequence 645, App	675	68	1.7	252	59	US-60-036-145-55	Sequence 55, App
603	87	2.2	541	73	US-60-170-374-946	Sequence 946, App	676	68	1.7	387	1	PCT-US01-08631-16599	Sequence 16599, A
604	86	2.2	201	107	US-60-500-337-83223	Sequence 83223, A	677	68	1.7	387	1	PCT-US02-25485-131	Sequence 131, App
605	86	2.2	357	31	US-09-726-788-5004	Sequence 905, App	678	68	1.7	387	1	US-10-219-882-131	Sequence 131, App
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608	86	2.2	479	72	US-60-160-245-554	Sequence 554, App	681	68	1.7	387	47	US-10-219-882-131	Sequence 131, App
609	86	2.2	648	74	US-60-185-216-964	Sequence 964, App	682	68	1.7	387	47	US-10-219-882-131	Sequence 131, App
610	86	2.2	648	89	US-60-324-185-5552	Sequence 5552, App	683	68	1.7	387	47	US-10-219-882-131	Sequence 131, App
611	86	2.2	881	31	US-09-758-439-171	Sequence 171, App	684	68	1.7	387	47	US-10-219-882-131	Sequence 131, App
612	86	2.2	881	47	US-10-201-915-111	Sequence 171, App	685	68	1.7	459	72	US-60-164-760-118	Sequence 225, App
613	86	2.2	961	73	US-60-172-373-15871	Sequence 15871, A	686	68	1.7	460	72	US-60-164-760-125	Sequence 225, App
614	86	2.2	32768	76	US-60-206-600-56	Sequence 56, App	687	68	1.7	756	93	US-60-365-184-52	Sequence 52, App
615	86	2.2	32768	76	US-60-207-316-9	Sequence 9, App	688	66	1.7	189	15	US-09-107-909-2171	Sequence 2171, App
616	86	2.2	32768	76	US-60-208-129-64	Sequence 64, App	689	66	1.7	189	22	US-09-534-943-15134	Sequence 15134, A
617	86	2.2	32768	76	US-60-208-965-77	Sequence 77, App	690	66	1.7	201	107	US-60-500-337-83290	Sequence 83290, A
618	86	2.2	32768	76	US-60-208-973-75	Sequence 75, App	691	66	1.7	385	25	US-09-617-081-1054	Sequence 1054, App
619	86	2.2	32768	76	US-60-208-973-76	Sequence 76, App	692	66	1.7	385	34	US-09-845-654-962	Sequence 962, App
620	86	2.2	32768	77	US-60-213-177-178	Sequence 178, App	693	64	1.6	201	107	US-60-500-337-83233	Sequence 83233, A
621	86	2.2	32768	79	US-60-229-525-196	Sequence 196, App	694	63	1.6	154	77	US-60-217-080-24235	Sequence 24235, A
622	86	2.2	32768	79	US-60-230-445-684	Sequence 684, App	695	62	1.6	1665	1	PCT-US03-37730-23	Sequence 23, App
623	85	2.2	193	77	US-60-217-080-23739	Sequence 23739, A	696	61	1.5	201	107	US-60-500-337-83335	Sequence 83335, A
624	85	2.2	375	77	US-60-217-080-23173	Sequence 23173, A	697	61	1.5	201	107	US-10-421-961A-4507	Sequence 4507, App
625	85	2.2	406	74	US-60-186-662-181	Sequence 181, App	698	60	1.5	303	51	US-60-534-943-15108	Sequence 15108, A
626	85	2.2	420	8	US-08-401-791A-10359	Sequence 10359, A	699	59	1.5	412	77	US-60-212-356-352	Sequence 352, App
627	85	2.2	420	8	US-08-401-791B-10359	Sequence 10359, A	700	58	1.5	247	14	US-09-036-889-32	Sequence 32, App
628	85	2.2	420	37	US-09-912-293-126709	Sequence 126709, A	701	58	1.5	247	14	US-09-036-889-32	Sequence 32, App
629	84	2.1	271	14	US-09-065-521-3370	Sequence 3370, App	702	58	1.5	247	14	US-09-036-889-32	Sequence 32, App
630	84	2.1	271	22	US-09-534-843-15159	Sequence 15159, A	703	58	1.5	247	14	US-09-036-889-32	Sequence 32, App
631	83	2.1	201	107	US-60-500-337-83287	Sequence 83287, A	704	58	1.5	449	35	US-09-864-761-01271	Sequence 3513, App
632	82	2.1	274	17	US-09-294-093A-829	Sequence 829, App	705	58	1.5	449	35	US-09-864-761-01271	Sequence 3513, App
633	82	2.1	274	17	US-09-294-093B-723	Sequence 723, App	706	58	1.5	449	35	US-10-182-993-3613	Sequence 3613, App
634	82	2.1	274	18	US-09-304-517A-44335	Sequence 44335, A	707	58	1.5	449	35	US-10-203-134-16640	Sequence 3640, App
635	82	2.1	274	19	US-09-371-146A-44335	Sequence 44335, A	708	58	1.5	449	35	US-10-203-134-16640	Sequence 3640, App
636	82	2.1	274	34	US-09-839-976-723	Sequence 723, App	709	58	1.5	449	35	US-10-203-134-16640	Sequence 3640, App
637	82	2.1	274	34	US-09-839-976A-723	Sequence 723, App	710	58	1.5	449	35	US-10-203-134-16640	Sequence 3640, App
638	82	2.1	274	42	US-09-985-678-44395	Sequence 44395, A	711	58	1.5	449	35	US-10-203-134-16640	Sequence 3640, App
639	82	2.1	274	64	US-60-082-567-723	Sequence 723, App	712	58	1.5	449	35	US-10-203-134-16640	Sequence 3640, App
640	78	2.0	601	39	US-09-947-907-16717	Sequence 16717, A	713	58	1.5	449	35	US-10-203-134-16640	Sequence 3640, App
641	77	1.9	77	1	PCT-US03-18714-18461	Sequence 18461, A	714	58	1.5	449	35	US-10-203-134-16640	Sequence 3640, App
642	77	1.9	77	1	PCT-US03-18714-18461	Sequence 18461, A	715	58	1.5	449	35	US-10-203-134-16640	Sequence 3640, App
643	77	1.9	146	27	US-09-659-737A-18461	Sequence 18461, A	716	58	1.5	449	35	US-10-203-134-16640	Sequence 3640, App
644	77	1.9	201	107	US-60-500-337-83177	Sequence 83177, A	717	57	1.4	95	1	PCT-US01-00663-16876	Sequence 16876, A
645	77	1.9	201	107	US-60-500-337-83178	Sequence 83178, A	718	57	1.4	95	1	US-09-864-761-26936	Sequence 26936, A
646	77	1.9	201	107	US-60-500-337-83189	Sequence 83189, A	719	57	1.4	95	1	US-10-182-993-3613	Sequence 3613, App
647	77	1.9	201	107	US-60-500-337-83190	Sequence 83190, A	720	57	1.4	95	1	US-10-203-134-16640	Sequence 16640, A
648	75	1.9	120	22	US-09-539-806-41291	Sequence 41291, A	721	57	1.4	95	1	US-10-203-134-16640	Sequence 16640, A
649	75	1.9	120	22	US-09-539-806B-41291	Sequence 41291, A	722	57	1.4	95	1	US-10-203-134-16640	Sequence 16640, A
650	75	1.9	201	107	US-60-500-337-83237	Sequence 83237, A	723	57	1.4	95	1	US-10-203-134-16640	Sequence 16640, A
651	73	1.8	413	13	US-08-971-050-577	Sequence 577, App	724	57	1.4	95	1	US-10-203-134-16640	Sequence 16640, A
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728	57	1.4	201	107	US-60-500-337-83225	Sequence 83225, A	C 802	42	1.1	5419	72	US-60-167-217-4203	Sequence 4203, App
729	57	1.4	303	1	PCT-US01-08631-1901	Sequence 1901, App	C 802	42	1.1	11085	21	US-09-528-237A-1362	Sequence 1362, App
730	56	1.4	201	107	US-60-500-337-83224	Sequence 83226, A	C 803	41	1.0	252	21	US-09-500-900-1190	Sequence 1190, App
731	56	1.4	201	107	US-60-500-337-83236	Sequence 83236, A	C 804	41	1.0	252	22	US-09-534-843-21731	Sequence 21731, A
732	56	1.4	403	16	US-09-248-797-3362	Sequence 3362, App	C 805	41	1.0	252	68	US-60-120-015-1190	Sequence 1190, App
733	56	1.4	403	18	US-09-346-956-1352	Sequence 1352, App	C 806	41	1.0	703	29	US-09-692-886A-4505	Sequence 4505, App
734	56	1.4	403	37	US-09-904-703-1352	Sequence 1352, App	C 807	40	1.0	182	17	US-09-394-086A-1350	Sequence 1350, App
735	56	1.4	403	38	US-09-925-564-3362	Sequence 3362, App	C 808	40	1.0	182	64	US-60-084-492-1789	Sequence 1789, App
736	55	1.4	186	72	US-60-162-245-1548	Sequence 1548, App	C 809	40	1.0	201	107	US-60-500-337-83185	Sequence 83185, A
C 737	55	1.4	199	1	PCT-US03-18714-18457	Sequence 18457, A	C 810	40	1.0	273	14	US-09-079-688-968	Sequence 968, App
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740	53	1.3	253	16	US-09-239-412-231	Sequence 231, App	C 813	39	1.0	204	8	US-08-401-791A-1354	Sequence 1354, App
741	53	1.3	253	22	US-09-534-843-21737	Sequence 21737, App	C 814	39	1.0	204	8	US-08-401-791B-1354	Sequence 1354, App
742	53	1.3	265	19	US-09-370-505-5936	Sequence 3366, App	C 815	39	1.0	204	37	US-09-512-293-22204	Sequence 22204, A
743	53	1.3	265	22	US-09-534-843-21738	Sequence 21738, A	C 816	38	1.0	278	22	US-09-534-846B-12933	Sequence 12933, A
744	53	1.3	265	65	US-60-096-463-1936	Sequence 3366, App	C 817	38	1.0	278	49	US-10-314-344-12933	Sequence 12933, A
745	53	1.3	288	15	US-09-145-501-4594	Sequence 4594, App	C 818	38	1.0	278	70	US-60-141-230-466	Sequence 466, App
746	53	1.3	288	22	US-09-534-843-21732	Sequence 21732, A	C 819	38	1.0	364	82	US-60-252-833-30784	Sequence 30784, A
747	53	1.3	311	20	US-09-428-151A-6910	Sequence 6910, App	C 820	38	1.0	505	1	PCT-US03-13853-10362	Sequence 10362, A
748	53	1.3	311	28	US-09-667-617-1117	Sequence 1117, App	C 821	38	1.0	505	94	US-60-377-240-10362	Sequence 10362, A
749	53	1.3	3903	48	US-10-261-175A-4	Sequence 4, App1	C 822	37	0.9	51	73	US-60-172-373-2795	Sequence 2795, App
750	53	1.3	4849	45	US-10-144-771-21878	Sequence 21878, A	C 823	37	0.9	144	1	PCT-US03-26220-14141	Sequence 14141, A
751	53	1.3	4849	93	US-60-360-207-21878	Sequence 21878, A	C 824	37	0.9	232	13	US-08-956-502-247	Sequence 247, App
752	51	1.3	51	89	US-60-324-185-5558	Sequence 5558, App	C 825	37	0.9	232	22	US-09-534-843-15132	Sequence 15132, A
753	51	1.3	247	31	US-09-726-174-3836	Sequence 3836, App	C 826	37	0.9	254	16	US-09-231-945-3855	Sequence 3855, App
754	51	1.3	438	27	US-09-652-916-1055	Sequence 1055, App	C 827	37	0.9	254	22	US-09-534-843-21734	Sequence 21734, A
755	51	1.3	450	6	US-08-276-163A-2615	Sequence 2615, App	C 828	37	0.9	285	13	US-08-395-244-1500	Sequence 1500, App
756	51	1.3	450	6	US-08-276-163B-2615	Sequence 2615, App	C 829	37	0.9	285	13	US-08-972-899-1550	Sequence 1500, App
757	51	1.3	450	6	US-08-276-163D-2615	Sequence 2615, App	C 830	37	0.9	339	37	US-09-912-292-6843	Sequence 6843, App
758	51	1.3	450	34	US-09-840-145-2615	Sequence 2615, App	C 831	37	0.9	339	37	US-09-912-292-6843	Sequence 6843, App
759	51	1.3	450	34	US-09-912-293-75759	Sequence 2615, App	C 832	36	0.9	156	15	US-09-148-482-1076	Sequence 1076, App
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3241 CCAAGAGTGAAGAAAGCAGAGGCTGAGCAGCTGGGGGAGATGAGAGGCTGGGAGC 3300  
3241 CCAAGAGTGAAGAAAGCAGAGGCTGAGCAGCTGGGGGAGATGAGAGGCTGGGAGC 3300  
3301 TACCGTGTGGAATATCAGAGGATTAAGTCTGCTGATCTGCTCAAGAGCTCGTG 3360  
3301 TACCGTGTGGAATATCAGAGGATTAAGTCTGCTGATCTGCTCAAGAGCTCGTG 3360  
3361 GAGGTGATGCTGGGGCCCCCAACCTTACCAAAATTCATGAGCTTCAAGCTCTGAG 3420  
3361 GAGGTGATGCTGGGGCCCCCAACCTTACCAAAATTCATGAGCTTCAAGCTCTGAG 3420  
3421 GACCTCCCCCAGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480  
3421 GACCTCCCCCAGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480  
3481 GTCACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540  
3481 GTCACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540  
3541 GACATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600  
3541 GACATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600  
3601 CCCAACCCGAGCGGATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660  
3601 CCCAACCCGAGCGGATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660  
3661 ACCTACGAGCGGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3720  
3661 ACCTACGAGCGGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3720  
3721 GCTTACATCTGCTTCAACCAAGTATGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGG 3780  
3721 GCTTACATCTGCTTCAACCAAGTATGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGG 3780  
3781 GTGAGAGCGGCGCAGCTGAGCGGCTCTTCAATGCAAAAGAGCTCAGAGGCTCAAGTTC 3840  
3781 GTGAGAGCGGCGCAGCTGAGCGGCTCTTCAATGCAAAAGAGCTCAGAGGCTCAAGTTC 3840  
3841 CTGTGTGAGCGGAGATGAGAGGATGATGATGATGATGATGATGATGATGATGATGATG 3900  
3841 CTGTGTGAGCGGAGATGAGAGGATGATGATGATGATGATGATGATGATGATGATGATG 3900  
3901 GTTACTTATGAGCTGAGACCGTAACTGATCATGATGATGATGATGATGATGATGATG 3960  
3901 GTTACTTATGAGCTGAGACCGTAACTGATCATGATGATGATGATGATGATGATGATG 3960

RESULT 2  
PCT-US02-33845-2  
Sequence 2, Application PCT/TUS0233845  
GENERAL INFORMATION:  
APPLICANT: Rigel Pharmaceuticals, Inc.  
APPLICANT: Leo, Cindy  
APPLICANT: Luo, Ying  
APPLICANT: Xu, Xiang  
TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE PROTEINS, COMPOSITIONS,  
FILE REFERENCE: 021044-005600PC  
CURRENT APPLICATION NUMBER: PCT/US02/33845  
CURRENT FILING DATE: 2003-05-30  
PRIOR APPLICATION NUMBER: US 10/029,115  
PRIOR FILING DATE: 2001-10-19





QY 1980 CCTTAACACAGATGGGGCCGAGAGGTCCGCGCAGGCCAGAGCTCCGTGACGACCTCG 2039  
DB 1980 CCTTAACACAGATGGGGCCGAGAGGTCCGCGCAGGCCAGAGCTCCGTGACGACCTCG 2039  
QY 2040 CAGCAATCTCGCTGGCAAAATCTATCTGCAAAAGCGGGCGAGCGGGGCACTCCAAAGCC 2099  
DB 2040 CAGCAATCTCGCTGGCAAAATCTATCTGCAAAAGCGGGCGAGCGGGGCACTCCAAAGCC 2099  
QY 2100 TCCAGGGGCCCCCTGAGCCCCCTGGCCCCGCGCAACCGCTAGTAACCCGCACTCG 2159  
DB 2100 TCCAGGGGCCCCCTGAGCCCCCTGGCCCCGCGCAACCGCTAGTAACCCGCACTCG 2159  
QY 2160 GAGGAGCGACCTCTGGCTGGGAAGCTCGAGCAGCGCTCTTCCAGCTCTCAAGGCACT 2219  
DB 2160 GAGGAGCGACCTCTGGCTGGGAAGCTCGAGCAGCGCTCTTCCAGCTCTCAAGGCACT 2219  
QY 2220 CCCCCAGGCTGGCTCACTGAGCGGAACCGCGTGGAGCTCTCTCCAACTGAGACGCTC 2279  
DB 2220 CCCCCAGGCTGGCTCACTGAGCGGAACCGCGTGGAGCTCTCTCCAACTGAGACGCTC 2279  
QY 2218 CCCCCAGGCTGGCTCACTGAGCGGAACCGCGTGGAGCTCTCTCCAACTGAGACGCTC 2277  
DB 2218 CCCCCAGGCTGGCTCACTGAGCGGAACCGCGTGGAGCTCTCTCCAACTGAGACGCTC 2277  
QY 2280 CCGTGTCTCTCCCTGGGGAATTAAGCCAGGCCGAGCAGCAGCGCTCAAGGCGGCGG 2339  
DB 2278 CCGTGTCTCTCCCTGGGGAATTAAGCCAGGCCGAGCAGCAGCGCTCAAGGCGGCGG 2337  
QY 2340 GCCCGCAGACTTGTGTGCTGTAAGAGCGGCACTCTGAGCAGAGCCCTCGGCTCCCA 2399  
DB 2338 GCCCGCAGACTTGTGTGCTGTAAGAGCGGCACTCTGAGCAGAGCCCTCGGCTCCCA 2397  
QY 2400 GAAAGCCATGACCTACTGCTCTGCAAGCAGAGAGGTGGAAGCATGAGAGCAGCAGGA 2459  
DB 2398 GAAAGCCATGACCTACTGCTCTGCAAGCAGAGAGGTGGAAGCATGAGAGCAGCAGGA 2457  
QY 2460 GGAAGCGGAGCGGGCCGAGAGGGGGAGAGAGTACCCTGGGGGGCGGAGGAGTGG 2519  
DB 2458 GGAAGCGGAGCGGGCCGAGAGGGGGAGAGAGTACCCTGGGGGGCGGAGGAGTGG 2517  
QY 2520 GGAATCAGACAGCTGACGACCATGAGTGTCCACGACGTCGAGAGATCAGCGGAGCCCA 2579  
DB 2518 GGAATCAGACAGCTGACGACCATGAGTGTCCACGACGTCGAGAGATCAGCGGAGCCCA 2577  
QY 2580 GCCCCCATACGAGGCGGCGGACCATGAGTGTCCACGACGTCGAGAGATCAGCGGAGCCCA 2639  
DB 2578 GCCCCCATACGAGGCGGCGGACCATGAGTGTCCACGACGTCGAGAGATCAGCGGAGCCCA 2637  
QY 2640 GGTGACATGCTGACAGCAATGGGTGACCAAACTGCTGAGCTGAGCTCAAGCCGACCTC 2699  
DB 2638 GGTGACATGCTGACAGCAATGGGTGACCAAACTGCTGAGCTGAGCTCAAGCCGACCTC 2697  
QY 2700 ACCCAACGAGAACAGCAAAAGGCCCAACCTCGAGAGATGAGAGTGTGACTTCA 2759  
DB 2698 ACCCAACGAGAACAGCAAAAGGCCCAACCTCGAGAGATGAGAGTGTGACTTCA 2757  
QY 2760 GTCTGTGGGGCTGTAAAGCCCCCTGGC-AAAGCTGTTTCAAGATGTTTGTGATCTAG 2818  
DB 2758 GTCTGTGGGGCTGTAAAGCCCCCTGGC-AAAGCTGTTTCAAGATGTTTGTGATCTAG 2817  
QY 2819 GGAATCTACAGAGCTGAGGAGCAGTGGGGAGCAGCATCCCATCAAGCCCTAGTGGGTGAG 2878  
DB 2818 GGAATCTACAGAGCTGAGGAGCAGTGGGGAGCAGCATCCCATCAAGCCCTAGTGGGTGAG 2877  
QY 2879 AGGGCACTGGCTCGACAGCTGACAGTACGAGCTGAGAGAGGTTCTGTGTCAACGTGA 2938  
DB 2878 AGGGCACTGGCTCGACAGCTGACAGTACGAGCTGAGAGAGGTTCTGTGTCAACGTGA 2937  
QY 2939 ATCCCAACCAACCCGGGCTCCACAGTGAACCCCTGAGATCCGGAAGTCAAGAGCCGAT 2998  
DB 2938 ATCCCAACCAACCCGGGCTCCACAGTGAACCCCTGAGATCCGGAAGTCAAGAGCCGAT 2997  
QY 2999 TCAACCTCGAGATCTCTGTGAGACCTTTGGGGGGGTCAACCTGCTGGTGGGAGCAGGA 3058  
DB 2998 TCAACCTCGAGATCTCTGTGAGACCTTTGGGGGGGTCAACCTGCTGGTGGGAGCAGGA 3057  
QY 3059 ACGGCTGATGTTGCTGACACCGAAGTGGGCAAGGTTGATGACTCATTTGGGCGCG 3118

DB 3058 ACGGCTGATGTTGCTGACACCGAAGTGGGCAAGGTTGATGACTCATTTGGGCGCG 3117  
QY 3119 GAGCTTCCACAGATGAGTGTGCTGAGAGGGCTCAACCTGCTATCAACATCTCAGGGA 3178  
DB 3118 GAGCTTCCACAGATGAGTGTGCTGAGAGGGCTCAACCTGCTATCAACATCTCAGGGA 3177  
QY 3179 AAAGAACAACTGGGCTGTATTATCTGTCTGCTCGGAGCAAGATTTGTGCAATG 3238  
DB 3178 AAAGAACAACTGGGCTGTATTATCTGTCTGCTCGGAGCAAGATTTGTGCAATG 3237  
QY 3229 ACCCAAGTGAAGAGAGAGAGGCTGAGACCCGTGGGGAGCATGAGAGGCTCGGGG 3298  
DB 3228 ACCCAAGTGAAGAGAGAGAGGCTGAGACCCGTGGGGAGCATGAGAGGCTCGGGG 3297  
QY 3299 ACTACCGGTTGTGAATAACAGAGCGAGATTAAAGTTCTGTGATCGCCCTCAAGAGCTCG 3358  
DB 3298 ACTACCGGTTGTGAATAACAGAGCGAGATTAAAGTTCTGTGATCGCCCTCAAGAGCTCG 3357  
QY 3359 TGAAGTGTATGCTGGGCCCCCAACCCCTACCAAAATTCATGAGCTTCAAGTCTTTG 3418  
DB 3358 TGAAGTGTATGCTGGGCCCCCAACCCCTACCAAAATTCATGAGCTTCAAGTCTTTG 3417  
QY 3419 CCGACTTCCCAACCGCTCTCTGTGTGACCTGACAGTGTGAGAGAGGGGAGCGGCTCA 3478  
DB 3418 CCGACTTCCCAACCGCTCTCTGTGTGACCTGACAGTGTGAGAGAGGGGAGCGGCTCA 3477  
QY 3479 AGGTATATATGAGCTGAGTGTGCTGAGTGTGCTGAGTGTGAGTGTGAGTGTGAGTGTG 3538  
DB 3478 AGGTATATATGAGCTGAGTGTGCTGAGTGTGCTGAGTGTGAGTGTGAGTGTGAGTGTG 3537  
QY 3539 ATGACATCTAATCTCTGTGACATTCAGAGCAGATCAGGCCCATGCAATCTTCC 3598  
DB 3538 ATGACATCTAATCTCTGTGACATTCAGAGCAGATCAGGCCCATGCAATCTTCC 3597  
QY 3599 TCCCAACACCGAGCGGATGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3657  
DB 3598 TCCCAACACCGAGCGGATGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3657  
QY 3658 AACAGTACGGGCGGATGATTAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3717  
DB 3658 AACAGTACGGGCGGATGATTAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3717  
QY 3718 GTGCTCATCTGTCTCCAAACAGATTAATGGGCTGTGAGGAGAAAGCCATTGAGATCCG 3777  
DB 3718 GTGCTCATCTGTCTCCAAACAGATTAATGGGCTGTGAGGAGAAAGCCATTGAGATCCG 3777  
QY 3778 TCTGTGAGAGCGGCTGACCTGAGCGGGTCTTATGCAAAACGAGCTCAAGGCTCAAG 3837  
DB 3778 TCTGTGAGAGCGGCTGACCTGAGCGGGTCTTATGCAAAACGAGCTCAAGGCTCAAG 3837  
QY 3838 TTCTGTGAGAGCGGAGTGAAGAGGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3897  
DB 3838 TTCTGTGAGAGCGGAGTGAAGAGGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3897  
QY 3898 CAAGTTTACTTATGACTCTGAACCGTAATGTCATGAACTGTGTGAAGGCG 3951  
DB 3898 CAAGTTTACTTATGACTCTGAACCGTAATGTCATGAACTGTGTGAAGGCG 3951

RESULT 3  
PCT-US03-37730-22  
Sequence 22, Application PC/TUS0337730  
GENERAL INFORMATION:  
APPLICANT: EXELIXIS, INC.  
TITLE OF INVENTION: MAPKs AS MODIFIERS OF THE RAC, AXIN, AND BETA-CATENIN PATHWAYS  
FILE REFERENCE: EX03-089C-PC  
CURRENT APPLICATION NUMBER: PCT/US03/37730  
PRIOR FILING DATE: 2003-11-24  
PRIOR APPLICATION NUMBER: US 60/429,061  
PRIOR FILING DATE: 2002-11-25  
PRIOR APPLICATION NUMBER: US 60/437,163

PRIOR FILING DATE: 2002-12-30  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 22  
LENGTH: 5014  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US03-37730-22

Query Match 55.7%; Score 2201; DB 1; Length 5014;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1745	AGTCCCTGACAGACCAAGCCCAACCCGAAACCTGCTGCTCCCTCCAGCCCTCCATGACCCCG	1804
Db	1995	AGTCCCTGACAGACCAAGCCCAACCCGAAACCTGCTGCTCCCTCCAGCCCTCCATGACCCCG	2054
Qy	1805	ACCCTGACATCCCGACCACTGACAGCCCAAGTGCCTGAGAGAGCTGTCAATCCGACGA	1864
Db	2055	ACCCTGACATCCCGACCACTGACAGCCCAAGTGCCTGAGAGAGCTGTCAATCCGACGA	2114
Qy	1865	ATTGAGACCCCACTCTGAGAGACCTGAGCCCAAGCCGAAATCCCGACCTGCTGCTG	1924
Db	2115	ATTGAGACCCCACTCTGAGAGACCTGAGCCCAAGCCGAAATCCCGACCTGCTGCTG	2174
Qy	1925	CAGATTAAGAGCCCAACCCCAAGGCTCTGAGAGACCTCAATATGCTGCTGCTGCTG	1984
Db	2175	CAGATTAAGAGCCCAACCCCAAGGCTCTGAGAGACCTCAATATGCTGCTGCTGCTG	2234
Qy	1985	ACACAGTGGGGCCGAGAGGATCCCGGACAGCCAGGAGCTCGTGCAGACTTCGACGA	2044
Db	2235	ACACAGTGGGGCCGAGAGGATCCCGGACAGCCAGGAGCTCGTGCAGACTTCGACGA	2294
Qy	2045	ACTCGGCTGGAATATCTATCTGCAAGGCGGGAGAGCGGGGCAACCCCAAGCTTCAG	2104
Db	2295	ACTCGGCTGGAATATCTATCTGCAAGGCGGGAGAGCGGGGCAACCCCAAGCTTCAG	2354
Qy	2105	GGCCCCCTGCTCAACCCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2164
Db	2355	GGCCCCCTGCTCAACCCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2414
Qy	2165	GGGAGCCCTGCTGGAAGAGCTCGGACAGGCTCTTCCAGCTCTCAAGGACCTTCGCC	2224
Db	2415	GGGAGCCCTGCTGGAAGAGCTCGGACAGGCTCTTCCAGCTCTCAAGGACCTTCGCC	2474
Qy	2225	AGGCTGCTCACTGAGAGGAAACCGGCTGAGAGCTCTTCCAACTGAGAGCTTCGCC	2284
Db	2475	AGGCTGCTCACTGAGAGGAAACCGGCTGAGAGCTCTTCCAACTGAGAGCTTCGCC	2534
Qy	2285	TGCTCTCCCTGCTGGAATTAAGCCCAAGCCGACAGACCTCTCAAGGACCTTCGCC	2344
Db	2535	TGCTCTCCCTGCTGGAATTAAGCCCAAGCCGACAGACCTCTCAAGGACCTTCGCC	2594
Qy	2245	CAGACTTGTGTGCTGTAAGAGGAGGAGCTCTGAGAGGAGCCCTCGGCTCCCAAGAG	2404
Db	2595	CAGACTTGTGTGCTGTAAGAGGAGGAGCTCTGAGAGGAGCCCTCGGCTCCCAAGAG	2654
Qy	2405	CCATGAGCTACTCGTCTGCTGAGAGGAGTGTGAAAGCAGTGAAGACGACGAGAGAG	2464
Db	2655	CCATGAGCTACTCGTCTGCTGAGAGGAGTGTGAAAGCAGTGAAGACGACGAGAGAG	2714
Qy	2465	GCGAAGGCGGGCCGACAGAGGAGGAGATACCCCTGAGAGGAGCTGAGAGGAGTA	2524
Db	2715	GCGAAGGCGGGCCGACAGAGGAGGAGATACCCCTGAGAGGAGCTGAGAGGAGTA	2774
Qy	2525	CAGACAGCTGACAGCAATGCTGCTGAGAGGAGTCAAGGAGGAGCTGAGAGGAGTA	2584
Db	2775	CAGACAGCTGACAGCAATGCTGCTGAGAGGAGTCAAGGAGGAGCTGAGAGGAGTA	2834
Qy	2585	CATACGAGGCGGACCAATGCTGCTGAGAGGAGCTGAGAGGAGGAGGAGGAGGAGG	2644
Db	2835	CATACGAGGCGGACCAATGCTGCTGAGAGGAGCTGAGAGGAGGAGGAGGAGGAGG	2894

Qy	2645	ATGCTGACAGCAATGGGTACACAAACCTGCTGAGTGTGTCCAGCCAGCCACTCAACCA	2704
Db	2895	ATGCTGACAGCAATGGGTACACAAACCTGCTGAGTGTGTCCAGCCAGCCACTCAACCA	2954
Qy	2705	CCGAGAACAGCAAGGCGCAAGCCCAACCTGGAAGGATGGAGTGTGACTCAAGTCTC	2764
Db	2955	CCGAGAACAGCAAGGCGCAAGCCCAACCTGGAAGGATGGAGTGTGACTCAAGTCTC	3014
Qy	2765	GTTGGCTGTGTAAGGCGCTGCTGAGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTG	2824
Db	3015	GTTGGCTGTGTAAGGCGCTGCTGAGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTG	3074
Qy	2825	ACGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2884
Db	3075	ACGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	3134
Qy	2885	CTCGGCTGACACAGCTGAGTACAGAGTGAAGAGGTTCTGTGTGCTCAAGCTGAATCCA	2944
Db	3135	CTCGGCTGACACAGCTGAGTACAGAGTGAAGAGGTTCTGTGTGCTCAAGCTGAATCCA	3194
Qy	2945	CCAAACCCCGGACCAAGTGAAGCCCTGAGATCCGGAAGTACAAAGAGGATTCACACT	3004
Db	3195	CCAAACCCCGGACCAAGTGAAGCCCTGAGATCCGGAAGTACAAAGAGGATTCACACT	3254
Qy	3005	CCGAGATCTCTGTGAGGCGCTTGTGGGGGTCAACTGTGTGTGGGACCGGAGAACGGGC	3064
Db	3355	CCGAGATCTCTGTGAGGCGCTTGTGGGGGTCAACTGTGTGTGGGACCGGAGAACGGGC	3314
Qy	3065	TGATGTTGCTGAGACGGAAGTGGGCAAGGTGTATGGAATGGAATGAGGAGGAGGAG	3124
Db	3315	TGATGTTGCTGAGACGGAAGTGGGCAAGGTGTATGGAATGGAATGAGGAGGAGGAG	3374
Qy	3125	TCCAGCAGATGATGTGTGAGAGGAGGCTCAACTGTGTCTATCACTCAAGGAGGAGG	3184
Db	3375	TCCAGCAGATGATGTGTGAGAGGAGGCTCAACTGTGTCTATCACTCAAGGAGGAGG	3434
Qy	3185	ACAACTGCGGGGTATATTAACCTGCTGAGGCTCGGGAACAAGTTCTGCAACAATGCCAG	3244
Db	3435	ACAACTGCGGGGTATATTAACCTGCTGAGGCTCGGGAACAAGTTCTGCAACAATGCCAG	3494
Qy	3245	AAATGAGAGAGAGAGGAGGCTGAGACCAAGTGGGGGACATGAGAGGCTGCGGGACCTAAC	3304
Db	3495	AAATGAGAGAGAGAGGAGGCTGAGACCAAGTGGGGGACATGAGAGGCTGCGGGACCTAAC	3554
Qy	3305	GTTGTTGGAATTAAGAGCGGATTAAGTTCTGTGCTATCGCCCTTAAGAGCTCGTGGAGG	3364
Db	3555	GTTGTTGGAATTAAGAGCGGATTAAGTTCTGTGCTATCGCCCTTAAGAGCTCGTGGAGG	3614
Qy	3365	TGTATGCTGGGCCCCCAACCCCTACCAAAATTCATGAGCTTCAAGCTTTCGCCAGC	3424
Db	3615	TGTATGCTGGGCCCCCAACCCCTACCAAAATTCATGAGCTTTCGCCAGC	3674
Qy	3425	TCCCCACCGGCTCTGCTGCTGAGCTGAGCAAGTGAAGAGGAGGAGGAGGAGGAGG	3484
Db	3675	TCCCCACCGGCTCTGCTGCTGAGCTGAGCAAGTGAAGAGGAGGAGGAGGAGGAGG	3734
Qy	3485	TCTATGCTGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3544
Db	3735	TCTATGCTGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3794
Qy	3545	TCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3604
Db	3795	TCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3854
Qy	3605	ACAACGAGCAGATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3664
Db	3855	ACAACGAGCAGATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3914
Qy	3665	ACGGGCGCATATTAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3724
Db	3915	ACGGGCGCATATTAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3974
Qy	3725	ACATCTGCTCAACCAATATGAGGCTGGGGTGAAGAAAGCATTGAATCCGCTCTGTGG	3784

Db 3975 ACATCTGCTCCAAACAGATTAATGGGGCTGGGGTGAAGAAAGCATTGAGATCCGCTCTGGG 4034  
Qy 3785 AGAGGGGACACCTGAGCGGGGCTTCATGCAACAAACGAGCTCAGAGGCTCAAGTTCCTGT 3844  
Db 4035 AGACGGGCGACCTGACGGGGCTTCATGCAACAAACGAGCTCAGAGGCTCAAGTTCCTGT 4094  
Qy 3845 GTGAGCGGAATGACAAGGTGTTTTTGTGCTCAGTCCGCTCTGGGGGAGCAGCCAAAGTTT 3904  
Db 4095 GTGAGCGGAATGACAAGGTGTTTTTGTGCTCAGTCCGCTCTGGGGGAGCAGCCAAAGTTT 4154  
Qy 3905 ACTTCATGACTCTGTAACCGTAACTGCATCATGTAACCTGTGTA 3945  
Db 4155 ACTTCATGACTCTGTAACCGTAACTGCATCATGTAACCTGTGTA 4195

RESULT 4  
PCT-US03-37730-26  
; Sequence 26, Application PC/TUS0337730  
; GENERAL INFORMATION:  
; APPLICANT: EXELIXIS, INC.  
; TITLE OF INVENTION: MAPKS AS MODIFIERS OF THE RAC, AXIN, AND BETA-CATENIN PATHWAYS  
; TITLE OF INVENTION: AND METHODS OF USE  
; FILE REFERENCE: EX03-089C-PC  
; CURRENT APPLICATION NUMBER: PCT/US03/37730  
; PRIOR FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: US 60/429,061  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: US 60/437,163  
; PRIOR FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 26  
; LENGTH: 4989  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US03-37730-26

Query Match 53.1%; Score 2099; DB 1; Length 4989;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2199; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1745 AGTCCCTGACGAGACGACCCCAACCCGAAACCTGGCTGCTTCCAGCTTCCATGACCCCG 1804  
Db 1995 AGTCCCTGACGAGACGACCCCAACCCGAAACCTGGCTGCTTCCAGCTTCCATGACCCCG 2054  
Qy 1805 ACCCTGCACTCCCGGACCCCACTGCGACGCGGAGTGCAGAGAGTGTCTATCCGCGAGA 1864  
Db 2055 ACCCTGCACTCCCGGACCCCACTGCGACGCGGAGTGCAGAGAGTGTCTATCCGCGAGA 2114  
Qy 1865 ATTGAGACCCCACTCTGTAAGGACCTGGGCGCCGAGCCCGAATCCCGAGGCTGGTCCGCG 1924  
Db 2115 ATTGAGACCCCACTCTGTAAGGACCTGGGCGCCGAGCCCGAATCCCGAGGCTGGTCCGCG 2174  
Qy 1925 CAGATTAACGAGGCGCCCAACCAAGTGTCTCAGAGGACCTCATCTATGCGCACTGCGCTTA 1984  
Db 2175 CAGATTAACGAGGCGCCCAACCAAGTGTCTCAGAGGACCTCATCTATGCGCACTGCGCTTA 2234  
Qy 1985 ACAACGATGGGCGCGGAGGTTCCCGGCGACGCCAGCGAGTCCGTGCGACAACCTCGAGAGA 2044  
Db 2235 ACAACGATGGGCGCGGAGGTTCCCGGCGACGCCAGCGAGTCCGTGCGACAACCTCGAGAGA 2294  
Qy 2045 ACTCGGCTGGGAAATCTATCTGCAAAAGCGGGGAGAGGCGGGGCAACCCCAAGCTCCAG 2104  
Db 2295 ACTCGGCTGGGAAATCTATCTGCAAAAGCGGGGAGAGGCGGGGCAACCCCAAGCTCCAG 2354  
Qy 2105 GGGCGGCTGCTAGCGGCTTGGCGCGCCCAAGCGCTCTAGTAACCCCGACCTCAGAGAGA 2164  
Db 2355 GGGCGGCTGCTAGCGGCTTGGCGCGCCCAAGCGCTCTAGTAACCCCGACCTCAGAGAGA 2414  
Qy 2165 GCGACCTGCTGGGAAAGCTGCGACAGCGTCTTCCAGCTCTCAAGGCGACCTTCCCC 2224  
Db 2415 GCGACCTGCTGGGAAAGCTGCGACAGCGTCTTCCAGCTCTCAAGGCGACCTTCCCC 2474

Qy 2225 AGGCTGCTCACTGAGCGGAACCGCTGGAGGCTCTCTCAAACTGGAAGCTTCCCTG 2284  
Db 2475 AGGCTGCTCACTGAGCGGAACCGCTGGAGGCTCTCTCAAACTGGAAGCTTCCCTG 2534  
Qy 2285 TGCTCTCCCTGGGAATTAACCAACCCCAACGACCAACCGCTCAACGCGCAGGCGGCGCG 2344  
Db 2535 TGCTCTCCCTGGGAATTAACCAACCCCAACGACCAACCGCTCAACGCGCAGGCGGCGCG 2594  
Qy 2345 CAGACTTGTGTGTGTAAGAGCGGACTCTGGAAGAGGCGGCTCGGCTCCCAAGAG 2404  
Db 2595 CAGACTTGTGTGTGTAAGAGCGGACTCTGGAAGAGGCGGCTCGGCTCCCAAGAG 2654  
Qy 2405 CCATGACTACTCGTCTGACGAGAGAGGTGAAAGCATGAGAGCAGCAGAGAGAG 2464  
Db 2655 CCATGACTACTCGTCTGACGAGAGAGGTGAAAGCATGAGAGCAGCAGAGAGAG 2714  
Qy 2465 GCGAAGGCGGCGCAGCAGAGGAGAGAGATTAACCCCTGGGGGCGCGAGCGATGGGGATA 2524  
Db 2715 GCGAAGGCGGCGCAGCAGAGGAGAGAGATTAACCCCTGGGGGCGCGAGCGATGGGGATA 2774  
Qy 2525 CAGACAGGCTGACGACCATGCTGTCAGAGAGATGAGAGATGACCGGAGCCAGCCCC 2584  
Db 2775 CAGACAGGCTGACGACCATGCTGTCAGAGAGATGAGAGATGACCGGAGCCAGCCCC 2834  
Qy 2585 CATACGGGGGCGGACCATGCTGTCAGAGAGATGAGAGATGAGAGATGAGAGATGAGAG 2644  
Db 2835 CATACGGGGGCGGACCATGCTGTCAGAGAGATGAGAGATGAGAGATGAGAGATGAGAG 2894  
Qy 2645 ATGCTGAGACGATGAGTGAACCAACCTGAGAGTGTGTCAGGCGGAGAGAGAGAGAG 2704  
Db 2895 ATGCTGAGACGATGAGTGAACCAACCTGAGAGTGTGTCAGGCGGAGAGAGAGAGAG 2954  
Qy 2705 CCGAGAGCAGCAAAAGGCGCAAGCCCACTCGAAGAGTGGAGTGTGATCAACAGTCTC 2764  
Db 2955 CCGAGAGCAGCAAAAGGCGCAAGCCCACTCGAAGAGTGGAGTGTGATCAACAGTCTC 3014  
Qy 2765 GTGGGCTGTAAAGGCGGCTGCGCAAGAGCTGTTCAAGATGTTGTGATCTAGAGATCT 2824  
Db 3015 GTGGGCTGTAAAGGCGGCTGCGCAAGAGCTGTTCAAGATGTTGTGATCTAGAGATCT 3074  
Qy 2825 ACCAGCTGAGAGGAGTGGGAGCAGCATCCCACTCAAGAGAGAGAGAGAGAGAGAGAG 2884  
Db 3075 ACCAGCTGAGAGGAGTGGGAGCAGCATCCCACTCAAGAGAGAGAGAGAGAGAGAGAG 3134  
Qy 2885 CTGGGCTGACAGCTGAGTACGAGCTGAGAGAGAGTGTGTGTGATCAACGTAATCCA 2944  
Db 3135 CTGGGCTGACAGCTGAGTACGAGCTGAGAGAGAGTGTGTGTGATCAACGTAATCCA 3194  
Qy 2945 CCAACACCGGCGCCCAAGTGAAGACCCCTGAGATCGGAGAGTACCAAGAGAGATTCAT 3004  
Db 3195 CCAACACCGGCGCCCAAGTGAAGACCCCTGAGATCGGAGAGTACCAAGAGAGATTCAT 3254  
Qy 3005 CCGAATCTCTGTGACAGCCCTTGGGGGAGTCAACCTGCTGTGGGAGCAGGAGAGCGGG 3064  
Db 3255 CCGAATCTCTGTGACAGCCCTTGGGGGAGTCAACCTGCTGTGGGAGCAGGAGAGCGGG 3314  
Qy 3065 TGATGTTCTGGAACCGAAGTGGGAGGCGCAAGGTATGAGACTCATTTGGGCGGCGAGCT 3124  
Db 3315 TGATGTTCTGGAACCGAAGTGGGAGGCGCAAGGTATGAGACTCATTTGGGCGGCGAGCT 3374  
Qy 3125 TCAGCAGATGATGATGCTGAGAGGAGCTCAACCTGCTCATCAACATCTCAGGAAAGGA 3184  
Db 3375 TCAGCAGATGATGATGCTGAGAGGAGCTCAACCTGCTCATCAACATCTCAGGAAAGGA 3434  
Qy 3185 ACAAACTGCGGATTAATCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3244  
Db 3435 ACAAACTGCGGATTAATCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3494  
Qy 3245 AAGTGAAGAGAGAGGAGGCTGAGACAGCGTGGGAGAGATGAGAGGAGGAGGAGGAG 3304  
Db 3495 AAGTGAAGAGAGAGGAGGCTGAGACAGCGTGGGAGAGATGAGAGGAGGAGGAGGAG 3554





Db 3285 ACCAGCCTGAGAGGCGAGTGGGAGCAGCATCCCATCAGAGCCCTAGTGGGTGAGAGGCGCA 3344  
OY 2885 CTCGGCTGACACGACGTGACATGACGATGAGAGAGGCTTCTGTGCTCAACCTGATATCCCA 2944  
Db 3345 CTCGGCTGACACGACGTGACATGACGATGAGAGAGGCTTCTGTGCTCAACCTGATATCCCA 3404  
OY 2945 CCAACACCGGGGCCACAGTGAAGACCCCTGAGATCCGGAAGTACAAAGAGCAGATTCAACT 3004  
Db 3405 CCAACACCGGGGCCACAGTGAAGACCCCTGAGATCCGGAAGTACAAAGAGCAGATTCAACT 3464  
OY 3005 CCGAGATCTCTGTGACAGCCCTTTG3GGGGTCAACCTGTGTG3GCACGAGAAAGGGC 3064  
Db 3465 CCGAGATCTCTGTGACAGCCCTTTG3GGGGTCAACCTGTGTG3GCACGAGAAAGGGC 3524  
OY 3065 TGAATTTCTGGAACCGAAGTGGGACGAGAGTGTATGGAATTCATTTGGGCGGCGACGCT 3124  
Db 3525 TGAATTTCTGGAACCGAAGTGGGACGAGAGTGTATGGAATTCATTTGGGCGGCGACGCT 3584  
OY 3125 TCACAGATGATGATGCTGAGAGGGCTCAACCTGTCTATCAACATCTCAGGAAAGGA 3184  
Db 3585 TCACAGATGATGATGCTGAGAGGGCTCAACCTGTCTATCAACATCTCAGGAAAGGA 3644  
OY 3185 ACAAACTGGGGGTGATTAACCTGTCTGTGCTCGGAAACAAGTTCGACAAATGACCCAG 3244  
Db 3645 ACAAACTGGGGGTGATTAACCTGTCTGTGCTCGGAAACAAGTTCGACAAATGACCCAG 3704  
OY 3245 AAGTGAAGAAGAAGAGGGCTGAGACCAACGTTGGGGGACATGAGAGGGCTGGGACACTAC 3304  
Db 3705 AAGTGAAGAAGAAGAGGGCTGAGACCAACGTTGGGGGACATGAGAGGGCTGGGACACTAC 3764  
OY 3305 GGTGTGTAATATACAGCGAGATTAAGTTCCTGTGCTATCGCCCTCAAGAGCTCCGTGAG 3364  
Db 3765 GGTGTGTAATATACAGCGAGATTAAGTTCCTGTGCTATCGCCCTCAAGAGCTCCGTGAG 3824  
OY 3365 TGTATGCTGGGCCCCCAAAACCTTACCAAAATTCATGAGCTTCAAGTCTTTGCCAGC 3424  
Db 3825 TGTATGCTGGGCCCCCAAAACCTTACCAAAATTCATGAGCTTCAAGTCTTTGCCAGC 3884  
OY 3425 TCCCCACCGCCCTGTGCTGTGCTGACACCTGACAGTGAAGAGGGGCGGCTCAAGGTCA 3484  
Db 3885 TCCCCACCGCCCTGTGCTGTGCTGACACCTGACAGTGAAGAGGGGCGGCTCAAGGTCA 3944  
OY 3485 TCTATGCTCCAGTGTGCTTCAATGCTGTGATGCTGAGTCCGAGGAAACAGTATGACA 3544  
Db 3945 TCTATGCTCCAGTGTGCTTCAATGCTGTGATGCTGAGTCCGAGGAAACAGTATGACA 4004  
OY 3545 TCTATGCTCCAGTGTGCTTCAATGCTGTGATGCTGAGTCCGAGGAAACAGTATGACA 3604  
Db 4005 TCTATGCTCCAGTGTGCTTCAATGCTGTGATGCTGAGTCCGAGGAAACAGTATGACA 4064  
OY 3605 ACAACGACGAGATGAGATGCTGTGCTGACAGAGACAGAGGTGTCTACGTCAACAGCT 3664  
Db 4065 ACAACGACGAGATGAGATGCTGTGCTGACAGAGACAGAGGTGTCTACGTCAACAGCT 4124  
OY 3665 ACGGGCGCATCTTAAGATGTGTGCTGACAGTGGGGGAGAGTCTTACTTCTGTGCT 3724  
Db 4125 ACGGGCGCATCTTAAGATGTGTGCTGACAGTGGGGGAGAGTCTTACTTCTGTGCT 4184  
OY 3725 ACATCTGCTCAACAGATTAATGAGGTGGGGTGAAGAACCAATGAGATCCGCTGTG 3784  
Db 4185 ACATCTGCTCAACAGATTAATGAGGTGGGGTGAAGAACCAATGAGATCCGCTGTG 4244  
OY 3785 AAGACGGGCACTCTGACAGGGGCTTCTATGACAAAGAGCTCAGAGGCTCAAGTTCCT 3844  
Db 4245 AAGACGGGCACTCTGACAGGGGCTTCTATGACAAAGAGCTCAGAGGCTCAAGTTCCT 4304  
OY 3845 GTGAGCGAATGACAAAGTGTGTTTGTGCTCAGTCCGCTCTGGGGGACAGCAGAGTT 3904  
Db 4305 GTGAGCGAATGACAAAGTGTGTTTGTGCTCAGTCCGCTCTGGGGGACAGCAGAGTT 4364  
OY 3905 ACTTCATGACTCTGAACCGTAACTGATCATGAATGCTGA 3945

Db 4365 ACTTCATGACTCTGAACCGTAACTGATCATGAATGCTGA 4405  
RESULT 6  
US-10-029-115-5  
; Sequence 5, Application US/10029115  
; GENERAL INFORMATION:  
; APPLICANT: Luo, Yiang  
; APPLICANT: Fu, Alan C  
; APPLICANT: Shen, Mary  
; TITLE OF INVENTION: Novel Germinal Center Kinase Cell Cycle Proteins, Compositions an  
; FILE REFERENCE: A-70229/RMS/DHR  
; CURRENT APPLICATION NUMBER: US/10/029,115  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 4033  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-029-115-5  
Query Match 48.3%; Score 1907; DB 43; Length 4033;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2197; Conservative 0; Mismatches 1; Indels 3; Gaps 1;  
OY 1745 AGTCCCTGACAGACCAAGCCCAACCCGAAACCTGAGCTGCTCCAGCTCCAGTACCCCG 1804  
Db 1836 AGTCCCTGACAGACCAAGCCCAACCCGAAACCTGAGCTGCTCCAGCTCCAGTACCCCG 1895  
OY 1805 ACCCTGACATCCCGACACCACTGACAGCCGACGATGCCGAGAGAGCTGTATCCGCCAGA 1864  
Db 1896 ACCCTGACATCCCGACACCACTGACAGCCGACGATGCCGAGAGAGCTGTATCCGCCAGA 1955  
OY 1865 ATTCAGACCCCACTCTGAAAGAGCTGAGCCGACGCGGAAATCCCGACCTGGGTCGCC 1924  
Db 1956 ATTCAGACCCCACTCTGAAAGAGCTGAGCCGACGCGGAAATCCCGACCTGGGTCGCC 2015  
OY 1925 CAGATTAAGAGGCCCCCAACCAAGGTGCTCAGAGGAGCTCTATTCGCACTGCGCTTA 1984  
Db 2016 CAGATTAAGAGGCCCCCAACCAAGGTGCTCAGAGGAGCTCTATTCGCACTGCGCTTA 2075  
OY 1985 ACACAGTGGGGCCGAGAGGTTCCGGCCAGCCAGCCAGTCCGTGCTCAGACTCGCAGCA 2044  
Db 2076 ACACAGTGGGGCCGAGAGGTTCCGGCCAGCCAGCCAGTCCGTGCTCAGACTCGCAGCA 2135  
OY 2045 ACTCCGCTGTGAAATCTATCTGCAAAAGCGGGGAGACCGGGGCAACCCCAAGCTCCAG 2104  
Db 2136 ACTCCGCTGTGAAATCTATCTGCAAAAGCGGGGAGACCGGGGCAACCCCAAGCTCCAG 2195  
OY 2105 GGGCCCTGTGAGGCCCCCTGAGCCGACCAAGCTCTAGTAAACCCGACCTCAGAGAGA 2164  
Db 2196 GGGCCCTGTGAGGCCCCCTGAGCCGACCAAGCTCTAGTAAACCCGACCTCAGAGAGA 2255  
OY 2165 GCGACCTGTGAGGAGCGCTGAGACAGGCTTTCAGGCTCTCAGCGGACCTTCCGCC 2224  
Db 2256 GCGACCTGTGAGGAGCGCTGAGACAGGCTTTCAGGCTCTCAGCGGACCTTCCGCC 2315  
OY 2225 AGGCTGCTCACTGAGAGGGAACCGCGTGGAGCTTCTCCAAATGAGCAGCTCCCTG 2284  
Db 2316 AGGCTGCTCACTGAGAGGGAACCGCGTGGAGCTTCTCCAAATGAGCAGCTCCCTG 2375  
OY 2285 TGCTCCCTGTGGAATTAAGCCAGACCCGACGACCAACGCTCAGGCGAGGCGGCGG 2344  
Db 2376 TGCTCCCTGTGGAATTAAGCCAGACCCGACGACCAACGCTCAGGCGAGGCGGCGG 2435  
OY 2345 CAGACTTGTGTGTGTAAGAGCGGACCTGTGAAGAGGCGGCTCGGCTCCAGAGAG 2404  
Db 2436 CAGACTTGTGTGTGTAAGAGCGGACCTGTGAAGAGGCGGCTCGGCTCCAGAGAG 2495  
OY 2405 CCATGACTACTGTGCTCAGCGAGAGGTGGAAGAGTGAAGACGAGCAGAGGAGAG 2464





Db 1964 CAGATAAGAGGCCCCACCCAAAGTGCTCAGAGGACCTCATCTATCCGCACTGCGCTTAA 2023  
Qy 1965 AACACAGTGGGGCCCGAGAGTCCCGGCGACGAGTCCGTCGAGAGCTCGACGA 2044  
Db 2024 AACACAGTGGGGCCCGAGAGTCCCGGCGACGAGTCCGTCGAGAGCTCGACGA 2083  
Qy 2045 ACTCCGCTGGCAATCTATCTGCAAAAGCGGGCAGAGCGGGCAAGCCCAAGCTTCAG 2104  
Db 2084 ACTCCGCTGGCAATCTATCTGCAAAAGCGGGCAGAGCGGGCAAGCCCAAGCTTCAG 2143  
Qy 2105 GAGCCCTGCTCAGGCCCCCTGGCCCCCGCAAGCTCTAGTAAGCCCGAAGCTCAGAGGA 2164  
Db 2144 GAGCCCTGCTCAGGCCCCCTGGCCCCCGCAAGCTCTAGTAAGCCCGAAGCTCAGAGGA 2203  
Qy 2165 GCGAACCTGGCTGGGAAAGCTTCGGGACAGGTCCTTCAGGCTCTGACGGGGCACTCCCG 2224  
Db 2204 GCGAACCTGGCTGGGAAAGCTTCGGGACAGGTCCTTCAGGCTCTGACGGGGCACTCCCG 2263  
Qy 2225 AGGCTGGCTCAGTGGAGCGGAAACCGCTGGGAGCTCTCCAAAGTGGACAGCTCCCTG 2284  
Db 2264 AGGCTGGCTCAGTGGAGCGGAAACCGCTGGGAGTCTCTCCAAAGTGGACAGCTCCCTG 2323  
Qy 2285 TGCTCTCCCTGGGAAATTAAGCCCAAGCCCGACGACCAAGCTCAGCGGCGGCGCGCG 2344  
Db 2324 TGCTCTCCCTGGGAAATTAAGCCCAAGCCCGACGACCAAGCTCAGCGGCGGCGCGCG 2383  
Qy 2345 CAGACTTGTGTGTGTAAGAGCGGACCTTGGAGAGAGGCGCTGGGCTCCCAAGAAAG 2404  
Db 2384 CAGACTTGTGTGTGTAAGAGCGGACCTTGGAGAGAGGCGCTGGGCTCCCAAGAAAG 2443  
Qy 2405 CCATGAGTACTCTGCTGCTCAGCGAGAGAGTGAAGAGCAGTGAAGACGACGAGAGAG 2464  
Db 2444 CCATGAGTACTCTGCTGCTCAGCGAGAGTGAAGAGCAGTGAAGAGCAGGAGAGAG 2503  
Qy 2465 GCGAAGCGGGCCAGAGAGGAGAGAGATATCCCTGGGGCCGCGAGCGGATG 2524  
Db 2504 GCGAAGCGGGCCAGAGAGGAGAGAGATATCCCTGGGGCCGCGAGCGGATG 2560  
Qy 2525 CAGACAGGCTCAGCAGATGCTGCTCAGAGTGAAGAGATCAAGCGGAGCCAGCGCC 2584  
Db 2561 CAGACAGGCTCAGCAGATGCTGCTCAGAGTGAAGAGATCAAGCGGAGCCAGCGCC 2620  
Qy 2585 CATACGGGGCCGACCATGCTGCTCAGCGAGCCCTGGAAGAGAGCGGAACTGCTG 2644  
Db 2621 CATACGGGGCCGACCATGCTGCTCAGCGAGCCCTGGAAGAGAGCGGAACTGCTG 2680  
Qy 2645 ATGCTGACAGCAATGGGTACAAACCTGCTGAGTGGTCAAGCCCAAGCTCAAGCA 2704  
Db 2681 ATGCTGACAGCAATGGGTACAAACCTGCTGAGTGGTCAAGCCCAAGCTCAAGCA 2740  
Qy 2705 CCGAAGACGCAAGGCGCAAGCCCTGGAAGAGTGGGTGAAGCTCAAGCTCA 2764  
Db 2741 CCGAAGACGCAAGGCGCAAGCCCTGGAAGAGTGGGTGAAGCTCAAGCTCA 2800  
Qy 2765 GTGGCTGGTAAAGGCCCCCTGGCAAGAGCTGCTCAGATGTTGTGATCTAGGAGAT 2824  
Db 2801 GTGGCTGGTAAAGGCCCCCTGGCAAGAGCTGCTCAGATGTTGTGATCTAGGAGAT 2860  
Qy 2825 ACCAGCTTGGAGCAGTGGGGAAGCATCCCATCAAGCCCTAGTGGTGAAGAGGCA 2884  
Db 2861 ACCAGCTTGGAGCAGTGGGGAAGCATCCCATCAAGCCCTAGTGGTGAAGAGGCA 2920  
Qy 2885 CTGGCTGACAGAGCTGCTGCTGAGAGAGGCTCTGCTGCTCAAGCTCAAGCTCA 2944  
Db 2921 CTGGCTGACAGAGCTGCTGCTGAGAGAGGCTCTGCTGCTCAAGCTCAAGCTCA 2980  
Qy 2945 CCAAGACCCGGGCGCAAGTGAAGCCCTGAGATCCGGAAGTCAAGAGCAATTCAGT 3004  
Db 2981 CCAAGACCCGGGCGCAAGTGAAGCCCTGAGATCCGGAAGTCAAGAGCAATTCAGT 3040  
Qy 3005 CCGAGATCTCTGTGTGAGGCTTTTGGGGGGTCAAGCTGTGTGTGGGCAAGAGAGG 3064  
Db 3041 CCGAGATCTCTGTGTGAGGCTTTTGGGGGGTCAAGCTGTGTGTGGGCAAGAGAGG 3100

Qy 3065 TGATGTTGCTGAGACCGAAGTGGGCAAGGCTGATGAGACTCATTTGGGGCGAGCGCT 3124  
Db 3101 TGATGTTGCTGAGACCGAAGTGGGCAAGGCTGATGAGACTCATTTGGGGCGAGCGCT 3160  
Qy 3125 TCACAGCAGATGATGTGTGGAGGGGCTCAACCTGCTCATCAACATCTCAGGAAAGGA 3184  
Db 3161 TCACAGCAGATGATGTGTGGAGGGGCTCAACCTGCTCATCAACATCTCAGGAAAGGA 3220  
Qy 3185 ACAACCTGGGGGTATTAACCTGCTGCTGCTCCGGAACAAGTTCGTGCAATGACAG 3244  
Db 3221 ACAACCTGGGGGTATTAACCTGCTGCTGCTCCGGAACAAGTTCGTGCAATGACAG 3280  
Qy 3245 AAGTGAAGAAAGCAGGGCTGAGCAACCTGAGGGGGAATGAGAGGCTGAGGCACTAAC 3304  
Db 3281 AAGTGAAGAAAGCAGGGCTGAGCAACCTGAGGGGGAATGAGAGGCTGAGGCACTAAC 3340  
Qy 3305 GTGTTGTAATTAAGAGCGGATTAAGTTCCTGCTGCTATGCTCCCTCAAGAGCTCCG 3364  
Db 3341 GTGTTGTAATTAAGAGCGGATTAAGTTCCTGCTGCTATGCTCCCTCAAGAGCTCCG 3400  
Qy 3365 TGATAGCCTGGGCCCCCAACCTTACCAACAAATTCATGAGCTTCCTTGGCGAGC 3424  
Db 3401 TGATAGCCTGGGCCCCCAACCTTACCAACAAATTCATGAGCTTCCTTGGCGAGC 3460  
Qy 3425 TCCCCCAAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3484  
Db 3461 TCCCCCAAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3520  
Qy 3485 TCTATGCTCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3544  
Db 3521 TCTATGCTCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3580  
Qy 3545 TCTATGCTCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3604  
Db 3581 TCTATGCTCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3640  
Qy 3605 ACACGAGGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3664  
Db 3641 ACACGAGGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3700  
Qy 3665 ACGGCGCATTAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3724  
Db 3701 ACGGCGCATTAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3760  
Qy 3725 ACATGCTGCTCAACGAGTAAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3784  
Db 3761 ACATGCTGCTCAACGAGTAAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3820  
Qy 3785 AGACGGGCGACCTGAGCGGGGCTTTCATGCAAAAGAGCTGAGAGCTCAAGTTCTGT 3844  
Db 3821 AGACGGGCGACCTGAGCGGGGCTTTCATGCAAAAGAGCTGAGAGCTCAAGTTCTGT 3880  
Qy 3845 GTAGCGGAATGAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3904  
Db 3881 GTAGCGGAATGAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3940  
Qy 3905 ACTCATGACTGGAAGCGTAAC 3927  
Db 3941 ACTCATGACTGGAAGCGTAAC 3963

RESULT 8  
US-10-725-329-11  
Sequence 11, Application US/10725329  
GENERAL INFORMATION:  
APPLICANT: PLOWMAN, GREGORY  
APPLICANT: MARTINEZ, RICARDO  
APPLICANT: WHYTE, DAVID  
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
FILE REFERENCE: 038602/0328  
CURRENT APPLICATION NUMBER: US/10/725,329  
CURRENT FILING DATE: 2003-12-02



QY 3665 ACGGCGCATCATTAAGAGTGTGTCTGTCAGTGGGGGAGAGATGCTTCTGTGGCCT 3724  
Db 3701 ACGGCGCATCATTAAGAGTGTGTCTGTCAGTGGGGGAGAGATGCTTCTGTGGCCT 3760  
QY 3725 ACATCTGCTCCAACAGATTAATGGGCTGGGGTGAAGAACCATTTGATCCGCTCTGTGG 3784  
Db 3761 ACATCTGCTCCAACAGATTAATGGGCTGGGGTGAAGAACCATTTGATCCGCTCTGTGG 3820  
QY 3785 AGACGGGCGACCTCGACGGGGCTTCATGTCAGAAACGAGCTGAGAGGCTCAAGTTCCCTGT 3844  
Db 3821 AGACGGGCGACCTCGACGGGGCTTCATGTCAGAAACGAGCTGAGAGGCTCAAGTTCCCTGT 3880  
QY 3845 GTGAGCGGATGACAAAGGTGTTTGTGCTCAGTCCGCTCTGCGGGCAGACCAAGTTT 3904  
Db 3881 GTGAGCGGATGACAAAGGTGTTTGTGCTCAGTCCGCTCTGCGGGCAGACCAAGTTT 3940  
QY 3905 ACTTCATGACTCTGAACCGTAAAC 3927  
Db 3941 ACTTCATGACTCTGAACCGTAAAC 3963

RESULT 9  
US-10-725-330-11  
; Sequence 11, Application US/10725330  
; GENERAL INFORMATION:  
; APPLICANT: PLOMMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHITE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 038602/0328  
; CURRENT APPLICATION NUMBER: US/10/725,330  
; PRIOR FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: US/09/688,1888  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 09/291,417  
; PRIOR FILING DATE: 1999-04-14  
; PRIOR APPLICATION NUMBER: 60/081,784  
; PRIOR FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 4133  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-725-330-11

Query Match 45.2%; Score 1787; DB 54; Length 4133;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2177; Conservative 0; Mismatches 3; Indels 3; Gaps 1;  
QY 1745 ACTCCCTGAGAGACCAAGCCCAACCTGCTGCTTCCAGCCTCCATGACCCGG 1804  
Db 1784 ACTCCCTGAGAGACCAAGCCCAACCTGCTGCTTCCAGCCTCCATGACCCGG 1843  
QY 1805 ACCCTGCAATCCCGCAACCACTGCAAGCCCAAGTCCCGAGAGCTGTCATCCGCA 1864  
Db 1844 ACCCTGCAATCCCGCAACCACTGCAAGCCCAAGTCCCGAGAGCTGTCATCCGCA 1903  
QY 1865 ATTGAGACCCCACTCTGAAGACTGTGCTGCAAGCCCAAGTCCCGAGCTGCTGCTG 1924  
Db 1904 ATTGAGACCCCACTCTGAAGACTGTGCTGCAAGCCCAAGTCCCGAGCTGCTGCTG 1963  
QY 1925 CAGATTAAGAGCCCAACCAAGTCCCTCAAGAGCTTATATGCGACATGCGCTTA 1984  
Db 1964 CAGATTAAGAGCCCAACCAAGTCCCTCAAGAGCTTATATGCGACATGCGCTTA 2023  
QY 1985 ACACGAGTGGGCGGAGGGTCCCGGCAAGCCCAAGCAATCCGTCAGACCTCGAGCA 2044  
Db 2024 ACACGAGTGGGCGGAGGGTCCCGGCAAGCCCAAGCAATCCGTCAGACCTCGAGCA 2083  
QY 2045 ACTCGGCTGGCAATCTATCTGCAAAAGCGGGCAGAGCGGGGCAACCCCAAGCTCCAG 2104  
Db 2084 ACTCGGCTGGCAATCTATCTGCAAAAGCGGGCAGAGCGGGGCAACCCCAAGCTCCAG 2143

QY 2105 GAGCCCTGCTCAAGCCCTGAGCCCGCAACGCTCTAATGTAACCCCAAGCTCAGAGGA 2164  
Db 2144 GAGCCCTGCTCAAGCCCTGAGCCCGCAACGCTCTAATGTAACCCCAAGCTCAGAGGA 2203  
QY 2165 GCGACCTGCTGAGGAAGCTGCGACAGCTGCTTCCAGCTCTCAAGGCACTCTCCG 2224  
Db 2204 GCGACCTGCTGAGGAAGCTGCGACAGCTGCTTCCAGCTCTCAAGGCACTCTCCG 2263  
QY 2225 AGGCTGCTCACTGAGAGGGAACCGGCTGAGAGCTCTCCAAACTGACAGCTCCCTG 2284  
Db 2264 AGGCTGCTCACTGAGAGGGAACCGGCTGAGAGCTCTCCAAACTGACAGCTCCCTG 2323  
QY 2285 TGCTCTCCCTGAGGAATTAAGCAAGCCCGACGACCAAGCTCTCAAGGCAAGCTCCG 2344  
Db 2324 TGCTCTCCCTGAGGAATTAAGCAAGCCCGACGACCAAGCTCTCAAGGCAAGCTCCG 2383  
QY 2345 CAGACTTTGTGTGCTGAAGAGCGGACTCTGAGAGAGGCTCTGAGCTTCCAAAGAG 2404  
Db 2384 CAGACTTTGTGTGCTGAAGAGCGGACTCTGAGAGAGGCTCTGAGCTTCCAAAGAG 2443  
QY 2405 CCAATGACTACTCTGCTGCTCAAGCGAGGAGTGAAGCAATGAGGACGACGAGGAG 2464  
Db 2444 CCAATGACTACTCTGCTGCTCAAGCGAGGAGTGAAGCAATGAGGAGGAGGAGGAG 2503  
QY 2465 GCGAAGCGGCGCAGACAGAGGAGGAGCAGAGATACCTCTGAGGCGCCGACGATGAG 2524  
Db 2504 GCGAAGCGGCGCAGACAGAGGAGGAGGAGATACCTCTGAGGCGCCGACGATGAG 2560  
QY 2525 CAGACAGCTGACCAATGCTGTGTCACAGCTGAGAGATTCACCGGACCCAGCCG 2584  
Db 2561 CAGACAGCTGACCAATGCTGTGTCACAGCTGAGAGATTCACCGGACCCAGCCG 2620  
QY 2585 CATACGGGGGCGGACCAATGCTGTGTCACAGCTGAGAGATTCACCGGACCCAGCCG 2644  
Db 2621 CATACGGGGGCGGACCAATGCTGTGTCACAGCTGAGAGATTCACCGGACCCAGCCG 2680  
QY 2645 ATGCTGACAGCAATGCTGTGTCACAACTGCTGAGCTGAGCTGAGCTGAGCTGAG 2704  
Db 2681 ATGCTGACAGCAATGCTGTGTCACAACTGCTGAGCTGAGCTGAGCTGAGCTGAG 2740  
QY 2705 CCGAAGACGCAAGAGCCCAAGCCCACTGAGAGAGTGGAGTGTGTAACCTGCTG 2764  
Db 2741 CCGAAGACGCAAGAGCCCAAGCCCACTGAGAGAGTGGAGTGTGTAACCTGCTG 2800  
QY 2765 GTGGCTGTGAAGGCTGCTGAGAGCTGCTGAGAGTGTGTAACCTGCTGAGAGCT 2824  
Db 2801 GTGGCTGTGAAGGCTGCTGAGAGCTGCTGAGAGTGTGTAACCTGCTGAGAGCT 2860  
QY 2825 ACCAGCTGAGAGCAGTGGGAGCAGCATCCCATCAAGCCCTAGTGGGTGAGAGGCA 2884  
Db 2861 ACCAGCTGAGAGCAGTGGGAGCAGCATCCCATCAAGCCCTAGTGGGTGAGAGGCA 2920  
QY 2885 CTGGCTGACCACTGACATGACGATGAGAGAGGTTCTGTGTCAACGTGAATCCCA 2944  
Db 2921 CTGGCTGACCACTGACATGACGATGAGAGAGGTTCTGTGTCAACGTGAATCCCA 2980  
QY 2945 CCAAGACCCGGGCGCAAGTGAACCCCTGAGATCCGGAAGTGAAGAGGCAATCACT 3004  
Db 2981 CCAAGACCCGGGCGCAAGTGAACCCCTGAGATCCGGAAGTGAAGAGGCAATCACT 3040  
QY 3005 CCGAGATCTCTGTGCAAGCCCTTTGGGGGCTCAACCTGCTGTGGGCAAGGAGAG 3064  
Db 3041 CCGAGATCTCTGTGCAAGCCCTTTGGGGGCTCAACCTGCTGTGGGCAAGGAGAG 3100  
QY 3065 TGATGTGCTGAGCCGAAGTGGGAGGCGCAAGCTGATGACTATTGGGCGGACGCT 3124  
Db 3101 TGATGTGCTGAGCCGAAGTGGGAGGCGCAAGCTGATGACTATTGGGCGGACGCT 3160  
QY 3125 TCCAGCAATGATGTGCTGAGAGGCTCAACCTGCTCATCACTTCAGGGAAGAGGA 3184  
Db 3161 TCCAGCAATGATGTGCTGAGAGGCTCAACCTGCTCATCACTTCAGGGAAGAGGA 3220

QY	3185	CAAACTGCGGGTGTATTACCTGTCGTGGCTCCGGAAACAAGTTCTGACAATGACCCAG	3244
Db	3221	ACAACTCGGGTGTATTACTGTCTCTGGCTCCGGAAACAAGTTCTGACAATGACCCAG	3280
QY	3245	AAGTGAAGAAGACGAGGGCTGGAACACCGTGGGGGACATGGAGGGCTGCGGGCACTAC	3304
Db	3281	AAGTGAAGAAGAAGAGGGCTGGACCAACGTGGGGGACATGGAGGGCTGCGGGCACTAC	3340
QY	3305	GTGTTGTGAATAACGAGCGGATTAAAGTTCTGTGTATGCTCCCTCAAGACTCCGTGAGG	3364
Db	3341	GTGTTGTGAATAACGAGCGGATTAAAGTTCTGTGTATGCTCCCTCAAGACTCCGTGAGG	3400
QY	3365	TGTATGCTGGGGCCCCCAAAACCTTACCAAAATTGATGGCTTCAAGTCTTTTGGCGAC	3424
Db	3401	TGTATGCTGGGGCCCCCAAAACCTTACCAAAATTATGAGCTTCAAGTCTTTTGGCGAC	3460
QY	3425	TCCCCACCGGCTCTGTCTGTGTGCACTGACAGTGAAGAGGGGACAGCGGCTCAAGTCA	3488
Db	3461	TCCCCACCGGCTCTGTCTGTGTGCACTGACAGTGAAGAGGGGACAGCGGCTCAAGTCA	3520
QY	3485	TCTATGCGTCCAGTGTGAGCTTCCATGCTGTGATGTGCACTCGGGGAAACAGCTATGCA	3544
Db	3521	TCTATGCGTCCAGTGTGAGCTTCCATGCTGTGATGTGCACTCGGGGAAACAGCTATGCA	3580
QY	3545	TCTATATCTCCCTGTGCAACTCCAGAGCCAGATTCAGCCCCCATGCCATCATCTTCTCCCCA	3604
Db	3581	TCTATATCTCCCTGTGCAACTCCAGAGCCAGATTCAGCCCCCATGCCATCATCTTCTCCCCA	3640
QY	3605	ACACCGACGGGATGGAGATGCTGCTGTGTCTACAGAGACGAGGGTGTCTACGTCAAACGT	3664
Db	3641	ACACCGACGGGATGGAGATGCTGCTGTGTCTACAGAGACGAGGGTGTCTACGTCAAACGT	3700
QY	3665	ACGGGCGGCATATTAAAGGATGTGTGTCTGCAGTGGGGGGAGATGCTACTTCTGTGAGCT	3724
Db	3701	ACGGGCGGCATATTAAAGGATGTGTGTCTGCAGTGGGGGGAGATGCTACTTCTGTGAGCT	3760
QY	3725	ACATCTGTCTCCAAACCAAGTAATGGGCTGGGGTGAAGAAAGCCATTGAGTCCGCTGTGG	3784
Db	3761	ACATCTGTCTCCAAACCAAGTAATGGGCTGGGGTGAAGAAAGCCATTGAGTCCGCTGTGG	3820
QY	3785	AGAGGGGCGACCTGAGCGGGGCTTCATGCAAAACGAGCTCAGAGGCTCAAGTTCCTGT	3844
Db	3821	AGAGGGGCGACCTGAGCGGGGCTTCATGCAAAACGAGCTCAGAGGCTCAAGTTCCTGT	3880
QY	3845	GTGAGCGGATGACAAAGGTGTTTTTGTGCTCAGTCCGCTGTGGGGGACAGCCAAAGTTT	3904
Db	3881	GTGAGCGGATGACAAAGGTGTTTTTGTGCTCAGTCCGCTGTGGGGGACAGCCAAAGTTT	3940
QY	3905	ACTTCATGACTCTGAAACCGTTAC	3927
Db	3941	ACTTCATGACTCTGAAACCGTTAC	3963
RESULT 10			
US-60-081-784-11			
; Sequence 11, Application US/60081784			
; GENERAL INFORMATION:			
; APPLICANT: GREGORY PLOWMAN and			
; APPLICANT: RICARDO MARTINEZ			
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES			
; NUMBER OF SEQUENCES: 95			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Lyon & Lyon			
; STREET: 633 West Fifth Street			
; CITY: Suite 4700			
; CITY: Los Angeles			
; STATE: California			
; COUNTRY: U.S.A.			
; ZIP: 90071-2066			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb			
; MEDIUM TYPE: Storage			
; COMPUTER: IBM Compatible			

	OPERATING SYSTEM:	IBM P.C.	DOS 5.0
	SOFTWARE:	Fasteo for Windows	2.0
	CURRENT APPLICATION DATA:		
	APPLICATION NUMBER:	US/60/081.784	
	FILING DATE:	Filed Herewith	
	CLASSIFICATION:		
	PRIOR APPLICATION DATA:		
	APPLICATION NUMBER:		
	FILING DATE:		
	ATTORNEY/AGENT INFORMATION:		
	NAME:	Wardburg, Richard J.	
	REGISTRATION NUMBER:	32,327	
	REFERENCE/DOCKET NUMBER:	232/279	
	TELECOMMUNICATION INFORMATION:		
	TELEPHONE:	(213) 489-1600	
	TELEFAX:	(213) 955-0440	
	TELEX:	67-3510	
	INFORMATION FOR SEQ ID NO:	11:	
	SEQUENCE CHARACTERISTICS:		
	LENGTH:	4133 base pairs	
	TYPE:	nucleic acid	
	STRANDEDNESS:	single	
	TOPOLOGY:	linear	
	FEATURES:		
	OTHER INFORMATION:	Mammalian (Human)	ZC3
	US-60-081-784-11		
Query Match	Best Local Similarity	45.2%; Score 1787; DB 64; Length 4133;	
	Matches 2177; Conservative	99.7%; Pred. No. 0; Mismatches 3; Indels 3; Gaps 1,	
OY	1745 AGTCCCTGCAGACCAACCACCGGAAACTGGCTGCTTTCCAGACCTCCCATGACCCC	1804	
Db	1784 AGTCCTGCAGACCAACCACCGGAAACTGGCTGCTTTCCAGACCTCCCATGACCCC	1843	
OY	1805 ACCGCGCATCCCCGACCACTGCACAGCGCCAGTGCCGAGAGCTGTATCCGCCAGA	1864	
Db	1844 ACCGCGCATCCCCGACCACTGCACAGCGCCAGTGCCGAGAGCTGTATCCGCCAGA	1904	
OY	1865 ATTGAGACCCCACTGTGAAGACCTGGCCCCAGCCCGAATCCCCCAAGCTTGGTCCGC	1924	
Db	1904 ATTGAGACCCCACTGTGAAGACCTGGCCCCAGCCCGAATCCCCCAAGCTTGGTCCGC	1964	
OY	1925 CAGATTAACGAGGCCCAACCCMAAGTGCTTCAGAGAACCTCATATGCGCACTGCGCTTA	1984	
Db	1964 CAGATTAACGAGGCCCAACCCMAAGTGCTTCAGAGAACCTCATATGCGCACTGCGCTTA	2024	
OY	1985 ACACCACTGGGGCCGGAGGGTCCGGCCAGCCAGCAAGTCCGTGCGCAAGCTTGGCAGCA	2044	
Db	2024 ACACCACTGGGGCCGGAGGGTCCGGCCAGCCAGCAAGTCCGTGCGCAAGCTTGGCAGCA	2084	
OY	2045 ACTCCGCTGGCAATCTATCTGCAAAAGCGGAGAGCGGGAGCACCCCAAAGCTCCAG	2104	
Db	2084 ACTCCGCTGGCAATCTATCTGCAAAAGCGGAGAGCGGGAGCACCCCAAAGCTCCAG	2144	
OY	2105 GGCCCGCTGCTCAGCCCCCTGGCCCGCCCAAGCGCTCTAGTAACCTCGACCTCAGAGGA	2164	
Db	2144 GGCCCGCTGCTCAGCCCCCTGGCCCGCCCAAGCGCTCTAGTAACCTCGACCTCAGAGGA	2204	
OY	2165 GCAGACCTGGGTGGGAACGCTCGGACAGCGTCTTCCAAGCTCTCAGGGGACCTTCCCC	2224	
Db	2204 GCAGACCTGGGTGGGAACGCTCGGACAGCGTCTTCCAAGCTCTCAGGGGACCTTCCCC	2244	
OY	2225 AGGCTGGGTCACTGGAGGGAAACGCGTGGAGGCTCTCCAACTGGACAGCTCCCTG	2284	
Db	2264 AGGCTGGGTCACTGGAGGGAAACGCGTGGAGGCTCTCTCCAAACGGACAGCTCCCTG	2324	
OY	2285 TGCTCTCCCTGGGAATAAAGCCCAAGCCGACGACACACGCTCAAGGCGAAGCGGCGCG	2344	
Db	2324 TGCTCTCCCTGGGAATAAAGCCCAAGCCGACGACACACGCTCAAGGCGAAGCGGCGCG	2384	
OY	2345 CAGACTTTGTCTCTGAAAAGGCGAAGCTGACGAGGCGCCCTCGGCTTCCCAAGAGG	2404	



Db 2384 CAGACTTGTGTGCTGTAAGAGCGGACTCTGACGAGGCGCTCGGCTCCCAAGAGG 2443  
 QY 2405 CCATGAGCTATCTGCTGCTCCAGCGAGGAGTGAAGAGAGTGAAGACGACGAGGAGAG 2464  
 Db 2444 CCATGAGCTATCTGCTGCTCCAGCGAGGAGTGAAGAGAGTGAAGACGACGAGGAGAG 2503  
 QY 2465 GCGAAGCGGCGCGACGAGGAGGAGAGATACCCCTGGGGGCGCGACGATGGGGATA 2524  
 Db 2504 GCGAAGCGGCGCGACGAGGAGGAGAGATACCCCTGGGGGCGCGATGGGGATA 2560  
 QY 2525 CAGACAGCGTCAACCATGATGCTGTCACGACGTGAGAGATCAACCGGAGCCCGCCG 2584  
 Db 2561 CAGACAGCGTCAACCATGATGCTGTCACGACGTGAGAGATCAACCGGAGCCCGCCG 2620  
 QY 2585 CATAGCGGGGCGCGACCATGATGCTGTCACGACGTGAGAGATCAACCGGAGCCCGCCG 2644  
 Db 2621 CATAGCGGGGCGCGACCATGATGCTGTCACGACGTGAGAGATCAACCGGAGCCCGCCG 2680  
 QY 2645 ATGCTGACGACGATGAGTACCAAACTGTCAGCTGAGTCCAGCCGACCTGACCCA 2704  
 Db 2681 ATGCTGACGACGATGAGTACCAAACTGTCAGCTGAGTCCAGCCGACCTGACCCA 2740  
 QY 2705 CCGAAGACGACGAGGCGCAAGCCCACTCGAAGAGTGGAGTGGTGACTACAGTCTC 2764  
 Db 2741 CCGAAGACGACGAGGCGCAAGCCCACTCGAAGAGTGGAGTGGTGACTACAGTCTC 2800  
 QY 2765 GTGGGCTGGTAAAGCCCTGCGACAGAGTCTGTTACGATGTTGGATCTAGGGATCT 2824  
 Db 2801 GTGGGCTGGTAAAGCCCTGCGACAGAGTCTGTTACGATGTTGGATCTAGGGATCT 2860  
 QY 2825 ACCAGCTGGAGGAGTGGGAGCAGCATCCCATCAACGAGCTAGTGGTGAAGAGGCA 2884  
 Db 2861 ACCAGCTGGAGGAGTGGGAGCAGCATCCCATCAACGAGCTAGTGGTGAAGAGGCA 2920  
 QY 2885 CTGGCTGCAACGACTGCACTGACGATGAGAGAGGTTCTGTGCTCAACGATCCCA 2944  
 Db 2921 CTGGCTGCAACGACTGCACTGACGATGAGAGAGGTTCTGTGCTCAACGATCCCA 2980  
 QY 2945 CCAACACCCCGGCGCAAGTGAAGACCCCGATCCGGAAGTCAAGAGGCAATCAACT 3004  
 Db 2981 CCAACACCCCGGCGCAAGTGAAGACCCCGATCCGGAAGTCAAGAGGCAATCAACT 3040  
 QY 3005 CCGAGATCTCTGTGAGCCCTTTGGGGGGTCAACCTGCTGTGGCAAGAGAGAGGCG 3064  
 Db 3041 CCGAGATCTCTGTGAGCCCTTTGGGGGGTCAACCTGCTGTGGCAAGAGAGAGGCG 3100  
 QY 3065 TGATGTTGCTGAGCCGAGTGGCGAGGGCAAGGTGATGAGTCAATGGGCGCGACCT 3124  
 Db 3101 TGATGTTGCTGAGCCGAGTGGCGAGGGCAAGGTGATGAGTCAATGGGCGCGACCT 3160  
 QY 3125 TCCAGAGATGATGCTGAGGGGGCTCAACCTGCTCAATCAACCTCAGGGAGAGGA 3184  
 Db 3161 TCCAGAGATGATGCTGAGGGGGCTCAACCTGCTCAATCAACCTCAGGGAGAGGA 3220  
 QY 3185 ACAAACTGCGGGTGTATTAACCTGCTCCGGAACAAGATTGCAAAATGACCCAG 3244  
 Db 3221 ACAAACTGCGGGTGTATTAACCTGCTCCGGAACAAGATTGCAAAATGACCCAG 3280  
 QY 3245 AAGTGAGAGAGAGAGGCGCTGAGCAACGTTGGGGGACATGAGGGCTGGGCACTACC 3304  
 Db 3281 AAGTGAGAGAGAGAGGCGCTGAGCAACGTTGGGGGACATGAGGGCTGGGCACTACC 3340  
 QY 3305 GTGTTGTGAATAACGAGCGGATTAAGTTCCTGCTCAATCCCTCAAGAGCTCCGTGAGG 3364  
 Db 3341 GTGTTGTGAATAACGAGCGGATTAAGTTCCTGCTCAATCCCTCAAGAGCTCCGTGAGG 3400  
 QY 3365 TGTATGCTGGGCGCCCAACCTCAACAATTCATGAGCTCTTTCGCGAGC 3424  
 Db 3401 TGTATGCTGGGCGCCCAACCTCAACAATTCATGAGCTCTTTCGCGAGC 3460  
 QY 3425 TCCCCACCGCCTCTGCTGTGACCTGACAGTGAAGAGAGGGGCGAGGCTCAAGTCA 3484  
 Db 3461 TCCCCACCGCCTCTGCTGTGACCTGACAGTGAAGAGAGGGGCGAGGCTCAAGTCA 3520

QY 3485 TCTATGCTCCAGTCTGGCTTCCATGCTGTGATGTGCACTGGGGAACAGCTATGACA 3544  
 Db 3521 TCTATGCTCCAGTCTGGCTTCCATGCTGTGATGTGCACTGGGGAACAGCTATGACA 3580  
 QY 3545 TCTATGCTCCAGTCTGGCTTCCATGCTGTGATGTGCACTGGGGAACAGCTATGACA 3604  
 Db 3581 TCTATGCTCCAGTCTGGCTTCCATGCTGTGATGTGCACTGGGGAACAGCTATGACA 3640  
 QY 3605 AACCGAGGAGATGAGTGTGCTGTGCTGAGAGAGAGGATGTCAAGTCAACAGT 3664  
 Db 3641 AACCGAGGAGATGAGTGTGCTGTGCTGAGAGAGAGGATGTCAAGTCAACAGT 3700  
 QY 3665 ACGGCGCATATTAGAGTGTGCTGTGCAATGGGGGAGATGCTTCTGTGAGCT 3724  
 Db 3701 ACGGCGCATATTAGAGTGTGCTGTGCAATGGGGGAGATGCTTCTGTGAGCT 3760  
 QY 3725 ACATGCTCCAAACCAATTAAGGCTGGGGTGAAGAACCAATTGAGTCCGCTGTGG 3784  
 Db 3761 ACATGCTCCAAACCAATTAAGGCTGGGGTGAAGAACCAATTGAGTCCGCTGTGG 3820  
 QY 3785 AGAGGCGCACCTGAGGAGGCTTCAAGCAACAGAGCTCAGAGCTCAAGTTCTGT 3844  
 Db 3821 AGAGGCGCACCTGAGGAGGCTTCAAGCAACAGAGCTCAGAGCTCAAGTTCTGT 3880  
 QY 3845 GTGAGCGGAATGACAGGATGTTTTTGTGCTGAGTCCGCTGGGGGAGAGCCAAATT 3904  
 Db 3881 GTGAGCGGAATGACAGGATGTTTTTGTGCTGAGTCCGCTGGGGGAGAGCCAAATT 3940  
 QY 3905 ACTTATGATCTGTGACCGCTAAC 3927  
 Db 3941 ACTTATGATCTGTGACCGCTAAC 3963

RESULT 11  
 PCT-US02-33845-6  
 ; Sequence 6, Application PC/TUS0233845  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rigel Pharmaceuticals, Inc.  
 ; APPLICANT: Leo, Cindy  
 ; APPLICANT: Luo, Ying  
 ; APPLICANT: Xu, Xiang  
 ; APPLICANT: Yu, Simon  
 ; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE PROTEINS, COMPOSITIONS,  
 ; FILE REFERENCE: 021044-005600PC  
 ; CURRENT APPLICATION NUMBER: PCT/US02/33845  
 ; CURRENT FILING DATE: 2003-05-30  
 ; PRIOR APPLICATION NUMBER: US 10/029,115  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 6 4032  
 ; LENGTH: 4032  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: mishapen/NIK-related Kinase isoform c  
 PCT-US02-33845-6

Query Match 43.4%; Score 1714; DB 1; Length 4032;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 2154; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

QY 1745 AGTCCCTGAGAGACCAAGCCCAACCCGAAACCTGGCTGCTCCAGGCTCCCAATGACCCG 1804  
 Db 1836 AGTCCCTGAGAGACCAAGCCCAACCCGAAACCTGGCTGCTCCAGGCTCCCAATGACCCG 1895  
 QY 1805 ACCCTGCAATCCCGGACCACTGCGACGCGCCAGTGGCCGAGAGACTGTCAATCCGCGAGA 1864  
 Db 1896 ACCCTGCAATCCCGGACCACTGCGACGCGCCAGTGGCCGAGAGACTGTCAATCCGCGAGA 1955  
 QY 1865 ATTGACACCCACCTCTGAAAGAGCTGGGCCCAAGCCCAATCCCAAGCTGGGTCGGCC 1924



Db 1956 ATTGAGACCCCACTCTGTAAGGACCTGGCCCAAGCCCAATCCCACTGGGTTCCGC 2015  
Qy 1925 CAGATTAACGAGGCCCCCAACCCAGAGGCTCTGAGAGGACCTCATATGCTCCACTGCTTTA 1984  
Db 2016 CAGATTAACGAGGCCCCCAACCCAGAGGCTCTGAGAGGACCTCATATGCTCCACTGCTTTA 2075  
Qy 1985 ACACAGTGGGGCCGAGAGGTCCTCCGAGCCAGCCAGAGTCCGTGGCCAGACTCCGAGCA 2044  
Db 2076 ACACAGTGGGGCCGAGAGGTCCTCCGAGCCAGCCAGAGTCCGTGGCCAGACTCCGAGCA 2135  
Qy 2045 ACTCGGCTGGCAATCTATCTGCAAAAGGCGGCGAGAGCGGGGCAACCCCAAGCTCCAG 2104  
Db 2136 ACTCGGCTGGCAATCTATCTGCAAAAGGCGGCGAGAGCGGGGCAACCCCAAGCTCCAG 2195  
Qy 2105 GGGCCCTGCTGAGCCCTGAGCCCGCCCAACGCTCTAGTAAACCCGAGCTCAGAGGA 2164  
Db 2196 GGGCCCTGCTGAGCCCTGAGCCCGCCCAACGCTCTAGTAAACCCGAGCTCAGAGGA 2255  
Qy 2165 GCGACCTGCTGGGGAAGCTTCGAGACGCTCTTCCAGCTCTGACGCGGCACTCCGCC 2224  
Db 2256 GCGACCTGCTGGGGAAGCTTCGAGACGCTCTTCCAGCTCTGACGCGGCACTCCGCC 2315  
Qy 2225 AGGCTGCTCACTGAGCGGAAACGCTGGGAGCTCTCCCAACTGAGCAGCTCCCTG 2284  
Db 2316 AGGCTGCTCACTGAGCGGAAACGCTGGGAGCTCTCCCAACTGAGCAGCTCCCTG 2375  
Qy 2285 TGCTCTCCCTGGGAAATTAAGCCAGCCGAGCAGCAGCTCAGCGCCAGCGCGCCG 2344  
Db 2376 TGCTCTCCCTGGGAAATTAAGCCAGCCGAGCAGCAGCTCAGCGCCAGCGCGCCG 2435  
Qy 2345 CAGACTTTGTGTGTGTAAGAGCGGACTCTGAGAGAGGCTCTGCGCTCCCAAGAG 2404  
Db 2436 CAGACTTTGTGTGTGTAAGAGCGGACTCTGAGAGAGGCTCTGCGCTCCCAAGAG 2495  
Qy 2405 CCATGAGACTACTCTGCTCGCAAGCGAGGTGTAAGAGCAGTGAAGGACAGAGAGAG 2464  
Db 2496 CCATGAGACTACTCTGCTCGCAAGCGAGGTGTAAGAGCAGTGAAGGACAGAGAGAG 2555  
Qy 2465 GCGAAGGCGGCGCAGCAGAGGAGGAGCAGAGTACCCTGGGGGCGCAGCGATGAGGATA 2524  
Db 2556 GCGAAGGCGGCGCAGCAGAGGAGGAGCAGAGTACCCTGGGGGCGCAGCGATGAGGATA 2612  
Qy 2525 CAGACAGCTGACGACCATGCTGTCCAGACGCTGAGAGAGTCAACCGGAGCCAGGCC 2584  
Db 2613 CAGACAGCTGACGACCATGCTGTCCAGACGCTGAGAGAGTCAACCGGAGCCAGGCC 2672  
Qy 2585 CATACGGGGGCGGACCATGCTGTCCAGACGCTGAGAGAGGAGGAGGAGGAGGAGGAGG 2644  
Db 2673 CATACGGGGGCGGACCATGCTGTCCAGACGCTGAGAGAGGAGGAGGAGGAGGAGGAGG 2732  
Qy 2645 ATGCTGACAGCATGCTGTACCAAACTGCTGAGCTGAGCTGAGCCAGCTCAACCA 2704  
Db 2733 ATGCTGACAGCATGCTGTACCAAACTGCTGAGCTGAGCTGAGCCAGCTCAACCA 2792  
Qy 2705 CCGAGAACAGCAAAAGCCAAAGCCCACTTGAAGAGTGGAGTGTGATCAACAGTCTC 2764  
Db 2793 CCGAGAACAGCAAAAGCCCACTTGAAGAGTGGAGTGTGATCAACAGTCTC 2852  
Qy 2765 GTGGGCTGTAAAGGCTCTGAGCAAGCTGTGTTCAAGATGTTGTGATCTAGGAGTCT 2824  
Db 2853 GTGGGCTGTAAAGGCTCTGAGCAAGCTGTGTTCAAGATGTTGTGATCTAGGAGTCT 2912  
Qy 2825 ACAGAGCTGAGAGGAGTGGGAGCAGCATCCCATCAAGCCCTAGTGGTGGAGAGGCA 2884  
Db 2913 ACAGAGCTGAGAGGAGTGGGAGCAGCATCCCATCAAGCCCTAGTGGTGGAGAGGCA 2972  
Qy 2885 CTGGGCTGACAGCTGACGATGAGAGGAGGTTCTGTGTTCAAGTGAATCCCA 2944  
Db 2973 CTGGGCTGACAGCTGACGATGAGAGGAGGTTCTGTGTTCAAGTGAATCCCA 3032  
Qy 2945 CCAACACCCGGGCGCAGTGAAGCCCTGAGATCCGAGAGTAAAGAGGATTCACCT 3004

Db 3003 CCAACACCCGGGCGCAGTGAAGCCCTGAGATCCGAGATGAAGAGGATTCACCT 3092  
Qy 3005 CCGAGATCTCTTGTGACAGCTTTGGGGGGTCAACCTGCTGTGGGAGCAGGAAACGGGC 3064  
Db 3093 CCGAGATCTCTTGTGACAGCTTTGGGGGGTCAACCTGCTGTGGGAGCAGGAAACGGGC 3152  
Qy 3065 TGATGTTGCTGAGCCGAAAGTGGGAGGAGTGTATGACCTGATTTGGGCGGAGCCT 3124  
Db 3153 TGATGTTGCTGAGCCGAAAGTGGGAGGAGTGTATGACCTGATTTGGGCGGAGCCT 3212  
Qy 3125 TCAGAGATGATGATGCTGAGAGGAGGCTCAACCTGCTCATCAATCTCAGGAAAAAGGA 3184  
Db 3213 TCAGAGATGATGATGCTGAGAGGAGGCTCAACCTGCTCATCAATCTCAGGAAAAAGGA 3272  
Qy 3185 ACAACCTGCGGATTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3244  
Db 3273 ACAACCTGCGGATTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3332  
Qy 3245 AAGTGAAGAGAGCAGGAGCTGAGCAGCCGAGGAGGAGATGAGAGGCTGCGGAGCTAAC 3304  
Db 3333 AAGTGAAGAGAGCAGGAGCTGAGCAGCCGAGGAGGAGATGAGAGGCTGCGGAGCTAAC 3392  
Qy 3305 GTGTTGTAATTAAGAGCGATTAAGTTCCTGATCATGCTCAGAGCTCGTGAAG 3364  
Db 3393 GTGTTGTAATTAAGAGCGATTAAGTTCCTGATCATGCTCAGAGCTCGTGAAG 3452  
Qy 3365 TGATGCTTGGGCCCCCAACCTTACCAAAATTCATGCTTCAAGTCTTTGCGGAGC 3424  
Db 3453 TGATGCTTGGGCCCCCAACCTTACCAAAATTCATGCTTCAAGTCTTTGCGGAGC 3512  
Qy 3425 TCCGCCACCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3484  
Db 3513 TCCGCCACCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3572  
Qy 3485 TCTATGCTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3544  
Db 3573 TCTATGCTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3632  
Qy 3545 TCTATGCTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3604  
Db 3633 TCTATGCTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3692  
Qy 3605 ACAACGAGGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3664  
Db 3693 ACAACGAGGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3752  
Qy 3665 ACAGGCGCATCATTAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3724  
Db 3753 ACAGGCGCATCATTAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3812  
Qy 3725 ACATGCTCTCAACCAATATGAGGCTGGGGTGAAGGACATTAAGATCCGCTCTGTGG 3784  
Db 3813 ACATGCTCTCAACCAATATGAGGCTGGGGTGAAGGACATTAAGATCCGCTCTGTGG 3872  
Qy 3785 AGAGGGGCGCTCTGAGAGGAGGCTTTCATGCAAAACGAGCTCAGAGCTCAAGTTCCGT 3844  
Db 3873 AGAGGGGCGCTCTGAGAGGAGGCTTTCATGCAAAACGAGCTCAGAGCTCAAGTTCCGT 3932  
Qy 3845 GTGAGCGGAATGAAGAGTGTGTTTCTGCTCAGTCCCTCTGGGGGAGCAGCCAGTTT 3904  
Db 3933 GTGAGCGGAATGAAGAGTGTGTTTCTGCTCAGTCCCTCTGGGGGAGCAGCCAGTTT 3992  
Qy 3905 A 3905  
Db 3993 A 3993

RESULT 12  
PCT-US02-01048-37  
; Sequence 37, Application PC/RUS0201048  
; GENERAL INFORMATION:  
; APPLICANT: EXLIXIS, INC.  
; TITLE OF INVENTION: Modulating Insulin Receptor Signaling

FILE REFERENCE: EX02-001C-PC  
CURRENT APPLICATION NUMBER: PCT/US02/01048  
CURRENT FILING DATE: 2002-01-11  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 76  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 37  
LENGTH: 3888  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US02-01048-37

Query Match 43.1%; Score 1701; DB 1; Length 3888;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1801; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2143 AGTAAACCCGACCTCAGAGAGAGCCGCTGCTGGGAAAGCTCGACAGGCTCTTCCA 2202  
2086 AGTAAACCCGACCTCAGAGAGAGCCGCTGCTGGGAAAGCTCGACAGGCTCTTCCA 2145  
2203 GCTCTCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 2262  
2146 GCTCTCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 2205  
2263 TCCAACTGAGAGCTCCCTGCTCTCCCTGGGATTAAGCCAGCCGACGACAC 2322  
2206 TCCAAACGGGACCTCCCTGCTCTCCCTGGGATTAAGCCAGCCGACGACAC 2265  
2323 GCTCTCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 2382  
2266 GCTCTCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 2325  
2383 GCTCTCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 2442  
2326 GCTCTCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 2385  
2443 AGTGAAG 2502  
2386 AGTGAAG 2445  
2503 GGGGGCCGAGCGAGTGGGATACAGACAGCTGACAGCAATGGTGTCCAGCTCGAG 2562  
2446 GGGGGCCGAGCGAGTGGGATACAGACAGCTGACAGCAATGGTGTCCAGCTCGAG 2505  
2563 GAGATCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 2622  
2506 GAGATCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 2565  
2623 GAG 2682  
2566 GAG 2625  
2683 GTCAG 2742  
2626 GTCAG 2685  
2743 GGGAGTGGAGATCAACAGCTGCTGGGCTGGTAAAGGCTGGGAGAGAGCTGTTCA 2802  
2686 GGGAGTGGAGATCAACAGCTGCTGGGCTGGTAAAGGCTGGGAGAGAGCTGTTCA 2745  
2803 ATGTTTGGAGATCAACAGCTGCTGGGCTGGTAAAGGCTGGGAGAGAGCTGTTCA 2862  
2746 ATGTTTGGAGATCAACAGCTGCTGGGCTGGTAAAGGCTGGGAGAGAGCTGTTCA 2805  
2863 GCTCTCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 2922  
2806 GCTCTCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 2865  
2923 TCTGGTGGAG 2982  
2866 TCTGGTGGAG 2925  
2983 AAGTAAAGAGAGAGATCACTCCGAGATCTCTGTGCAAGCCCTTGGGGGCTCAACTG 3042

2926 AAGTAAAGAGAGAGATCACTCCGAGATCTCTGTGCAAGCCCTTGGGGGCTCAACTG 2985  
3043 CTGGTGGAG 3102  
2986 CTGGTGGAT 3045  
3103 GAGATCACTGGAT 3162  
3046 GAGATCACTGGAT 3105  
3163 ATCAACATCTGAT 3222  
3106 ATCAACATCTGAT 3165  
3223 AAGATTCGACCAATGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 3282  
3166 AAGATTCGACCAATGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 3225  
3283 ATGAT 3342  
3226 ATGAT 3285  
3343 GCTCTCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 3402  
3286 GCTCTCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 3345  
3403 GCTCTCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 3462  
3346 GCTCTCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 3405  
3463 GAGGGGAT 3522  
3406 GAGGGGAT 3465  
3523 GACTGGGGAT 3582  
3466 GACTGGGGAT 3525  
3583 CATGCAATCACTCTCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 3642  
3526 CATGCAATCACTCTCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 3585  
3643 GAGGAGTGTCTAAGTCAACAGTACGAGGAGATCAATTAAGATGGTGTCTGAGTGG 3702  
3586 GAGGAGTGTCTAAGTCAACAGTACGAGGAGATCAATTAAGATGGTGTCTGAGTGG 3645  
3703 GAGATGCTTACTTCTGTGGCTTCACTTGTCTTCAACAGATTAATGGGCTGGGATGA 3762  
3646 GAGATGCTTACTTCTGTGGCTTCACTTGTCTTCAACAGATTAATGGGCTGGGATGA 3705  
3763 GCTCTCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 3822  
3706 GCTCTCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 3765  
3823 GCTCTCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 3882  
3766 GCTCTCAACGGGACCTCCCGAGCTGCTCACTGGAGCGGAACCGGCTGGAGCTCC 3825  
3883 TCTGGGGAT 3942  
3826 TCTGGGGAT 3885  
3943 TGA 3945  
3886 TGA 3888

RESULT 13  
PCT-US03-37730-21  
Sequence 21, Application PCT/US0337730  
GENERAL INFORMATION:  
APPLICANT: EXELIXIS, INC.





Qy	GAGATGCCCTACTTCGTGCGCCTACATCTGCCTCAACCGAGTAATGGCTGGGGTGAAGAA	3703
Db	GAGATGCCCTACTTCGTGCGCCTACATCTGCCTCAACCGAGTAATGGCTGGGGTGAAGAA	3646
Qy	GCCATTGAGATCCGCTCTGTGGAGACGGGCGCACCTCGACGGGGTCTTCATGCACAAGA	3763
Db	GCCATTGAGATCCGCTCTGTGGAGACGGGCGCACCTCGACGGGGTCTTCATGCACAAGA	3706
Qy	GCTAAGAGGCTCAAGTTCTCTGTGAGGCGAATGACAAGGTTGTTTTTGCTCAAGTCCGC	3823
Db	GCTAAGAGGCTCAAGTTCTCTGTGAGGCGAATGACAAGGTTGTTTTTGCTCAAGTCCGC	3766
Qy	TCTGGGGGCGACGCGCAAGTTTACTTCATGACTCTGAAACCGTAACGTGCATCATGAATCG	3883
Db	TCTGGGGGCGACGCGCAAGTTTACTTCATGACTCTGAAACCGTAACGTGCATCATGAATCG	3826
Qy	TGA 3945	
Db	TGA 3888	

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RESULT 15
US-10-170-235-34328
; Sequence 34328, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; FILE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
; FILE REFERENCE: C0001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 34328
; LENGTH: 4436
; TYPE: DNA
; ORGANISM: HUMAN
; US-10-170-235-34328

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Job time : 8040 secs



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OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 20:03:44 ; Search time 69 Seconds  
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9646.236 Million cell updates/sec

Title: US-10-029-115-1

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
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#### SUMMARIES

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4	26	0.7	549	1 PCT-US03-13184-19	Sequence 19, Appl
5	26	0.7	549	6 US-10-424-986-19	Sequence 19, Appl
6	26	0.7	676	6 US-10-767-701-26464	Sequence 26464, A
7	26	0.7	3786	5 US-09-744-794C-46	Sequence 46, Appl
8	24	0.6	81440	6 US-10-451-467A-659	Sequence 659, Appl
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11	22	0.6	829	6 US-10-767-701-10485	Sequence 10485, A
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223	17	0.4	201	6	US-10-767-471-3741	Sequence 3741, Ap
224	17	0.4	201	6	US-10-767-471-3749	Sequence 3775, Ap
225	17	0.4	201	6	US-10-767-471-3775	Sequence 3775, Ap
226	17	0.4	201	6	US-10-767-471-3818	Sequence 3818, Ap
227	17	0.4	201	6	US-10-767-471-3825	Sequence 3825, Ap
228	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
229	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
230	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
231	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
232	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
233	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
234	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
235	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
236	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
237	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
238	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
239	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
240	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
241	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
242	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
243	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
244	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap
245	17	0.4	201	6	US-10-767-471-3826	Sequence 3826, Ap

C 246	17	0.4	201	6	US-10-767-471-6185	Sequence 6185, Ap	C 319	17	0.4	426	6	US-10-767-701-17752	Sequence 17752, A
C 247	17	0.4	201	6	US-10-767-471-6190	Sequence 6190, Ap	C 320	17	0.4	426	6	US-10-773-236-183	Sequence 183, App
C 248	17	0.4	201	6	US-10-767-471-6202	Sequence 6202, Ap	C 321	17	0.4	445	6	US-10-767-701-18780	Sequence 18790, A
C 249	17	0.4	201	6	US-10-767-471-6207	Sequence 6207, Ap	C 322	17	0.4	449	6	US-10-767-701-20747	Sequence 20747, A
C 250	17	0.4	201	6	US-10-767-471-6218	Sequence 6218, Ap	C 323	17	0.4	455	6	US-10-767-701-16556	Sequence 15556, A
C 251	17	0.4	201	6	US-10-767-471-6223	Sequence 6223, Ap	C 324	17	0.4	455	6	US-10-767-701-22346	Sequence 22346, A
C 252	17	0.4	201	6	US-10-767-471-6233	Sequence 6233, Ap	C 325	17	0.4	472	6	US-10-767-701-14585	Sequence 14585, A
C 253	17	0.4	201	6	US-10-767-471-6243	Sequence 6243, Ap	C 326	17	0.4	472	6	US-10-767-701-28439	Sequence 28439, A
C 254	17	0.4	201	6	US-10-767-471-6253	Sequence 6253, Ap	C 327	17	0.4	475	6	US-10-767-701-957	Sequence 957, App
C 255	17	0.4	201	6	US-10-767-471-6263	Sequence 6263, Ap	C 328	17	0.4	477	6	US-10-767-701-122309	Sequence 122309, A
C 256	17	0.4	201	6	US-10-767-471-6273	Sequence 6273, Ap	C 329	17	0.4	480	6	US-10-767-701-18117	Sequence 18117, A
C 257	17	0.4	201	6	US-10-767-471-6283	Sequence 6283, Ap	C 330	17	0.4	482	6	US-10-767-701-13654	Sequence 13654, A
C 258	17	0.4	201	6	US-10-767-471-6293	Sequence 6293, Ap	C 331	17	0.4	489	6	US-10-767-701-21098	Sequence 21098, A
C 259	17	0.4	201	6	US-10-767-471-6303	Sequence 6303, Ap	C 332	17	0.4	490	6	US-10-767-701-15747	Sequence 15747, A
C 260	17	0.4	201	6	US-10-767-471-6313	Sequence 6313, Ap	C 333	17	0.4	493	6	US-10-767-701-29436	Sequence 29436, A
C 261	17	0.4	201	6	US-10-767-471-6323	Sequence 6323, Ap	C 334	17	0.4	493	6	US-10-767-701-31233	Sequence 31233, A
C 262	17	0.4	201	6	US-10-767-471-6333	Sequence 6333, Ap	C 335	17	0.4	502	6	US-10-767-701-22439	Sequence 22439, A
C 263	17	0.4	201	6	US-10-767-471-6343	Sequence 6343, Ap	C 336	17	0.4	507	6	US-10-767-701-22107	Sequence 22107, A
C 264	17	0.4	201	6	US-10-767-471-6353	Sequence 6353, Ap	C 337	17	0.4	513	6	US-10-767-701-22544	Sequence 22544, A
C 265	17	0.4	201	6	US-10-767-471-6363	Sequence 6363, Ap	C 338	17	0.4	514	6	US-10-767-701-1047	Sequence 1047, Ap
C 266	17	0.4	201	6	US-10-767-471-6373	Sequence 6373, Ap	C 339	17	0.4	518	6	US-10-767-701-16187	Sequence 16187, A
C 267	17	0.4	201	6	US-10-767-471-6383	Sequence 6383, Ap	C 340	17	0.4	519	6	US-10-767-701-23039	Sequence 23039, A
C 268	17	0.4	201	6	US-10-767-471-6393	Sequence 6393, Ap	C 341	17	0.4	521	6	US-10-767-701-4639	Sequence 4639, Ap
C 269	17	0.4	201	6	US-10-767-471-6403	Sequence 6403, Ap	C 342	17	0.4	524	6	US-10-767-701-28854	Sequence 28854, A
C 270	17	0.4	201	6	US-10-767-471-6413	Sequence 6413, Ap	C 343	17	0.4	526	6	US-10-767-701-21490	Sequence 21490, A
C 271	17	0.4	201	6	US-10-767-471-6423	Sequence 6423, Ap	C 344	17	0.4	527	6	US-10-767-701-24650	Sequence 24650, A
C 272	17	0.4	201	6	US-10-767-471-6433	Sequence 6433, Ap	C 345	17	0.4	527	6	US-10-767-701-29434	Sequence 29434, A
C 273	17	0.4	201	6	US-10-767-471-6443	Sequence 6443, Ap	C 346	17	0.4	528	6	US-10-767-701-3459	Sequence 3459, Ap
C 274	17	0.4	201	6	US-10-767-471-6453	Sequence 6453, Ap	C 347	17	0.4	528	6	US-10-767-701-28700	Sequence 28700, A
C 275	17	0.4	201	6	US-10-767-471-6463	Sequence 6463, Ap	C 348	17	0.4	529	6	US-10-767-701-1352	Sequence 1352, Ap
C 276	17	0.4	201	6	US-10-767-471-6473	Sequence 6473, Ap	C 349	17	0.4	529	6	US-10-767-701-26767	Sequence 26767, A
C 277	17	0.4	201	6	US-10-767-471-6483	Sequence 6483, Ap	C 350	17	0.4	531	6	US-10-767-701-3219	Sequence 3219, Ap
C 278	17	0.4	201	6	US-10-767-471-6493	Sequence 6493, Ap	C 351	17	0.4	531	6	US-10-767-701-20525	Sequence 20525, A
C 279	17	0.4	201	6	US-10-767-471-6503	Sequence 6503, Ap	C 352	17	0.4	534	6	US-10-767-701-2093	Sequence 2093, Ap
C 280	17	0.4	201	6	US-10-767-471-6513	Sequence 6513, Ap	C 353	17	0.4	538	6	US-10-767-701-4099	Sequence 4099, A
C 281	17	0.4	201	6	US-10-767-471-6523	Sequence 6523, Ap	C 354	17	0.4	538	6	US-10-767-701-25663	Sequence 25663, A
C 282	17	0.4	201	6	US-10-767-471-6533	Sequence 6533, Ap	C 355	17	0.4	541	6	US-10-767-701-30710	Sequence 30710, A
C 283	17	0.4	201	6	US-10-767-471-6543	Sequence 6543, Ap	C 356	17	0.4	546	6	US-10-767-701-26891	Sequence 26891, A
C 284	17	0.4	201	6	US-10-767-471-6553	Sequence 6553, Ap	C 357	17	0.4	548	6	US-10-770-021-48	Sequence 48, App1
C 285	17	0.4	201	6	US-10-767-471-6563	Sequence 6563, Ap	C 358	17	0.4	549	6	US-10-767-701-22708	Sequence 22708, A
C 286	17	0.4	201	6	US-10-767-471-6573	Sequence 6573, Ap	C 359	17	0.4	550	6	US-10-767-701-4187	Sequence 4187, Ap
C 287	17	0.4	201	6	US-10-767-471-6583	Sequence 6583, Ap	C 360	17	0.4	550	6	US-10-767-701-1623	Sequence 1623, Ap
C 288	17	0.4	201	6	US-10-767-471-6593	Sequence 6593, Ap	C 361	17	0.4	553	6	US-10-767-701-28729	Sequence 28729, A
C 289	17	0.4	201	6	US-10-767-471-6603	Sequence 6603, Ap	C 362	17	0.4	556	6	US-10-767-701-31023	Sequence 31023, A
C 290	17	0.4	201	6	US-10-767-471-6613	Sequence 6613, Ap	C 363	17	0.4	559	6	US-10-767-701-6197	Sequence 6197, Ap
C 291	17	0.4	201	6	US-10-767-471-6623	Sequence 6623, Ap	C 364	17	0.4	562	6	US-10-767-701-26537	Sequence 26537, A
C 292	17	0.4	201	6	US-10-767-471-6633	Sequence 6633, Ap	C 365	17	0.4	563	6	US-10-767-701-1936	Sequence 1936, Ap
C 293	17	0.4	201	6	US-10-767-471-6643	Sequence 6643, Ap	C 366	17	0.4	564	6	US-10-767-701-30941	Sequence 30941, A
C 294	17	0.4	201	6	US-10-767-471-6653	Sequence 6653, Ap	C 367	17	0.4	567	6	US-10-767-701-20568	Sequence 20568, A
C 295	17	0.4	201	6	US-10-767-471-6663	Sequence 6663, Ap	C 368	17	0.4	567	6	US-10-767-701-24257	Sequence 24257, A
C 296	17	0.4	201	6	US-10-767-471-6673	Sequence 6673, Ap	C 369	17	0.4	571	6	US-10-767-701-22450	Sequence 22450, A
C 297	17	0.4	201	6	US-10-767-471-6683	Sequence 6683, Ap	C 370	17	0.4	571	6	US-10-767-701-25449	Sequence 25449, A
C 298	17	0.4	201	6	US-10-767-471-6693	Sequence 6693, Ap	C 371	17	0.4	572	6	US-10-767-701-26285	Sequence 26285, A
C 299	17	0.4	201	6	US-10-767-471-6703	Sequence 6703, Ap	C 372	17	0.4	575	6	US-10-767-701-15585	Sequence 15585, A
C 300	17	0.4	201	6	US-10-767-471-6713	Sequence 6713, Ap	C 373	17	0.4	577	6	US-10-767-701-25575	Sequence 25575, A
C 301	17	0.4	201	6	US-10-767-471-6723	Sequence 6723, Ap	C 374	17	0.4	578	6	US-10-767-701-15136	Sequence 15136, A
C 302	17	0.4	201	6	US-10-767-471-6733	Sequence 6733, Ap	C 375	17	0.4	579	6	US-10-767-701-21829	Sequence 21829, A
C 303	17	0.4	201	6	US-10-767-471-6743	Sequence 6743, Ap	C 376	17	0.4	580	6	US-10-767-701-44590	Sequence 44590, Ap
C 304	17	0.4	201	6	US-10-767-471-6753	Sequence 6753, Ap	C 377	17	0.4	583	6	US-10-767-701-4088	Sequence 4088, Ap
C 305	17	0.4	201	6	US-10-767-471-6763	Sequence 6763, Ap	C 378	17	0.4	583	6	US-10-767-701-6043	Sequence 6043, Ap
C 306	17	0.4	201	6	US-10-767-471-6773	Sequence 6773, Ap	C 379	17	0.4	585	6	US-10-767-701-25344	Sequence 25344, A
C 307	17	0.4	201	6	US-10-767-471-6783	Sequence 6783, Ap	C 380	17	0.4	590	6	US-10-767-701-24813	Sequence 24813, A
C 308	17	0.4	201	6	US-10-767-471-6793	Sequence 6793, Ap	C 381	17	0.4	598	6	US-10-767-701-15161	Sequence 15161, A
C 309	17	0.4	201	6	US-10-767-471-6803	Sequence 6803, Ap	C 382	17	0.4	598	6	US-10-767-701-23205	Sequence 23205, A
C 310	17	0.4	201	6	US-10-767-471-6813	Sequence 6813, Ap	C 383	17	0.4	599	6	US-10-767-701-20919	Sequence 20919, A
C 311	17	0.4	201	6	US-10-767-471-6823	Sequence 6823, Ap	C 384	17	0.4	604	6	US-10-767-701-6212	Sequence 6212, Ap
C 312	17	0.4	201	6	US-10-767-471-6833	Sequence 6833, Ap	C 385	17	0.4	606	6	US-10-767-701-7068	Sequence 7068, Ap
C 313	17	0.4	201	6	US-10-767-471-6843	Sequence 6843, Ap	C 386	17	0.4	606	6	US-10-767-701-30057	Sequence 30057, A
C 314	17	0.4	201	6	US-10-767-471-6853	Sequence 6853, Ap	C 387	17	0.4	610	6	US-10-767-701-528	Sequence 528, App
C 315	17	0.4	201	6	US-10-767-471-6863	Sequence 6863, Ap	C 388	17	0.4	613	6	US-10-767-701-6693	Sequence 6693, Ap
C 316	17	0.4	201	6	US-10-767-471-6873	Sequence 6873, Ap	C 389	17	0.4	613	6	US-10-767-701-26438	Sequence 26438, A
C 317	17	0.4	201	6	US-10-767-471-6883	Sequence 6883, Ap	C 390	17	0.4	614	6	US-10-767-701-22480	Sequence 22480, A
C 318	17	0.4	201	6	US-10-767-471-6893	Sequence 6893, Ap	C 391	17	0.4	615	6	US-10-767-701-446	Sequence 446, App

392	17	0.4	617	6	US-10-767-701-24499	Sequence 24499, A	465	17	0.4	877	6	US-10-767-701-9252	Sequence 8252, App
393	17	0.4	622	6	US-10-767-701-5162	Sequence 5162, App	466	17	0.4	879	6	US-10-451-46704-495	Sequence 495, App
394	17	0.4	628	6	US-10-767-701-1475	Sequence 1475, App	467	17	0.4	895	6	US-10-767-701-1396	Sequence 1396, App
395	17	0.4	630	6	US-10-767-701-24256	Sequence 24256, A	468	17	0.4	900	6	US-10-767-701-10688	Sequence 10688, A
396	17	0.4	633	6	US-10-767-701-8878	Sequence 8878, App	469	17	0.4	920	6	US-10-767-701-11392	Sequence 11392, App
397	17	0.4	635	6	US-10-767-701-28748	Sequence 28748, A	470	17	0.4	921	6	US-10-767-701-1665	Sequence 1665, App
398	17	0.4	639	6	US-10-773-236-166	Sequence 166, App	471	17	0.4	932	6	US-10-767-701-10977	Sequence 10977, A
399	17	0.4	635	6	US-10-767-701-25816	Sequence 25816, A	472	17	0.4	936	6	US-10-646-6204-8	Sequence 8, App1
400	17	0.4	640	6	US-10-767-701-20022	Sequence 20022, A	473	17	0.4	945	6	US-10-767-701-10900	Sequence 10900, A
401	17	0.4	641	6	US-10-767-701-4739	Sequence 4739, App	474	17	0.4	952	6	US-10-767-701-10472	Sequence 10472, A
402	17	0.4	643	6	US-10-767-701-23935	Sequence 23935, A	475	17	0.4	977	6	US-10-767-701-12410	Sequence 12410, A
403	17	0.4	646	6	US-10-767-701-8433	Sequence 8433, App	476	17	0.4	987	6	US-10-767-701-14401	Sequence 14401, A
404	17	0.4	646	6	US-10-767-701-24337	Sequence 24337, A	477	17	0.4	988	6	US-10-767-701-13978	Sequence 13978, A
405	17	0.4	646	6	US-10-767-701-25564	Sequence 25564, A	478	17	0.4	994	6	US-10-767-701-5362	Sequence 5362, App
406	17	0.4	647	6	US-10-767-701-12518	Sequence 12518, A	479	17	0.4	1004	6	US-10-767-701-13622	Sequence 13622, A
407	17	0.4	648	6	US-10-767-701-6082	Sequence 6082, App	480	17	0.4	1018	6	US-10-767-701-5625	Sequence 5625, App
408	17	0.4	651	6	US-10-767-701-7875	Sequence 7875, App	481	17	0.4	1022	6	PCT-US03-13184-1	Sequence 1, App1
409	17	0.4	651	6	US-10-767-701-20291	Sequence 20291, A	482	17	0.4	1022	6	US-10-424-986-1	Sequence 1, App1
410	17	0.4	658	6	US-10-767-701-4622	Sequence 4622, App	483	17	0.4	1022	6	US-10-773-236-137	Sequence 137, App
411	17	0.4	658	6	US-10-767-701-25290	Sequence 25290, A	484	17	0.4	1028	6	US-10-767-701-15054	Sequence 15054, App
412	17	0.4	660	6	US-10-767-701-2317	Sequence 2317, App	485	17	0.4	1028	6	US-10-767-701-15083	Sequence 15083, A
413	17	0.4	664	6	US-10-767-701-21524	Sequence 21524, A	486	17	0.4	1029	6	US-10-767-701-11693	Sequence 11693, A
414	17	0.4	665	6	US-10-767-701-5902	Sequence 5902, App	487	17	0.4	1030	6	US-10-767-701-14529	Sequence 14529, A
415	17	0.4	666	6	US-10-767-701-4674	Sequence 4674, App	488	17	0.4	1051	6	US-10-767-701-12214	Sequence 12214, A
416	17	0.4	666	6	US-10-767-701-5231	Sequence 5231, App	489	17	0.4	1052	6	US-10-767-701-12098	Sequence 12098, A
417	17	0.4	667	6	US-10-767-701-2274	Sequence 2274, App	490	17	0.4	1055	6	US-10-773-236-168	Sequence 168, App
418	17	0.4	668	6	US-10-767-701-11335	Sequence 11335, A	491	17	0.4	1061	6	US-10-767-701-14361	Sequence 14361, A
419	17	0.4	669	6	US-10-767-701-15584	Sequence 15584, A	492	17	0.4	1076	6	US-10-767-701-13091	Sequence 13091, A
420	17	0.4	672	6	US-10-767-701-9244	Sequence 9244, App	493	17	0.4	1088	6	US-10-773-226-202	Sequence 202, App
421	17	0.4	675	6	US-10-767-701-9163	Sequence 9163, App	494	17	0.4	1091	6	US-10-767-701-10763	Sequence 10763, App
422	17	0.4	675	6	US-10-767-701-25919	Sequence 25919, A	495	17	0.4	1104	1	PCT-US03-13184-25	Sequence 25, App1
423	17	0.4	681	6	US-10-767-701-7185	Sequence 7185, App	496	17	0.4	1104	6	US-10-767-701-14359	Sequence 14359, App
424	17	0.4	684	6	US-10-767-701-10756	Sequence 10756, A	497	17	0.4	1104	6	US-10-424-986-25	Sequence 25, App1
425	17	0.4	692	6	US-10-767-701-14720	Sequence 14720, A	498	17	0.4	1142	6	US-10-767-701-15574	Sequence 15574, A
426	17	0.4	698	6	US-10-767-701-6049	Sequence 6049, App	499	17	0.4	1154	6	US-10-767-701-9353	Sequence 9353, App
427	17	0.4	702	6	US-10-767-701-2548	Sequence 2548, App	500	17	0.4	1165	6	US-10-767-701-12235	Sequence 12235, A
428	17	0.4	704	6	US-10-767-701-3712	Sequence 3712, App	501	17	0.4	1183	6	US-10-773-236-53	Sequence 53, App1
429	17	0.4	715	6	US-10-767-701-7305	Sequence 7305, App	502	17	0.4	1188	6	US-10-773-236-169	Sequence 169, App
430	17	0.4	722	6	US-10-767-701-2037	Sequence 2037, App	503	17	0.4	1195	6	US-10-773-236-167	Sequence 167, App
431	17	0.4	722	6	US-10-767-701-4403	Sequence 4403, App	504	17	0.4	1200	6	US-10-767-701-13685	Sequence 13685, A
432	17	0.4	726	6	US-10-767-701-5462	Sequence 5462, App	505	17	0.4	1201	6	US-10-767-701-12659	Sequence 12659, A
433	17	0.4	735	6	US-10-767-701-5312	Sequence 5312, App	506	17	0.4	1216	6	US-10-773-226-92	Sequence 92, App1
434	17	0.4	735	6	US-10-767-701-13868	Sequence 13868, A	507	17	0.4	1218	6	US-10-767-701-14553	Sequence 14553, A
435	17	0.4	737	6	US-10-767-701-12728	Sequence 12728, A	508	17	0.4	1224	6	US-10-767-701-12453	Sequence 12453, A
436	17	0.4	737	6	US-10-767-701-19718	Sequence 19718, A	509	17	0.4	1231	6	US-10-767-701-4505	Sequence 4505, App
437	17	0.4	742	6	US-10-767-701-10893	Sequence 10893, A	510	17	0.4	1251	6	US-10-767-701-7224	Sequence 7224, App
438	17	0.4	743	6	US-10-767-701-1452	Sequence 1452, App	511	17	0.4	1263	6	US-10-767-701-10309	Sequence 10309, App
439	17	0.4	749	6	US-10-767-701-9670	Sequence 9670, App	512	17	0.4	1273	6	US-10-767-701-13420	Sequence 13420, A
440	17	0.4	749	6	US-10-767-701-10143	Sequence 10143, A	513	17	0.4	1274	6	US-10-767-701-12967	Sequence 12967, A
441	17	0.4	756	6	US-10-767-701-11281	Sequence 11281, A	514	17	0.4	1278	6	US-10-767-701-13540	Sequence 13540, A
442	17	0.4	756	6	US-10-767-701-1518	Sequence 1518, App	515	17	0.4	1290	5	US-09-744-794C-57	Sequence 57, App1
443	17	0.4	757	6	US-10-767-701-1442	Sequence 1442, App	516	17	0.4	1325	6	US-10-767-701-12769	Sequence 12769, A
444	17	0.4	761	6	US-10-767-701-14188	Sequence 14188, App	517	17	0.4	1361	6	US-10-451-46704-305	Sequence 305, App
445	17	0.4	765	6	US-10-767-701-9091	Sequence 9091, App	518	17	0.4	1427	6	US-10-767-701-11848	Sequence 11848, A
446	17	0.4	772	6	US-10-767-701-10435	Sequence 10435, A	519	17	0.4	1438	6	US-10-767-701-14180	Sequence 14180, A
447	17	0.4	772	6	US-10-767-701-7956	Sequence 7956, App	520	17	0.4	1439	6	US-10-767-701-12374	Sequence 12374, A
448	17	0.4	786	6	US-10-767-701-7932	Sequence 7932, App	521	17	0.4	1486	6	US-10-767-701-13587	Sequence 13587, A
449	17	0.4	793	6	US-10-767-701-20286	Sequence 20286, A	522	17	0.4	1528	6	US-10-767-701-14584	Sequence 14584, A
450	17	0.4	800	6	US-10-767-701-10261	Sequence 10261, A	523	17	0.4	1532	6	US-10-767-701-15555	Sequence 15555, A
451	17	0.4	804	6	US-10-767-701-15063	Sequence 15063, A	524	17	0.4	1593	6	US-10-767-701-15100	Sequence 15100, A
452	17	0.4	805	6	US-10-767-701-6791	Sequence 6791, App	525	17	0.4	1605	6	US-10-767-701-15564	Sequence 15564, A
453	17	0.4	810	6	US-10-767-701-8586	Sequence 8586, App	526	17	0.4	1605	6	US-10-767-701-6811	Sequence 6811, App
454	17	0.4	811	6	US-10-767-701-9159	Sequence 9159, App	527	17	0.4	1621	6	US-10-767-701-12166	Sequence 12166, A
455	17	0.4	823	6	US-10-767-701-13046	Sequence 13046, A	528	17	0.4	1721	6	US-10-451-46704-261	Sequence 261, App
456	17	0.4	824	6	US-10-767-701-2654	Sequence 2654, App	529	17	0.4	1726	6	PCT-US03-135026-18	Sequence 18, App1
457	17	0.4	834	6	US-10-767-701-13697	Sequence 13697, A	530	17	0.4	1769	6	US-10-767-701-15580	Sequence 15580, A
458	17	0.4	838	6	US-10-767-701-10262	Sequence 10262, A	531	17	0.4	1836	6	US-10-773-236-11	Sequence 11, App1
459	17	0.4	841	6	US-10-767-701-13998	Sequence 13998, A	532	17	0.4	1869	7	US-60-543-038-22	Sequence 22, App1
460	17	0.4	841	6	US-10-767-701-13998	Sequence 13998, A	533	17	0.4	1890	6	US-10-773-236-15	Sequence 15, App1
461	17	0.4	852	6	US-10-767-701-850	Sequence 850, App	534	17	0.4	1899	6	US-10-679-140-15	Sequence 15, App1
462	17	0.4	857	6	US-10-767-701-9672	Sequence 9672, App	535	17	0.4	1899	6	US-10-679-140-16	Sequence 16, App1
463	17	0.4	863	6	US-10-767-701-14360	Sequence 14360, A	536	17	0.4	1914	6	US-10-772-656-9	Sequence 9, App1
464	17	0.4	874	6	US-10-767-701-12304	Sequence 12304, A	537	17	0.4	1943	1	PCT-US04-02851-43	Sequence 43, App1

C 538	17	0.4	1943	6	US-10-768-158-43	Sequence 43, Appl	611	17	0.4	48234	6	US-10-767-471-10706	Sequence 10706, A
C 539	17	0.4	1959	6	US-10-772-656-18	Sequence 19, Appl	612	17	0.4	50010	6	US-10-767-471-10874	Sequence 10874, A
C 540	17	0.4	1960	6	US-10-767-701-1919	Sequence 14919, A	613	17	0.4	51323	6	US-10-417-375A-135	Sequence 135, App
C 541	17	0.4	1968	6	US-10-772-656-13	Sequence 13, Appl	614	17	0.4	55759	6	US-10-767-471-10656	Sequence 10656, A
C 542	17	0.4	1973	1	PCT-US03-31120A-1	Sequence 1, Appl	615	17	0.4	55966	6	US-10-767-471-10663	Sequence 10663, A
C 543	17	0.4	1931	6	US-10-772-656-23	Sequence 23, Appl	616	17	0.4	72779	6	US-10-767-471-10659	Sequence 10659, A
C 544	17	0.4	2037	6	US-10-772-656-17	Sequence 17, Appl	617	17	0.4	81440	6	US-10-451-467A-659	Sequence 659, App
C 545	17	0.4	2037	6	US-10-767-701-1441	Sequence 15441, A	618	17	0.4	87716	6	US-10-767-471-10648	Sequence 10648, A
C 546	17	0.4	2070	6	US-10-767-701-10360	Sequence 10360, A	619	17	0.4	91697	6	US-10-417-375A-36	Sequence 36, Appl
C 547	17	0.4	2103	6	US-10-772-656-27	Sequence 27, Appl	620	17	0.4	104438	6	US-10-767-471-10731	Sequence 10731, A
C 548	17	0.4	2109	6	US-10-772-656-21	Sequence 21, Appl	621	17	0.4	134598	6	US-10-767-471-10655	Sequence 10655, A
C 549	17	0.4	2135	6	US-10-767-701-1474	Sequence 14474, A	622	17	0.4	134598	6	US-10-767-471-10655	Sequence 10655, A
C 550	17	0.4	2181	6	US-10-772-656-25	Sequence 25, Appl	623	17	0.4	144323	6	US-10-767-471-10881	Sequence 10881, A
C 551	17	0.4	2311	6	US-10-772-656-3	Sequence 3, Appl	624	17	0.4	162329	6	US-10-767-471-10637	Sequence 10637, A
C 552	17	0.4	2311	6	US-10-772-656-7	Sequence 7, Appl	625	17	0.4	170548	6	US-10-767-471-10703	Sequence 10627, A
C 553	17	0.4	2334	1	PCT-US03-35026-48	Sequence 48, Appl	626	17	0.4	184809	6	US-10-767-471-10627	Sequence 63, Appl
C 554	17	0.4	2367	1	US-10-417-884A-2884	Sequence 2884, Ap	627	17	0.4	219715	6	US-10-417-375A-63	Sequence 63, Appl
C 555	17	0.4	2384	1	PCT-US04-02851-45	Sequence 45, Appl	628	17	0.4	219715	6	US-10-417-375A-63	Sequence 63, Appl
C 556	17	0.4	2384	6	US-10-768-158-45	Sequence 45, Appl	629	17	0.4	230101	6	US-10-767-471-10691	Sequence 10691, A
C 557	17	0.4	2389	6	US-10-772-656-1	Sequence 1, Appl	630	17	0.4	234734	6	US-10-767-471-10827	Sequence 10827, A
C 558	17	0.4	2389	6	US-10-772-656-5	Sequence 5, Appl	631	17	0.4	252907	6	US-10-417-375A-66	Sequence 66, Appl
C 559	17	0.4	2614	6	US-10-767-701-14986	Sequence 14986, A	632	17	0.4	252907	6	US-10-417-375A-66	Sequence 66, Appl
C 560	17	0.4	2693	6	US-10-679-140-12	Sequence 12, Appl	633	17	0.4	265113	6	US-10-767-471-10658	Sequence 10658, A
C 561	17	0.4	2693	6	US-10-679-140-14	Sequence 14, Appl	634	17	0.4	354592	6	US-10-765-790-70	Sequence 70, Appl
C 562	17	0.4	2828	6	US-10-767-701-15465	Sequence 15465, A	635	17	0.4	401433	6	US-10-765-790-79	Sequence 79, Appl
C 563	17	0.4	3038	6	US-10-767-701-15095	Sequence 15095, A	636	17	0.4	496635	6	US-10-765-790-12	Sequence 12, Appl
C 564	17	0.4	3169	6	US-10-632-815-5	Sequence 5, Appl	637	17	0.4	546025	6	US-10-767-471-10717	Sequence 10717, A
C 565	17	0.4	3303	1	PCT-US04-03417-9	Sequence 9, Appl	638	17	0.4	546025	6	US-10-767-471-10717	Sequence 10717, A
C 566	17	0.4	3303	6	US-10-772-636-9	Sequence 9, Appl	639	17	0.4	705636	6	US-10-765-790-30	Sequence 30, Appl
C 567	17	0.4	3985	1	PCT-US04-02851-13	Sequence 13, Appl	640	17	0.4	765267	6	US-10-767-471-10616	Sequence 10616, A
C 568	17	0.4	3985	6	US-10-768-158-13	Sequence 13, Appl	641	17	0.4	780759	6	US-10-767-471-10626	Sequence 10626, A
C 569	17	0.4	4219	1	PCT-US04-02188-76	Sequence 76, Appl	642	17	0.4	780759	6	US-10-767-471-10626	Sequence 10626, A
C 570	17	0.4	4219	6	US-10-764-425-76	Sequence 76, Appl	643	17	0.4	1126118	6	US-10-767-471-10615	Sequence 10615, A
C 571	17	0.4	4220	6	US-10-451-467A-671	Sequence 671, App	644	16	0.4	21	6	US-10-770-726-17518	Sequence 17518, A
C 572	17	0.4	4326	1	PCT-US03-27748-2	Sequence 2, Appl	645	16	0.4	24	6	US-10-708-204-3979	Sequence 3979, Ap
C 573	17	0.4	4372	6	US-10-603-196-1	Sequence 1, Appl	646	16	0.4	35	5	US-09-941-492A-35	Sequence 35, Appl
C 574	17	0.4	4403	6	US-10-767-471-304	Sequence 304, App	647	16	0.4	35	5	US-09-941-492A-79	Sequence 79, Appl
C 575	17	0.4	4424	6	US-10-767-471-302	Sequence 302, App	648	16	0.4	126	6	US-10-767-701-20480	Sequence 20480, A
C 576	17	0.4	4549	6	US-10-767-471-303	Sequence 303, App	649	16	0.4	162	6	US-10-767-471-2508	Sequence 9518, Ap
C 577	17	0.4	4549	6	US-10-767-471-241	Sequence 241, App	650	16	0.4	162	6	US-10-767-471-2516	Sequence 9516, Ap
C 578	17	0.4	6747	6	US-10-767-471-242	Sequence 242, App	651	16	0.4	162	6	US-10-767-471-2524	Sequence 9524, Ap
C 579	17	0.4	6798	6	US-10-765-790-38	Sequence 38, Appl	652	16	0.4	162	6	US-10-767-471-2532	Sequence 9532, Ap
C 580	17	0.4	7098	6	US-10-767-471-498	Sequence 498, App	653	16	0.4	163	6	US-10-767-471-2509	Sequence 9509, Ap
C 581	17	0.4	7240	6	US-10-767-471-499	Sequence 499, App	654	16	0.4	163	6	US-10-767-471-2517	Sequence 9517, Ap
C 582	17	0.4	7241	6	US-10-767-471-494	Sequence 494, App	655	16	0.4	163	6	US-10-767-471-2525	Sequence 9525, Ap
C 583	17	0.4	7914	6	US-10-767-471-263	Sequence 263, App	656	16	0.4	163	6	US-10-767-471-2533	Sequence 9533, Ap
C 584	17	0.4	7918	6	US-10-767-471-265	Sequence 265, App	657	16	0.4	164	6	US-10-767-471-2510	Sequence 9510, Ap
C 585	17	0.4	7922	6	US-10-767-471-258	Sequence 258, App	658	16	0.4	164	6	US-10-767-471-2518	Sequence 9518, Ap
C 586	17	0.4	7976	6	US-10-767-471-493	Sequence 493, App	659	16	0.4	164	6	US-10-767-471-2526	Sequence 9526, Ap
C 587	17	0.4	8118	6	US-10-767-471-497	Sequence 497, App	660	16	0.4	164	6	US-10-767-471-2534	Sequence 9534, Ap
C 588	17	0.4	8554	6	US-10-767-471-495	Sequence 495, App	661	16	0.4	200	6	US-10-767-471-2530	Sequence 2530, Ap
C 589	17	0.4	9250	6	US-10-767-471-492	Sequence 492, App	662	16	0.4	201	6	US-10-767-471-2010	Sequence 2010, Ap
C 590	17	0.4	11409	6	US-10-767-471-603	Sequence 603, App	663	16	0.4	201	6	US-10-767-471-2031	Sequence 2031, Ap
C 591	17	0.4	14111	6	US-10-767-471-10879	Sequence 10879, A	664	16	0.4	201	6	US-10-767-471-12215	Sequence 4215, Ap
C 592	17	0.4	14321	6	US-10-767-471-191	Sequence 191, App	665	16	0.4	201	6	US-10-767-471-12219	Sequence 4219, Ap
C 593	17	0.4	14641	6	US-10-767-471-193	Sequence 193, App	666	16	0.4	201	6	US-10-767-471-12221	Sequence 4221, Ap
C 594	17	0.4	14760	6	US-10-767-471-192	Sequence 192, App	667	16	0.4	201	6	US-10-767-471-12225	Sequence 4225, Ap
C 595	17	0.4	14800	6	US-10-767-471-195	Sequence 195, App	668	16	0.4	201	6	US-10-767-471-12249	Sequence 4249, Ap
C 596	17	0.4	15251	6	US-10-451-467A-669	Sequence 669, App	669	16	0.4	201	6	US-10-767-471-12253	Sequence 4253, Ap
C 597	17	0.4	15407	6	US-10-767-471-10684	Sequence 10684, A	670	16	0.4	201	6	US-10-767-471-12255	Sequence 4255, Ap
C 598	17	0.4	15526	6	US-10-767-471-10792	Sequence 10792, A	671	16	0.4	201	6	US-10-767-471-12259	Sequence 4259, Ap
C 599	17	0.4	22218	6	US-10-767-471-10583	Sequence 10583, A	672	16	0.4	201	6	US-10-767-471-1311	Sequence 7311, Ap
C 600	17	0.4	23047	6	US-10-767-471-10609	Sequence 10609, A	673	16	0.4	201	6	US-10-767-471-1316	Sequence 7316, Ap
C 601	17	0.4	24841	6	US-10-767-471-10753	Sequence 10753, A	674	16	0.4	201	6	US-10-767-471-1317	Sequence 7317, Ap
C 602	17	0.4	27779	6	US-10-767-471-10834	Sequence 10834, A	675	16	0.4	201	6	US-10-767-471-1369	Sequence 7369, Ap
C 603	17	0.4	28591	6	US-10-767-471-10841	Sequence 10841, A	676	16	0.4	201	6	US-10-767-471-1374	Sequence 7374, Ap
C 604	17	0.4	28786	6	US-10-767-471-10789	Sequence 10789, A	677	16	0.4	201	6	US-10-767-471-1375	Sequence 7375, Ap
C 605	17	0.4	34016	6	US-10-767-471-10556	Sequence 10556, A	678	16	0.4	201	6	US-10-767-471-17429	Sequence 7429, Ap
C 606	17	0.4	36989	6	US-10-767-471-10812	Sequence 10812, A	679	16	0.4	201	6	US-10-767-471-17434	Sequence 7434, Ap
C 607	17	0.4	37255	6	US-10-767-471-10594	Sequence 10594, A	680	16	0.4	201	6	US-10-767-471-17487	Sequence 7487, Ap
C 608	17	0.4	38092	7	US-60-542-038-23	Sequence 23, Appl	681	16	0.4	201	6	US-10-767-471-17492	Sequence 7492, Ap
C 609	17	0.4	39320	6	US-10-767-471-10781	Sequence 10781, A	682	16	0.4	201	6	US-10-767-471-17492	Sequence 7492, Ap
C 610	17	0.4	43692	6	US-10-767-471-10557	Sequence 10557, A	683	16	0.4	201	6	US-10-767-471-17493	Sequence 7493, Ap

C 684	16	0.4	201	6	US-10-767-471-7545	Sequence 7545, Ap	C 757	16	0.4	401	6	US-10-767-701-26902	Sequence 26902, A
C 685	16	0.4	201	6	US-10-767-471-7548	Sequence 7548, Ap	C 758	16	0.4	406	6	US-10-767-701-687	Sequence 687, App
C 686	16	0.4	201	6	US-10-767-471-7550	Sequence 7550, Ap	C 759	16	0.4	416	6	US-10-767-701-28694	Sequence 28694, A
C 687	16	0.4	201	6	US-10-767-471-7600	Sequence 7600, Ap	C 760	16	0.4	425	6	US-10-767-701-1879	Sequence 1879, Ap
C 688	16	0.4	201	6	US-10-767-471-7603	Sequence 7603, Ap	C 761	16	0.4	425	6	US-10-773-236-170	Sequence 170, App
C 689	16	0.4	201	6	US-10-767-471-7605	Sequence 7605, Ap	C 762	16	0.4	443	6	US-10-767-701-21086	Sequence 21086, A
C 690	16	0.4	201	6	US-10-767-471-7657	Sequence 7657, Ap	C 763	16	0.4	445	6	US-10-767-701-17312	Sequence 17312, A
C 691	16	0.4	201	6	US-10-767-471-7659	Sequence 7659, Ap	C 764	16	0.4	453	6	US-10-767-701-25614	Sequence 25614, A
C 692	16	0.4	201	6	US-10-767-471-7713	Sequence 7713, Ap	C 765	16	0.4	457	6	US-10-767-701-25071	Sequence 25071, A
C 693	16	0.4	201	6	US-10-767-471-7714	Sequence 7714, Ap	C 766	16	0.4	457	6	US-10-767-701-30104	Sequence 30104, A
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C 695	16	0.4	201	6	US-10-767-471-9545	Sequence 9545, Ap	C 768	16	0.4	463	6	US-10-767-701-23815	Sequence 23815, A
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C 697	16	0.4	201	6	US-10-767-471-9560	Sequence 9560, Ap	C 770	16	0.4	476	6	US-10-767-701-27027	Sequence 27027, Ap
C 698	16	0.4	201	6	US-10-767-471-9561	Sequence 9561, Ap	C 771	16	0.4	484	6	US-10-767-701-8248	Sequence 8248, Ap
C 699	16	0.4	201	6	US-10-767-471-9562	Sequence 9562, Ap	C 772	16	0.4	487	6	US-10-767-701-15034	Sequence 15034, A
C 700	16	0.4	201	6	US-10-767-471-10142	Sequence 10142, A	C 773	16	0.4	488	6	US-10-767-701-2951	Sequence 2951, Ap
C 701	16	0.4	201	6	US-10-767-471-10145	Sequence 10145, A	C 774	16	0.4	494	6	US-10-767-701-21599	Sequence 21599, Ap
C 702	16	0.4	201	6	US-10-767-471-12480	Sequence 12480, A	C 775	16	0.4	496	6	US-10-767-701-28044	Sequence 28044, A
C 703	16	0.4	201	6	US-10-767-471-13139	Sequence 13139, A	C 776	16	0.4	497	6	US-10-767-701-2690	Sequence 2690, Ap
C 704	16	0.4	201	6	US-10-767-471-14198	Sequence 14198, A	C 777	16	0.4	497	6	US-10-767-701-16148	Sequence 16148, A
C 705	16	0.4	201	6	US-10-767-471-14299	Sequence 14299, A	C 778	16	0.4	499	6	US-10-767-701-28049	Sequence 28049, A
C 706	16	0.4	201	6	US-10-767-471-19433	Sequence 19433, A	C 779	16	0.4	500	6	US-10-767-701-26449	Sequence 26449, A
C 707	16	0.4	201	6	US-10-767-471-23046	Sequence 23046, A	C 780	16	0.4	503	6	US-10-767-701-29148	Sequence 29148, A
C 708	16	0.4	201	6	US-10-767-471-23546	Sequence 23546, A	C 781	16	0.4	506	6	US-10-767-701-11279	Sequence 11279, A
C 709	16	0.4	201	6	US-10-767-471-23552	Sequence 23552, A	C 782	16	0.4	509	6	US-10-767-701-1658	Sequence 1658, Ap
C 710	16	0.4	201	6	US-10-767-471-23555	Sequence 23555, A	C 783	16	0.4	509	6	US-10-767-701-4850	Sequence 4850, Ap
C 711	16	0.4	201	6	US-10-767-471-23561	Sequence 23561, A	C 784	16	0.4	511	6	US-10-767-701-19716	Sequence 19716, A
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C 713	16	0.4	201	6	US-10-767-471-24475	Sequence 24475, A	C 786	16	0.4	515	6	US-10-767-701-29483	Sequence 29483, A
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C 717	16	0.4	201	6	US-10-767-471-29555	Sequence 29555, A	C 790	16	0.4	534	6	US-10-767-701-7280	Sequence 7280, Ap
C 718	16	0.4	201	6	US-10-767-471-29590	Sequence 29590, A	C 791	16	0.4	540	6	US-10-767-701-2640	Sequence 2640, Ap
C 719	16	0.4	201	6	US-10-767-471-36542	Sequence 36542, A	C 792	16	0.4	545	6	US-10-767-701-21961	Sequence 21961, A
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## ALIGNMENTS

RESULT 1  
US-10-764-503-30  
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? IDENTIFYING NATURALLY OCCURRING ANTISENS?
? TITLE OF INVENTION: METHODS AND SYSTEMS FOR IDENTIFYING NATURALLY OCCURRING ANTISENS?
? TITLE OF INVENTION: TRANSCRIPTS AND METHODS, KITS AND ARRAYS UTILIZING SAME?
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Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1739; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

0y 7 ATGGGCGACCCAGCCCCCGCCGCGACCTTGAGCAGCATGCACTTGTCCGCTCGCGGAC 66  
Db 185 ATGGGCGACCCAGCCCCCGCCGCGACCTTGAGCAGCATGCACTTGTCCGCTCGCGGAC 244  
0y 67 CTTGCTGGGATCTTTTGAGCTTTGTGAGAGTGTCGTGGCAATGGAACCTTAAGGACAGGTGTAC 126

Db	245	CTGTCTGGGATCTTTGAGCTTTGTGAGGTGTGGGCAATGGAACTTAACGACAGGTGTAC	304
Qy	127	AAAGGTGGGCAATGTCAGAACGGGGCAGCTGGCTGCCATCAAGTCATGATGTTCACGGAG	186
Db	305	AAAGGTGGGCAATGTCAGAACGGGGCAGCTGGCTGCCATCAAGGTCAATGATGTTCACGGAG	364
Qy	187	GACGAGGAGGAAAGATCAACAAGGAAATCAATGCTGAAAAAAGTACTCTCAACACCGC	246
Db	365	GACGAGGAGGAAAGATCAACAAGGAAATCAATGCTGAAAAAAGTACTCTCAACACCGC	424
Qy	247	AACATGCCACCTACTACGAGCCTTCATCAAGAAAGACCCCGGGAAAAAGATGACAG	306
Db	425	AACATGCCACCTACTACGAGCCTTCATCAAGAAAGACCCCGGGAAAAAGATGACAG	484
Qy	307	CTCTGGCTGTGATGAGATTCTGTGGTCTGGTTCACTGACTGAACCTGTGTAAGAACACA	366
Db	485	CTCTGGCTGTGATGAGATTCTGTGGTCTGGTTCACTGAACCTGTGTAAGAACACA	544
Qy	367	AAAGGCAACGCCCTGAAGAGAGACTGATGCGCTATATCTGCAGGAGATCCCAAGGGT	426
Db	545	AAAGGCAACGCCCTGAAGAGAGACTGATGCGCTATATCTGCAGGAGATCCCAAGGGT	604
Qy	427	CTGGCCCATCTCCATGCGCCCAACAGGTATCATCGAACATCAAGGGGAGAAATGTGCTG	486
Db	605	CTGGCCCATCTCCATGCGCCCAACAGGTATCATCGAACATCAAGGGGAGAAATGTGCTG	664
Qy	487	CTGCACAGGAATGCTGAGTCAAGCTAATGGAATTTGGGGTGAATGCTCAGCTGCACGC	546
Db	665	CTGCACAGGAATGCTGAGTCAAGCTAATGGAATTTGGGGTGAATGCTCAGCTGCACGC	724
Qy	547	ACCGTGGGCAAGCGGAACATTTTATTTGGGACTCTCCCTACTGATGCTCCAGAGGTATCT	606
Db	725	ACCGTGGGCAAGCGGAACATTTTATTTGGGACTCTCCCTACTGATGCTCCAGAGGTATCT	784
Qy	607	GGCTGTATGGAACCCGTAATGCCACTATGATTAACAGAGTGAATATTTGGTCTCTAGA	666
Db	785	GGCTGTATGGAACCCGTAATGCCACTATGATTAACAGAGTGAATATTTGGTCTCTAGA	844
Qy	667	ATCAACAGCCATCGAGATGCGAGAGGAGCCGCCCTCTGTGTGCATGCAACCCCATGCGA	726
Db	845	ATCAACAGCCATCGAGATGCGAGAGGAGCCGCCCTCTGTGTGCATGCAACCCCATGCGA	904
Qy	727	GGCCCTCTCTCATTTCTCGGAAACCTTCGCCGCCAGGCTCAAGTCTCAAGAGTGTCTAAG	786
Db	905	GGCCCTCTCTCATTTCTCGGAAACCTTCGCCGCCAGGCTCAAGTCTCAAGAGTGTCTAAG	964
Qy	787	AAAGTTCAATGACTTCAATGACACATGTCTCATCAAGACTTAACGAGCGGCCCAACCGAG	846
Db	965	AAAGTTCAATGACTTCAATGACACATGTCTCATCAAGACTTAACGAGCGGCCCAACCGAG	1024
Qy	847	GAGCAGCTACTGAAGTTTCCCTTATCGGGGACCAAGCCACGAGCGGCAAGTCCGATC	906
Db	1025	GAGCAGCTACTGAAGTTTCCCTTATCGGGGACCAAGCCACGAGCGGCAAGTCCGATC	1084
Qy	907	CAGCTTAAGACCAATTAACCGATCCCGGAAGAAACGGGGTGAAGAAAGAGACAGAA	966
Db	1085	CAGCTTAAGACCAATTAACCGATCCCGGAAGAAACGGGGTGAAGAAAGAGACAGAA	1144
Qy	967	TATGAGTACAGCGGCAAGAGAGAGAGATGACAGCCATGGAAGAGAAAGAGCCAGC	1026
Db	1145	TATGAGTACAGCGGCAAGAGAGAGAGATGACAGCCATGGAAGAGAAAGAGCCAGC	1204
Qy	1027	TCCATCAATGAACGTCGCGAGAGTGCATCTACAGCGGGAGTTTCTCCGCTCCAGCAG	1086
Db	1205	TCCATCAATGAACGTCGCGAGAGTGCATCTACAGCGGGAGTTTCTCCGCTCCAGCAG	1264
Qy	1087	GAATAATAAGCACTCAAGAGGCTTTAAAAACAGCAGCAGCAGCTGCAGCAGCAGCAG	1146
Db	1265	GAATAATAAGCACTCAAGAGGCTTTAAAAACAGCAGCAGCAGCTGCAGCAGCAGCAG	1324
Qy	1147	CGAGACCCCGAGCACAATCAACACCTGTGTGCACAGCGGGCAGCGGGCGCATATGAGAG	1206

Db 1325 CGAGACCCCGAGGACACATCAACCTGCTGACACGCGGAGCGGCGATAGAGAG 1384  
Qy 1207 CAGAAAGAGAGCGCGCGCGGTGAGAGCAACGCGCGGAGCGGAGAGCGGAGAG 1286  
Db 1385 CAGAAAGAGAGCGCGCGCGGTGAGAGCAACGCGCGGAGCGGAGAGCGGAGAG 1444  
Qy 1267 CTGAG 1326  
Db 1445 CTGAG 1504  
Qy 1327 GAGCGCGGAG 1386  
Db 1505 GAGCGCGGAG 1564  
Qy 1387 CAGTCAAAAGCTCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1446  
Db 1565 CAGTCAAAAGCTCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1624  
Qy 1447 CAGCAGAAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1506  
Db 1625 CAGCAGAAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1684  
Qy 1507 AGGAAGCCCTGTATCAATATATGTCGGGAGATGATCCCGCTGACAAACAGCCTGAGCC 1566  
Db 1685 AGGAAGCCCTGTATCAATATATGTCGGGAGATGATCCCGCTGACAAACAGCCTGAGCC 1744  
Qy 1567 CGAGAGGTAG 1626  
Db 1745 CGAGAGGTAG 1804  
Qy 1627 AAGCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1686  
Db 1805 AAGCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1864  
Qy 1687 CCCCTTTCAGAGACTCTCTATATCAGAGAGCGGCTGAGAGCCCGCAGAGAGAGAG 1746  
Db 1865 CCCCTTTCAGAGACTCTCTATATCAGAGAGCGGCTGAGAGCCCGCAGAGAGAGAG 1924

RESULT 2  
PCT-US03-13184-20  
; Sequence 20, Application PC/TUS0313184  
; GENERAL INFORMATION:  
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY  
; TITLE OF INVENTION: DI-1 NUCLEIC ACIDS, POLYPEPTIDES AND RELATED METHODS  
; FILE REFERENCE: CTCH-PWO-001  
; CURRENT APPLICATION NUMBER: PCT/US03/13184  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: 60/375904  
; PRIOR FILING DATE: 2002-04-26  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 20  
; LENGTH: 219  
; TYPE: DNA  
; ORGANISM: Sus scrofa  
PCT-US03-13184-20

Query Match 0.7%; Score 26; DB 1; Length 219;  
Best Local Similarity 100.0%; Pred. No. 0.0031;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1443 GCAGCAGCAGCAACAGCAGCAGCAGCAGC 1468  
Db 80 GCAGCAGCAGCAACAGCAGCAGCAGCAGC 105

RESULT 3  
US-10-424-986-20  
; Sequence 20, Application US/10424986  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSON et. al.  
; TITLE OF INVENTION: DI-1 NUCLEIC ACIDS, POLYPEPTIDES AND RELATED METHODS

FILE REFERENCE: CTCH-P01-001  
; CURRENT APPLICATION NUMBER: US/10/424,986  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: 60/375904  
; PRIOR FILING DATE: 2002-04-26  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 20  
; LENGTH: 219  
; TYPE: DNA  
; ORGANISM: Sus scrofa  
US-10-424-986-20

Query Match 0.7%; Score 26; DB 6; Length 219;  
Best Local Similarity 100.0%; Pred. No. 0.0031;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1443 GCAGCAGCAGCAACAGCAGCAGCAGCAGC 1468  
Db 80 GCAGCAGCAGCAACAGCAGCAGCAGCAGC 105

RESULT 4  
PCT-US03-13184-19  
; Sequence 19, Application PC/TUS0313184  
; GENERAL INFORMATION:  
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY  
; TITLE OF INVENTION: DI-1 NUCLEIC ACIDS, POLYPEPTIDES AND RELATED METHODS  
; FILE REFERENCE: CTCH-PWO-001  
; CURRENT APPLICATION NUMBER: PCT/US03/13184  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: 60/375904  
; PRIOR FILING DATE: 2002-04-26  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19  
; LENGTH: 549  
; TYPE: DNA  
; ORGANISM: Sus scrofa  
PCT-US03-13184-19

Query Match 0.7%; Score 26; DB 1; Length 549;  
Best Local Similarity 100.0%; Pred. No. 0.0031;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1443 GCAGCAGCAGCAACAGCAGCAGCAGCAGC 1468  
Db 188 GCAGCAGCAGCAACAGCAGCAGCAGCAGC 213

RESULT 5  
US-10-424-986-19  
; Sequence 19, Application US/10424986  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSON et. al.  
; TITLE OF INVENTION: DI-1 NUCLEIC ACIDS, POLYPEPTIDES AND RELATED METHODS  
; FILE REFERENCE: CTCH-P01-001  
; CURRENT APPLICATION NUMBER: US/10/424,986  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: 60/375904  
; PRIOR FILING DATE: 2002-04-26  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19  
; LENGTH: 549  
; TYPE: DNA  
; ORGANISM: Sus scrofa  
US-10-424-986-19

Query Match 0.7%; Score 26; DB 6; Length 549;  
Best Local Similarity 100.0%; Pred. No. 0.0031;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1443 GCAGCAGCAGCAGCAGCAGCAGCAGC 1468  
Db 188 GCAGCAGCAGCAGCAGCAGCAGCAGC 213

RESULT 6  
US-10-767-701-26464  
; Sequence 26464, Application US/10767701  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(5353)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 26464  
; LENGTH: 676  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 30974808  
US-10-767-701-26464

Query Match 0.7%; Score 26; DB 6; Length 676;  
Best Local Similarity 100.0%; Pred. No. 0.0031;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1443 GCAGCAGCAGCAGCAGCAGCAGCAGC 1468  
Db 617 GCAGCAGCAGCAGCAGCAGCAGCAGC 642

RESULT 7  
US-09-744-794C-46  
; Sequence 46, Application US/09744794C  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE CORPORATION, HILLMAN, Jennifer L.;  
; APPLICANT: LAU, Preeti G.; TANG, Y. Tom;  
; APPLICANT: CORLEY, Neil C.; GUEGLER, Karl J.;  
; APPLICANT: BAUGHN, Mariah R.; PATTERSON, Chandra S.;  
; APPLICANT: BANDMAN, Olga; AU-YOUNG, Janice K.;  
; APPLICANT: GORGONE, Gina A.; YUE, Henry; M.;  
; APPLICANT: AZIMZAI, Valda; REDDY, Roopa M.;  
; APPLICANT: LU, Dying Aina M.; SHIH, Leo L.  
; TITLE OF INVENTION: HUMAN CELL SURFACE RECEPTORS  
; FILE REFERENCE: PF-0565 USN  
; CURRENT APPLICATION NUMBER: US/09/744,794C  
; CURRENT FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PERL Program  
; SEQ ID NO 46  
; LENGTH: 3786  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No: 2299715CB1  
US-09-744-794C-46

Query Match 0.7%; Score 26; DB 5; Length 3786;  
Best Local Similarity 100.0%; Pred. No. 0.0031;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 598 GAGTCATGCGCTGTGATGAGAACC 623  
Db 731 GAGTCATGCGCTGTGATGAGAACC 756

RESULT 8  
US-10-451-467A-659/c

; Sequence 659, Application US/10451467A  
; GENERAL INFORMATION:  
; APPLICANT: CONTRERAS, ROLAND HENRI  
; APPLICANT: EBERHARDT, INES  
; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS  
; APPLICANT: REEMANS, RIEKA JOSEPHINA  
; TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN  
; TITLE OF INVENTION: YEAST AND FUNGI  
; FILE REFERENCE: JAB-1667  
; CURRENT APPLICATION NUMBER: US/10/451,467A  
; CURRENT FILING DATE: 2003-06-19  
; PRIOR APPLICATION NUMBER: EP 00870318.3  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: EP 01870002.1  
; PRIOR FILING DATE: 2001-01-04  
; PRIOR APPLICATION NUMBER: EP 01870003.9  
; PRIOR FILING DATE: 2001-01-09  
; NUMBER OF SEQ ID NOS: 732  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 659  
; LENGTH: 81440  
; TYPE: DNA  
; ORGANISM: Candida albicans  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (41180)..(41180)  
; OTHER INFORMATION: N = A, G, T or C  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (41181)..(41181)  
; OTHER INFORMATION: N = A, G, T or C  
; NAME/KEY: misc.feature  
; LOCATION: (41211)..(41211)  
; OTHER INFORMATION: N = A, G, T or C  
US-10-451-467A-659

Query Match 0.6%; Score 24; DB 6; Length 81440;  
Best Local Similarity 100.0%; Pred. No. 0.031;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1443 GCAGCAGCAGCAGCAGCAGCAGCAGC 1466  
Db 66636 GCAGCAGCAGCAGCAGCAGCAGCAGC 66613

RESULT 9  
US-10-767-701-6073  
; Sequence 6073, Application US/10767701  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(5353)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 6073  
; LENGTH: 789  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS33754\_1  
US-10-767-701-6073

Query Match 0.6%; Score 23; DB 6; Length 789;  
Best Local Similarity 100.0%; Pred. No. 0.096;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1446 GCAGCAGCAGCAGCAGCAGCAGCAGC 1468

Db 189 GCAGCAGCAGCAGCAGCAGC 211

## RESULT 10

US-09-941-492A-63/c  
; Sequence 63, Application US/09941492A  
; GENERAL INFORMATION:  
; APPLICANT: Mitchell, Lloyd  
; APPLICANT: Garcia-Blanco, Mariano M.  
; APPLICANT: Puttareju, Madalah  
; APPLICANT: Mansfield, Gary S.  
; TITLE OF INVENTION: METHODS OF COMPOSITIONS FOR USE IN  
; TITLE OF INVENTION: SPLICOSOME MEDIATED RNA TRANS-SPLICING  
; FILE REFERENCE: A31304-BAE (072874.0156)  
; CURRENT FILING DATE: US/09/941,492A  
; PRIOR APPLICATION NUMBER: 09/838,858  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 09/756,096  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 09/158,863  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 09/133,717  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: 09/087,233  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 08/766,354  
; PRIOR FILING DATE: 1996-12-13  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 63  
; LENGTH: 196  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Trans-spliced product containing Escherichia coli  
; OTHER INFORMATION: lacZ gene sequences  
US-09-941-492A-63

Query Match 0.6%; Score 22; DB 5; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1444 CAGCAGCAGCAGCAGCAGC 1465  
Db 146 CAGCAGCAGCAGCAGCAGC 125

## RESULT 11

US-10-767-701-10485  
; Sequence 10485, Application US/10767701  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT FILING DATE: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 10485  
; LENGTH: 829  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS16079\_1  
US-10-767-701-10485

Query Match 0.6%; Score 22; DB 6; Length 829;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1443 GCAGCAGCAGCAGCAGCAGC 1464  
Db 175 GCAGCAGCAGCAGCAGCAGC 196

## RESULT 12

US-10-767-701-11901  
; Sequence 11901, Application US/10767701  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT FILING DATE: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 11901  
; LENGTH: 1123  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS34030\_1  
US-10-767-701-11901

Query Match 0.6%; Score 22; DB 6; Length 1123;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1442 TGCAGCAGCAGCAGCAGCAGC 1463  
Db 413 TGCAGCAGCAGCAGCAGCAGC 434

## RESULT 13

PCT-US04-02974-37  
; Sequence 37, Application PC/TUS0402974  
; GENERAL INFORMATION:  
; APPLICANT: Wright, Susan C.  
; APPLICANT: Larrick, James W.  
; APPLICANT: Nock, Steffen R.  
; APPLICANT: Wilson, David S.  
; TITLE OF INVENTION: Cell-Killing Molecules and Methods of Use Thereof  
; FILE REFERENCE: ABASUS-08804  
; CURRENT FILING DATE: PCT/US04/02974  
; CURRENT FILING DATE: 2004-02-02  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 37  
; LENGTH: 1137  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
PCT-US04-02974-37

Query Match 0.6%; Score 22; DB 1; Length 1137;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1447 CAGCAGCAGCAGCAGCAGC 1468  
Db 328 CAGCAGCAGCAGCAGCAGC 349

## RESULT 14

US-10-770-668-37  
; Sequence 37, Application US/10770668  
; GENERAL INFORMATION:  
; APPLICANT: Wright, Susan C.  
; APPLICANT: Larrick, James W.  
; APPLICANT: Nock, Steffen R.  
; APPLICANT: Wilson, David S.  
; TITLE OF INVENTION: Cell-Killing Molecules and Methods of Use Thereof

; FILE REFERENCE: ABSALUS-08602  
; CURRENT APPLICATION NUMBER: US/10/770,668  
; CURRENT FILING DATE: 2004-02-02  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 37  
; LENGTH: 1137  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-10-770-668-37

Query Match 0.6%; Score 22; DB 6; Length 1137;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1447 CAGCAGCAACAGCAGCAGCAGC 1468  
DB 328 CAGCAGCAACAGCAGCAGCAGC 349

RESULT 15  
US-10-767-701-2898/c  
; Sequence 2898, Application US/10767701  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 2898  
; LENGTH: 1139  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS49114\_1  
US-10-767-701-2898

Query Match 0.6%; Score 22; DB 6; Length 1139;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1446 GCAGCAGCAACAGCAGCAGCAG 1467  
DB 800 GCAGCAGCAACAGCAGCAGCAG 779

Search completed: March 3, 2004, 05:28:39  
Job time : 85 secs





Db	302	GGGAAATCCTCAGGGGCTCGGGCCATCTCCATGGCCCAAGAAGTATCCATGCAACATCA	361
Qy	470	AGGGCAGAAATGTGCTGTCTGACAGAGAAATGCTGAGGTCAAGCTAATGAAATTTTGGGGTGA	529
Db	362	AGGGCAGAAATGTGCTGTCTGACAGAGAAATGCTGAGGTCAAGCTAATGAAATTTTGGGGTGA	421
Qy	530	GTGCTCAGCTGGAACCGCAACCGTGGGCACACGGAAACATTTCAATGGGACTCCCTACTGGA	589
Db	422	GTGCTCAGCTGGAACCGCAACCGTGGGCACACGGAAACATTTCAATGGGACTCCCTACTGGA	481
Qy	590	TGGCTCCAGAGGTCAATGCGCTGTGATGAGAAACCTGATGCCACTATGATTTACAGAGTG	649
Db	482	TGGCTCCAGAGGTCAATGCGCTGTGATGAGAAACCTGATGCCACTATGATTTACAGAGTG	541
Qy	650	ATATTGGTCTCTAGAAATCAACGCCATCGAGATGGCAGAGGAGACCCCTCTGTGTG	709
Db	542	ATATTGGTCTCTAGAAATCAACGCCATCGAGATGGCAGAGGAGACCCCTCTGTGTG	601
Qy	710	ACATGCAACCCCATGCGAGCCCTCTTCTCATTTCTTGGAACCTTCGCCCAGGCTGAAGT	769
Db	602	ACATGCAACCCCATGCGAGCCCTCTTCTCATTTCTTGGAACCTTCGCCCAGGCTGAAGT	661
Qy	770	CCAAAGATGGCTTAAGAAATTCATTTGACTTATGACAATGCTCATCAAGACTTACC	829
Db	662	CCAAAGATGGCTTAAGAAATTCATTTGACTTATGACAATGCTCATCAAGACTTACC	721
Qy	830	TGAGCGGCCCAACCCACGAGACGACTAGTAAGTTTCCCTTCAATCCGGGACCAAGCCACGG	889
Db	722	TGAGCGGCCCAACCCACGAGACGACTAGTAAGTTTCCCTTCAATCCGGGACCAAGCCACGG	781
Qy	890	AGCGCAGGTCCGCATCCAGCTTAAAGACACATTTGACCGATCCCGGAAAGCCGGGCTG	949
Db	782	AGCGCAGGTCCGCATCCAGCTTAAAGACACATTTGACCGATCCCGGAAAGCCGGGCTG	841
Qy	950	AGAAAGAGAGACAGAAATATGAGTACAGCGGCACGAGAGAGAAATGACACCTATGAG	1006
Db	842	AGAAAGAGAGACAGAAATATGAGTACAGCGGCACGAGAGAGAAATGACACCTATGAG	901
Qy	1010	AGGAAGAGAGGCAAGCTCCATCATGAAGCGTCCCTGAGAGTCACTCTAAGCCGGGAGT	1066
Db	902	AGGAAGAGAGGCAAGCTCCATCATGAAGCGTCCCTGAGAGTCACTCTAAGCCGGGAGT	961
Qy	1070	TTCTTCGGCTCCAGCAGGAAATTAAGACAATCAGAGGCTTTAAACAGCAGCAGCAGC	1122
Db	962	TTCTTCGGCTCCAGCAGGAAATTAAGACAATCAGAGGCTTTAAACAGCAGCAGCAGC	1022
Qy	1130	TGCACAGCAGCAGCAGCGAGACCCCGAGGCACACATCAACACTCTGTGCACACGCGC	1186
Db	1022	TGCACAGCAGCAGCAGCGAGACCCCGAGGCACACATCAACACTCTGTGCACACGCGC	1082
Qy	1190	AGCGCGCAGATGAGAGAGCAGAAAGAGAGCGCGCGCGGTGAGAGAGCAACGCGCGCGG	1245
Db	1082	AGCGCGCAGATGAGAGAGCAGAAAGAGAGCGCGCGCGGTGAGAGAGCAACGCGCGCGG	1141
Qy	1250	AGCGGGAACAGCGGAAAGCTGACAGAGAAAGAGACACAGCGCGGCTGAGAGACATGACAG	1305
Db	1142	AGCGGGAACAGCGGAAAGCTGACAGAGAAAGAGACACAGCGCGGCTGAGAGACATGACAG	1201
Qy	1310	CTCTGCGGCGGAGAGAGAGCGCGCGGACAGCGGAGCTGAGCA-----	1352
Db	1202	CTCTGCGGCGGAGAGAGAGCGCGCGGACAGCGGAGCTGAGCA-----	1265
Qy	1353	-----	1352
Db	1262	GGCTTAGAGAGAGCAGCGACAGCTCGAGATCCTTCAAGCAACAGCTGCTCCAGAAACAG	1321
Qy	1353	-----GGATATCAAGCGGGAAGCAGCTGAGAGAGCAGCGGACAGTACGAAGCTCTCC	1402
Db	1352	CCCTGCTCTGGAATTAACAAGCGGAAGCAGCTGAGAGAGCAGCGGAGTCTAGAACCTCTCC	1381
Qy	1403	AGAGCAGACTGACAGAGAGCAATGCTCTAATCTTAAGTCTCTGACAGAGCAACAGCAGC	1462
Db	1382	AGAGCAGACTGACAGAGAGCAATGCTCTAATCTTAAGTCTCTGACAGAGCAACAGCAGC	1441

QY	1465	AGCAGCTTCGAAAACACAGACGAGAGAGCTCCCTGGCGGAGACGAAAGCCCTGTACC	1522
Db	1442	AGCAGCTTCGAAAACACAGACGAGAGAGCTCCCTGGCGGAGACGAAAGCCCTGTACC	1501
QY	1523	ATTATGGTCGGGGCATGATCCCGCTGACAAACCAAGCCTGGGCCGAGAGGTAGAGAGA	1582
Db	1502	ATTATGGTCGGGGCATGATCCCGCTGACAAACCAAGCCTGGGCCGAGAGGTAGAGAGA	1561
QY	1583	GAACAGAGATGAACAGACGACGAACTCTCCCTTGGCCAGAGAGCAACGACGACGACCGG	1642
Db	1562	GAACAGAGATGAACAGACGACGAACTCTCCCTTGGCCAGAGAGCAACGACGACGACCGG	1621
QY	1643	GGCCGTGAGCCCCCATCGCCCCCAGGSCCTCCCGAGGGGCCCGCAGACCCCTTTCCGACTC	1702
Db	1622	GGCCGTGAGCCCCCATCGCCCCCAGGSCCTCCCGAGGGGCCCGCAGACCCCTTTCCGACTC	1681
QY	1703	CTCCTATGACAGAGCCCGGTGGAGGCCCGCAGAGAGGAGCCGCA-----	1744
Db	1682	CTCCTATGACAGAGCCCGGTGGAGGCCCGCAGAGAGGAGCCGCA-----	1741
QY	1745	-----AGTCCCTGACGAGCCAGC	1762
Db	1742	GGGTCCCACTGAGGCCATATGACGACCTGTATCCCGCATCCCACTCCCTGACGAGCCAGC	1801
QY	1763	CCACCCGGAACCTTGGCTGCTCTTCCAGACCTTCCCATGACCCCGACCCCTTGCAATCCCGCAC	1822
Db	1802	CCACCCGGAACCTTGGCTGCTCTTCCAGACCTTCCCATGACCCCGACCCCTTGCAATCCCGCAC	1861
QY	1823	CCAATGCGCAGGCCCAAGTCCCGAGAGAGCTGTCAATCCCGCAGAAATTGACATCCCACTCTG	1882
Db	1862	CCAATGCGCAGGCCCAAGTCCCGAGAGAGCTGTCAATCCCGCAGAAATTGACATCCCACTCTG	1921
QY	1883	AAGGACCTGGCCCCCAGGCCGGAATCCCGCAGCTGGGTCCGSCCGAGATPACGAGGCCCCAC	1942
Db	1922	AAGGACCTGGCCCCCAGGCCGGAATCCCGCAGCTGGGTCCGSCCGAGATPACGAGGCCCCAC	1981
QY	1943	CCAAAGTGCTCAGAGGACCTCATCTATCCGCACTGCTCTTTACACCAATGAGGSCCGAG	2002
Db	1982	CCAAAGTGCTCAGAGGACCTCATCTATCCGCACTGCTCTTTACACCAATGAGGSCCGAG	2041
QY	2003	GGTCCCGGCGAGCCCAAGGAGTCCGTGCGACGAACTCGGACGAGAACTCGGCGTGGCAAAATCT	2062
Db	2042	GGTCCCGGCGAGCCCAAGGAGTCCGTGCGACGAACTCGGACGAGAACTCGGCGTGGCAAAATCT	2101
QY	2063	ATCTGCAAAAGCGGGGCGAGAGCGGGGCAACCCCAAAAGCTCCAGAGGCCCTCTGCTCAGGCC	2122
Db	2102	ATCTGCAAAAGCGGGGCGAGAGCGGGGCAACCCCAAAAGCTCCAGAGGCCCTCTGCTCAGGCC	2161
QY	2123	CTGGCCCCGCCAAGGCTCTTATGTAACCCCGACTCTCAGAGAGAGGAGACCCGTGGCGGAAC	2182
Db	2162	CTGGCCCCGCCAAGGCTCTTATGTAACCCCGACTCTCAGAGAGAGGAGACCCGTGGCGGAAC	2221
QY	2183	GCTGGGACAGGCTCTTTCAGGCTCTCTCAGCGGACCTTCCCGCAGGCTGGGCTCACTGGAGC	2242
Db	2222	GCTGGGACAGGCTCTTTCAGGCTCTCTCAGCGGACCTTCCCGCAGGCTGGGCTCACTGGAGC	2281
QY	2243	GGAAACCGGTGGAGGCTCTCTCAAACTGGACAGCTCCCTGTGCTCTCCCTGGGAAATA	2302
Db	2282	GGAAACCGGTGGAGGCTCTCTCAAACTGGAGCTCCCTGTGCTCTCCCTGGGAAATA	2341
QY	2303	AAGGCAAGCCCGAAGCAACCGCTCAGAGGCGGSCCGGCGCGAGACTTTGTGTGTGCTGA	2362
Db	2342	AAGGCAAGCCCGAAGCAACCGCTCAGAGGCGGSCCGGCGCGAGACTTTGTGTGTGCTGA	2401
QY	2363	AAGAGCGGACTCTTGAAGAGGCCCTTGCGCTCCCAAGAAAGCCATGAGCTTACTGTCGT	2422
Db	2402	AAGAGCGGACTCTTGAAGAGGCCCTTGCGCTCCCAAGAAAGCCATGAGCTTACTGTCGT	2461
QY	2423	CCAGCGAGAGGTGAAAAGCAGTGAAGACGACGAGAGAGAAAGCGAGAGGGCGGCACACAG	2482
Db	2462	CCAGCGAGAGGTGAAAAGCAGTGAAGACGACGAGAGAGAAAGCGAGAGGGCGGCACACAG	2521

Qy	2483	AGGGAGGAGATACCCCTGGGGGCGGAGGATGGGGATACAGACGCTCAGACCA	2542
Db	2522	AGGGAGGAGATACCCCTGGGGGCGGAGGATGGGGATACAGACGCTCAGACCA	2578
Qy	2543	TGTTGTCACAGACCTCGAGAGATCACCGGAGCCAGCCCATACGGGGCGGACCA	2602
Db	2579	TGTTGTCACAGACCTCGAGAGATCACCGGAGCCAGCCCATACGGGGCGGACCA	2638
Qy	2603	TGTTGTCACAGACCTCGAGAGATCACCGGAGCCAGCCCATACGGGGCGGACCA	2662
Db	2639	TGTTGTCACAGACCTCGAGAGATCACCGGAGCCAGCCCATACGGGGCGGACCA	2698
Qy	2663	TGTTGTCACAGACCTCGAGAGATCACCGGAGCCAGCCCATACGGGGCGGACCA	2722
Db	2699	TGTTGTCACAGACCTCGAGAGATCACCGGAGCCAGCCCATACGGGGCGGACCA	2758
Qy	2723	AAAGCCCACTCGAGAGATCACCGGAGCCAGCCCATACGGGGCGGACCA	2782
Db	2759	AAAGCCCACTCGAGAGATCACCGGAGCCAGCCCATACGGGGCGGACCA	2818
Qy	2783	CTGGCAGAGCTCGTTCAAGATGTTTGATCTAGAGATCTAGAGCTCGAGGCAAGT	2842
Db	2819	CTGGCAGAGCTCGTTCAAGATGTTTGATCTAGAGATCTAGAGCTCGAGGCAAGT	2878
Qy	2843	GGGACAGATCCCACTCAAGCCCTAGGGGTGAGAGGGCACTGGGCTCGAGCAAGT	2902
Db	2879	GGGACAGATCCCACTCAAGCCCTAGGGGTGAGAGGGCACTGGGCTCGAGCAAGT	2938
Qy	2903	AGTACGATGAGAGAGGTTCTGTGATCAAGTATCCCAAGACCCGGGCGGACCA	2962
Db	2939	AGTACGATGAGAGAGGTTCTGTGATCAAGTATCCCAAGACCCGGGCGGACCA	2998
Qy	2963	GTGAGACCTCGAGATCCGGAAGTACAGAGCGATTCACTCGAGATCTGTGAG	3022
Db	2999	GTGAGACCTCGAGATCCGGAAGTACAGAGCGATTCACTCGAGATCTGTGAG	3058
Qy	3023	CCCTTTGGGGGTCAACCTGTGTGGGCAAGGAGTGTGTGTGTGTGTGTGTGTGT	3082
Db	3059	CCCTTTGGGGGTCAACCTGTGTGGGCAAGGAGTGTGTGTGTGTGTGTGTGTGT	3118
Qy	3083	GTGGGCAAGGAGTGTATGAGCTCATTTGGGCGGCGAGCTTCCAGAGATGATGTGC	3142
Db	3119	GTGGGCAAGGAGTGTATGAGCTCATTTGGGCGGCGAGCTTCCAGAGATGATGTGC	3178
Qy	3143	TGAGAGGGCTCAACCTGTGTATCACCATCTCAGGAAAGAAACAACTGGGGGTAT	3202
Db	3179	TGAGAGGGCTCAACCTGTGTATCACCATCTCAGGAAAGAAACAACTGGGGGTAT	3238
Qy	3203	ACCTGTCTGT	3262
Db	3239	ACCTGTCTGT	3298
Qy	3263	GCTGGACCAAGGAGTGTATGAGCTCATTTGGGCGGCGAGCTTCCAGAGATGATGTGC	3322
Db	3299	GCTGGACCAAGGAGTGTATGAGCTCATTTGGGCGGCGAGCTTCCAGAGATGATGTGC	3358
Qy	3323	GGATTAAAGTCTGTGTATCGCCCTCAAGAGCTCCGTGAGGTGTATGCTGGGCGG	3382
Db	3359	GGATTAAAGTCTGTGTATCGCCCTCAAGAGCTCCGTGAGGTGTATGCTGGGCGG	3418
Qy	3383	AACTTACCAAAATTCATGAGCTTGTGCGGAGCTTCCCGGAGCGGCGGCTGTGC	3442
Db	3419	AACTTACCAAAATTCATGAGCTTGTGCGGAGCTTCCCGGAGCGGCGGCTGTGC	3478
Qy	3443	TGTTGACCTGACAGTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	3502
Db	3479	TGTTGACCTGACAGTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	3538
Qy	3503	GCTTTCATGCTGT	3562
Db	3539	GCTTTCATGCTGT	3598
Qy	3563	TCAGAGGCAATACAGGCGGCTATCTTCTCCCAACAGCGGAGTGAAGA	3622

Db	3599	TCAGAGGCAATACAGGCGGCTATCTTCTCCCAACAGCGGAGTGAAGA	3658
Qy	3623	TGTTGTCACAGACCTCGAGAGATCACCGGAGCCAGCCCATACGGGGCGGACCA	3682
Db	3659	TGTTGTCACAGACCTCGAGAGATCACCGGAGCCAGCCCATACGGGGCGGACCA	3718
Qy	3683	ATGTTGTCACAGACCTCGAGAGATCACCGGAGCCAGCCCATACGGGGCGGACCA	3742
Db	3719	ATGTTGTCACAGACCTCGAGAGATCACCGGAGCCAGCCCATACGGGGCGGACCA	3778
Qy	3743	TAATGGCTGGGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	3802
Db	3779	TAATGGCTGGGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	3838
Qy	3803	GGTCTTCATCACAAGAGCTCAGAGGCTCAAGGCTCTGTGTGTGTGTGTGTGTGT	3862
Db	3839	GGTCTTCATCACAAGAGCTCAGAGGCTCAAGGCTCTGTGTGTGTGTGTGTGTGT	3898
Qy	3863	TGTTTTCCTCAGTCCGCTGTGGGGCAGACGCAAGTTTACTTCAATGACTGAAC	3922
Db	3899	TGTTTTCCTCAGTCCGCTGTGGGGCAGACGCAAGTTTACTTCAATGACTGAAC	3958
Qy	3923	GTAACGATCATGAACTGTGAAAGGSC	3951
Db	3959	GTAACGATCATGAACTGTGAAAGGSC	3987

RESULT 2  
US-09-291-417D-11  
Sequence 11, Application US/09291417D  
Patent No. 6680170  
GENERAL INFORMATION:  
APPLICANT: PLOWMAN, GREGORY  
APPLICANT: MARTINEZ, RICARDO  
APPLICANT: MYHE, DAVID  
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
FILE REFERENCE: 038602/0329  
CURRENT APPLICATION NUMBER: US/09/291,417D  
CURRENT FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: 60/081,784  
PRIOR FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 155  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 11  
LENGTH: 4133  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-291-417D-11

Query Match 92.0%; Score 3635; DB 4; Length 4133;  
Best Local Similarity 95.9%; Pred. No. 0;  
Matches 3824; Conservative 0; Mismatches 15; Indels 150; Gaps 3;

Qy	110	CTTACGACAGTGTATCAAGGCTGCGCATGTCAAGAGCGGCGAGCTGCTCCATCAAGG	169
Db	2	CATTGGGAGGTGTATGAGGCTGCGCATGTCAAGAGCGGCGAGCTGCTCCATCAAGG	61
Qy	170	TCATGATGTACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	229
Db	62	TCATGATGTACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	121
Qy	230	AGTACTTACACCGCAATGCGCACTTACGAGGCTTCAATCAAGAGAGGCGGCGG	289
Db	122	AGTACTTACACCGCAATGCGCACTTACGAGGCTTCAATCAAGAGAGGCGGCGG	181
Qy	290	CGGAAAGAGTACAGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	349
Db	182	CGGAAAGAGTACAGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	241
Qy	350	ACCTGTAAAGACAAAGGCAAGCGCTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGG	409
Db	242	ACCTGTAAAGACAAAGGCAAGCGCTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGG	301

OY	410	GGGAGAAATCCTCAAGGGGTCTGGGCGCATCTCCAGTCCCAAGGTAATCCATCCAGACATCA	465
Db	302	GGGAAATCCTCAAGGGGTCTGGGCGCATCTCCAGTCCCAAGGTAATCCATCCAGACATCA	361
OY	470	AGGGGACAGATGTGTGTGTGCTGACAGAGAAATGCTGAGGTCAAGCTAGTGAATTTTGGGGTGA	529
Db	352	AGGGGACAGATGTGTGTGTGCTGACAGAGAAATGCTGAGGTCAAGCTAGTGAATTTTGGGGTGA	421
OY	530	GTGCTCAGCTGGAACGGCACCGTGGGCGACGGAACCTTTCATTTGGGACTCCCTACTGGA	589
Db	422	GTGCTCAGCTGGAACGGCACCGTGGGCGACGGAACCTTTCATTTGGGACTCCCTACTGGA	481
OY	590	TGGCTCCAGAGGTCATTCGCTGTGTGATGAAGACCTTCATGCCATTCATTTGATTCAGAGGTG	649
Db	482	TGGCTCCAGAGGTCATTCGCTGTGTGATGAAGACCTTCATGCCATTCATTTGATTCAGAGGTG	541
OY	650	ATATTTTGGTCTGTAGGAATCAGAGCCATCGAGATGGACAGGGAGGCGCCCTCTGTGTG	709
Db	542	ATATTTTGGTCTGTAGGAATCAGAGCCATCGAGATGGACAGGGAGGCGCCCTCTGTGTG	601
OY	710	ACATGCAACCCCATGGAGCGCTCTTCCTCATCTCTGGAACCTCCGCGCCAGGCTCAAGT	769
Db	602	ACATGCAACCCCATGGAGCGCTCTTCCTCATCTCTGGAACCTCCGCGCCAGGCTCAAGT	661
OY	770	CCAAAGATGTCTTAAGAAATTCATTGACTTCATTTGACATGTCTCATCAAGACTTACC	829
Db	662	CCAAAGATGTCTTAAGAAATTCATTGACTTCATTTGACATGTCTCATCAAGACTTACC	721
OY	830	TGAGCGCCGCCACCCACGAGACGCTACTGAAGTTTCCCTTCATCCGGAACCAAGCCACGG	889
Db	722	TGAGCGCCGCCACCCACGAGACGCTACTGAAGTTTCCCTTCATCCGGAACCAAGCCACGG	781
OY	890	AGCGGCAAGTCCGCAATCCAGTTAAGAGCACATTTGACCGATCCCGGAGAAAGCGGGGTG	949
Db	782	AGCGGCAAGTCCGCAATCCAGTTAAGAGCACATTTGACCGATCCCGGAGAAAGCGGGGTG	841
OY	950	AGAAAGAGGAGACAGAAATATGAGTACAGCGGCGACGAGGAGGAAGATGACAGCCATGAG	1000
Db	842	AGAAAGAGGAGACAGAAATATGAGTACAGCGGCGACGAGGAGGAAGATGACAGCCATGAG	901
OY	1010	AGGAAGGAGAGGCAAGCTCCATCATGAAAGTGTGCTGGAGAGTGCATCAAGCGGGAGT	1066
Db	902	AGGAAGGAGAGGCAAGCTCCATCATGAAAGTGTGCTGGAGAGTGCATCAAGCGGGAGT	961
OY	1070	TTCTCCGGCTCCAGCAGGAAAAATTAAGAGCACTCAGAGGCTTTTAAACAGCAGCAGCAGC	1122
Db	962	TTCTCCGGCTCCAGCAGGAAAAATTAAGAGCACTCAGAGGCTTTTAAACAGCAGCAGCAGC	1022
OY	1130	TGCACAGTACAGCAGCAGCAGACCCCGAGGCGACATCAAAACACTCTGTGCACACAGCGG	1188
Db	1022	TGCACAGTACAGCAGCAGCAGACCCCGAGGCGACATCAAAACACTCTGTGCACACAGCGG	1088
OY	1190	AGCGGCGCATTAAGAGAGCAGAAAGAGAGACGGCGCGCGCTGTGAGAGAGCAACAGCGCGG	1244
Db	1082	AGCGGCGCATTAAGAGAGCAGAAAGAGAGAGAGCGCGCGCGCTGTGAGAGAGCAACAGCGCGG	1144
OY	1250	AGCGGAGCAGCGGAAAGCTGACAGAGAAAGACAGCAGCGCGGCTGAGAGACATGCAGG	1300
Db	1142	AGCGGAGCAGCGGAAAGCTGACAGAGAAAGACAGCAGCGCGGCTGAGAGACATGCAGG	1200
OY	1310	CTCTGCGGCGGGAGAGAGAGCGCGCGCAGCGGAGGCTGTAGCA-----	1355
Db	1202	CTCTGCGGCGGGAGAGAGAGCGCGCGCAGCGGAGGCTGTAGCA-----	1266
OY	1353	-----	1355
Db	1262	GGCTTAGAGAGAGCAGCAGCAGCTCGAATCTTTACAGAAACAGCGTCCAGAAACAGG	1322
OY	1353	-----GGAATTCACGCGGAAGCAGCTGAGAGAGCAGCGGCGCTCAGAACTCTCC	1400
Db	1322	CCCTCTGCTGGAATTCACGCGGAAGCAGCTGAGAGAGCAGCGGCGCTCAGAACTCTCC	1388

OY	1403	AGAGCGAGCTGCACAGAGAGATGCTCAATCCGAAAGTCCCTGACAGCAGCAACAGCAGC	1462
Db	1382	AGAGCGAGCTGCACAGAGAGATGCTCAATCCGAAAGTCCCTGACAGCAGCAACAGCAGC	1441
OY	1463	AGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCTGCTCGGAGCAGGAAGCCCTGTATCC	1522
Db	1442	AGCAGCTTCAGAAACAGCAGCAGCAGCTCTGCTCGGAGCAGGAAGCCCTGTATCC	1501
OY	1523	ATTATGCTCGGGGCATGATATCCGCTGACAAACAGCTCTGGGCCCCGAGAGGTAGAAAGA	1582
Db	1502	ATTATGCTCGGGGCATGATATCCGCTGACAAACAGCTCTGGGCCCCGAGAGGTAGAAAGA	1561
OY	1583	GAACAGAGATGAACAAGACAGAAACTCTCCCTTGGCCAAAGAGCAACCCAGGCGACAGG	1642
Db	1562	GAACAGAGATGAACAAGACAGAAACTCTCTTGGCCAAAGAGCAACCCAGGCGACAGG	1621
OY	1643	GGCCTGAGCCCCCATGCCCCAGGCGCTCCCGAGGGCCCCAGAGACCCCTTTCACAGATC	1702
Db	1622	GGCCTGAGCCCCCATGCCCGAGGCTCTCCCGAGGGCCCCAGAGACCCCTTTCACAGATC	1681
OY	1703	CTCCTATGCAAGGCGCGGTGAGGCCCAAGAGGAGCCGACA-----	1744
Db	1682	CTCCTATGCAAGGCGCGGTGAGGCCCAAGAGGAGCCGACAAAGAGCTGTGTGACACAC	1741
OY	1745	-----AGTCCCTGACAGGACAGC	1762
Db	1742	GGGTCCCACTGAAGCCATATGACAGCACTGTATCCCGATCCCATCTCTGACAGACACAGC	1801
OY	1763	CCACCCGAAACCTGGGCTGCTTCCGACGCTCCATGACCCGACCCGACCTGCAATCCGCGCAC	1822
Db	1802	CCACCCGAAACCTGGGCTGCTTCCGACGCTCCATGACCCGACCCGACCTGCAATCCGCGCAC	1861
OY	1823	CCACTGCGACGCGCCAGTGCCCGAGAGCTGTATCGGCGAAGATTGACCCCACTCTG	1882
Db	1862	CCACTGCGACGCGCCAGTGCCCGAGAGCTGTATCGGCGAAGATTGACCCCACTCTG	1921
OY	1883	AAGGACTGTGCCCCAGGCCCAATCCCCAGGCTGGGTCCGCGCAAGATTAAGAGGCCCCAC	1942
Db	1922	AAGGACTGTGCCCCAGGCCCAATCCCCAGGCTGGGTCCGCGCAAGATTAAGAGGCCCCAC	1961
OY	1943	CCAAGGTGCTCTCAGAGGACCTCATCTATGCGCACTGCGCTTTAACAACGATGAGGGCCGAG	2002
Db	1982	CCAAGGTGCTCTCAGAGGACCTCATCTATGCGCACTGCGCTTTAACAACGATGAGGGCCGAG	2041
OY	2003	GGTCCCGGCGACGCCAGGCAAGTCCGTCAGACCTCGACACAACTCCGCTGTGCAAAATCT	2062
Db	2042	GGTCCCGGCGACGCCAGGCAAGTCCGTCAGACCTCGACACAACTCCGCTGTGCAAAATCT	2101
OY	2063	ATCTGCAAAAGCGGGCGAGAGCGGGGCAACCCCAAGCTCCAGGGCCCCCTGTCTATGCCCC	2122
Db	2102	ATCTGCAAAAGCGGGCGAGAGCGGGGCAACCCCAAGCTCCAGGGCCCCCTGTCTATGCCCC	2161
OY	2123	CTGGCCCGGCCCAAGGCTCTAGTAACCCCGACCTCAGAGAGAGGAGCCCTGGCTGGGAAC	2182
Db	2162	CTGGCCCGGCCCAAGGCTCTAGTAACCCCGACCTCAGAGAGAGGAGCCCTGGCTGGGAAC	2221
OY	2183	GCTGGAGCAGGCTCTTTCAGGCTCTCAGCGGACCTTCCCGCAGGCTGAGCTCATCTGAGGC	2242
Db	2222	GCTGGAGCAGGCTCTTTCAGGCTCTCAGCGGACCTTCCCGCAGGCTGAGCTCATCTGAGGC	2281
OY	2243	GGAAACCGGTGGAGGCTCTTCCAAACTGACAGCTCCCTGTGTCTCTCCCTTGGGAATA	2302
Db	2282	GGAAACCGGTGGAGGCTCTTCCAAACCGGACAGCTCCCTGTGTCTCTCCCTTGGGAATA	2341
OY	2303	AAGCCAAAGCCGAGACCAACGCTCAGGGCCAGGCGGGCCCGCAGACTTGTGTGTGCTGA	2362
Db	2342	AAGCCAAAGCCGAGACCAACGCTCAGGGCCAGGCGGGCCCGCAGACTTGTGTGTGCTGA	2401
OY	2363	AAGAGCGGACTCTGGAAGAGGCCCCCTGAGCTCCCAAGAAAGGCATGACTATCTGCTGCT	2422
Db	2402	AAGAGCGGACTCTGGAAGAGGCCCCCTGAGCTCCCAAGAAAGGCATGACTATCTGCTGCT	2461
OY	2423	CCACCGAGAGGTGAAAGCATGTAGAGACGACGAGAGAGAGCGAAAGCGGCGCAGCAGC	2482

Db 2462 CCAAGGAGAGGTGAAAAGCACTGAGACGACGAGAGAGGACCAAGCCGGCCAGAG 2521  
Qy 2483 AGGGAGAGAGATACCCCTGGGGGCGCAGGATGGGAGATACAGACAGCTCAGACCA 2542  
Db 2522 AGGGAGAGAGATACCCCTGGGGGCGCAGGATGGGAGATACAGACAGCTCAGACCA 2578  
Qy 2543 TGGTGTTCACAGACGTGAGAGATACACGGGAGCCAGCCCTCCATACGGGGGCGGACCA 2602  
Db 2579 TGGTGTTCACAGACGTGAGAGATACACGGGAGCCAGCCCTCCATACGGGGGCGGACCA 2638  
Qy 2603 TGGTGTTCACAGACGTGAGAGATACACGGGAGCCAGCCCTCCATACGGGGGCGGACCA 2662  
Db 2639 TGGTGTTCACAGACGTGAGAGATACACGGGAGCCAGCCCTCCATACGGGGGCGGACCA 2698  
Qy 2663 ACACAAACCTGCTGAGCTGAGTCCAGCCAGCCATCAACCAACGAGAAACAGAAAGCC 2722  
Db 2699 ACACAAACCTGCTGAGCTGAGTCCAGCCAGCCATCAACCAACGAGAAACAGAAAGCC 2758  
Qy 2723 AAAAGCCCACTCCGAAAGATGGAGTGGATCTACATCTCTGGGGCTGGTAAAGGCC 2782  
Db 2759 AAAAGCCCACTCCGAAAGATGGAGTGGATCTACATCTCTGGGGCTGGTAAAGGCC 2818  
Qy 2783 CTGGCAAGAGCTGCTTACAGATGTTTGTGATCTAGGATCTACAGCCTGAGGACATG 2842  
Db 2819 CTGGCAAGAGCTGCTTACAGATGTTTGTGATCTAGGATCTACAGCCTGAGGACATG 2878  
Qy 2843 GGAAGAGATCCCAATCAAGCCCTAGTGGTGGAGAGGAGCACTGGGCTGACCAAGTGC 2902  
Db 2879 GGAAGAGATCCCAATCAAGCCCTAGTGGTGGAGAGGAGCACTGGGCTGACCAAGTGC 2938  
Qy 2903 AGTACGAGTGAAGAGAGGTTCTGTGTGCAACGTGAATCCCAACCAACCCGGGCCCA 2962  
Db 2939 AGTACGAGTGAAGAGAGGTTCTGTGTGCAACGTGAATCCCAACCAACCCGGGCCCA 2998  
Qy 2963 GTGAGACCCCTGAGATCCGGAAGTACAGAAAGCATTAACCTCCGAGATCTGTGAG 3022  
Db 2999 GTGAGACCCCTGAGATCCGGAAGTACAGAAAGCATTAACCTCCGAGATCTGTGAG 3058  
Qy 3023 CCTTTTGGGGGGTCAACCTGTGTGTGGGACAGGAGCAAGGCTGATGTTGTGACCGAA 3082  
Db 3059 CCTTTTGGGGGGTCAACCTGTGTGTGGGACAGGAGCAAGGCTGATGTTGTGACCGAA 3118  
Qy 3083 GTGGGAGGGGCAAGGTGATGATCTATTTGGGCGGCGACCTTCCAGAGATGATGTC 3142  
Db 3119 GTGGGAGGGGCAAGGTGATGATCTATTTGGGCGGCGACCTTCCAGAGATGATGTC 3178  
Qy 3143 TGGAGGGGCTCAACCTGCTCATCACTCAAGGAGAAAGAAACAACTGGGGGTGATT 3202  
Db 3179 TGGAGGGGCTCAACCTGCTCATCACTCAAGGAGAAAGAAACAACTGGGGGTGATT 3238  
Qy 3203 ACTGTCTGTGCTCCGGAACAAGATTCTGCAACATGACCCAGAGTGGAGAGAGAGCAG 3262  
Db 3239 ACTGTCTGTGCTCCGGAACAAGATTCTGCAACATGACCCAGAGTGGAGAGAGAGCAG 3298  
Qy 3263 GCTGAGCAACCGTGGGGGACATGAGGGCTGGGGCACTACCGTGTGTGAATAACGAGC 3322  
Db 3299 GCTGAGCAACCGTGGGGGACATGAGGGCTGGGGCACTACCGTGTGTGAATAACGAGC 3358  
Qy 3323 GGATTTAAGTTCCTGGTCACTGGCCCTCAAGAGCTCGTGGAGGTGATGCTGGGGCCCCA 3382  
Db 3359 GGATTTAAGTTCCTGGTCACTGGCCCTCAAGAGCTCGTGGAGGTGATGCTGGGGCCCCA 3418  
Qy 3383 AACCTTACCAAAATTCAATGAGCTTCAAGTCTTTCAGCACTCCCAACGAGCTCTGC 3442  
Db 3419 AACCTTACCAAAATTCAATGAGCTTCAAGTCTTTCAGCACTCCCAACGAGCTCTGC 3478  
Qy 3443 TGGTGAACCTGACAGTGAAGAGAGGGGCAAGGGCTCAAGGTCACTTATGGCTTCAGTGTG 3502  
Db 3479 TGGTGAACCTGACAGTGAAGAGAGGGGCAAGGGCTCAAGGTCACTTATGGCTTCAGTGTG 3538  
Qy 3503 GCTTCCAGTGTGATGATCTCGGGGAAACAGTATGACATCACTCCCTGTGCA 3562

Db 3539 GCTTCCAGTGTGATGATGCTCGGGGAAACAGTATGACATCTACATCCCTGTGACA 3598  
Qy 3563 TCCAGACCCAGATACACCCCATATCCCTTCTCCCAACGAGGAGCATGAGA 3622  
Db 3599 TCCAGACCCAGATACACCCCATATCCCTTCTCCCAACGAGGAGCATGAGA 3658  
Qy 3623 TGTGTGTGCTGACAGAGACAGAGGTTCTACGTCAACAGTACAGGCGCATATTAAG 3682  
Db 3659 TGTGTGTGCTGACAGAGACAGAGGTTCTACGTCAACAGTACAGGCGCATATTAAG 3718  
Qy 3683 ATGTGTGTGCTGACAGTGGGGGAGATGCTTACTTGTGGCTTACATCTGCTCAACGA 3742  
Db 3719 ATGTGTGTGCTGACAGTGGGGGAGATGCTTACTTGTGGCTTACATCTGCTCAACGA 3778  
Qy 3743 TAAATGGCTGGGTGAGAAAGCCATTGAGATCCCTCTGTGAGAACGGGCCACTCGAG 3802  
Db 3779 TAAATGGCTGGGTGAGAAAGCCATTGAGATCCCTCTGTGAGAACGGGCCACTCGAG 3838  
Qy 3803 GGGTCTTCAATGCAAAACAGCTCAGAGCTCAAGTCTGTGTGAGCGGAAATGACAAG 3862  
Db 3839 GGGTCTTCAATGCAAAACAGCTCAGAGCTCAAGTCTGTGTGAGCGGAAATGACAAG 3898  
Qy 3863 TGTTTTTCCTCAAGTCCCTCTGGGGGAGAGCAAGCCAAATTACTTATCACTGAAC 3922  
Db 3899 TGTTTTTCCTCAAGTCCCTCTGGGGGAGAGCAAGCCAAATTACTTATCACTGAAC 3958  
Qy 3923 GTAACTGATATGATGATCTGTGAAAGGC 3951  
Db 3959 GTAACTGATATGATGATCTGTGAAAGGC 3987

RESULT 3  
US-09-645-456A-2  
; Sequence 2, Application US/09645456A  
; Patent No. 6562580  
; GENERAL INFORMATION:  
; APPLICANT: Pu, C. Alan  
; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AND  
; FILE REFERENCE: A-68344/RMS/DHR  
; CURRENT APPLICATION NUMBER: US/09/645, 456A  
; CURRENT FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US/09/425, 324  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 3996  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-09-645-456A-2

Query Match 35.6%; Score 1407.2; DB 4; Length 3996;  
Beet Local Similarity 62.5%; Pred. No. 6.4e-285; Indels 153; Gaps 15;  
Matches 2528; Conservative 0; Mismatches 1363;

Qy 7 ATGGGAGACCCAGCCCGCCGAGCTGGAGCAATGCACTGTCCGCTCGGGAGC 66  
Db 1 ATGGGAGACCACTCCCGGGCTCGAAGCTGATGAATGATCTCTGGGCTCTGAGGAC 60  
Qy 67 CTGTCTGGGATCTTTGAGCTTGTGAGGTGTGCGCAATGAACTTACAGCAAGTGTAC 126  
Db 61 CTGTCAAGGATCTTTGATGATGTTGTAATCTGTTGAAATGAAATACATCGGGCAAGTTAT 120  
Qy 127 AAGGTGGCATGTCAAGAGGGGCACTGGCTGCCATCAAGGTCAATGATGATGACGAG 186  
Db 121 AAGGTGTATGTCAAAAGGGGCAAGCTTGCAACCAAGTTATGATGATGACAGGG 180  
Qy 187 GACGAGAGAGAGATCAACAGAGATCAATGCTGAAAAGTACTCTACACCGC 246  
Db 181 GATGAGAGAGAGAAATCAACAGAAATTAACTGTTGAAGAAATTTCTCATCACCGG 240



QY 247 AACATGCACTTACTAGGAGCTTTCATCAAGAAAGAGCCCGGAAAGATGACCG 306  
DB 241 AATATTGTACATCATATGATGCTTTATCAAAAAGAACCCACAGGATGATGACCA 300  
QY 307 CTCTGCTGATGATGAGTTCTGTGTGCTGTGTTCAAGTACCTGTTAAAGAACCA 366  
DB 301 CTTTGGTGTATGAGTTTGTGTGTGTGTGCTGTGCTGACGACCTGATCAAGAACCA 360  
QY 367 AAAGCAAGCCCTGAAAGAGAGCTGTATGCTTATATTCAGAGGAGATCTCAGGGT 426  
DB 361 AAAGTATCACCTGTAAGAGAGATGATGATCATCATCTGACGGGAAATCTTACGGGG 420  
QY 427 CTGGCCATCTCCATGCCCCAAGGATGATCAATGACATCAAGGGGAGAAATGCTG 486  
DB 421 CTGAGTCACTTGACCAAGATTAAGTATTCATCGATATTAAGGCAAAATGCTTG 480  
QY 487 CTGACAGAAATGCTGAGGTCAAGCTAGTGAATTTTGGGTGAGTGTCTCAGCTGACCG 546  
DB 481 CTGATGAAATGCAAGAGTTAACTAGTGAATTTTGGGTGAGTGTCTCAGCTGATGA 540  
QY 547 ACCGTGGGAGACGAACTTTTATTTGGGATCTCTTATGATGCTTCAAGGTATC 606  
DB 541 ACAGTGGGAGAGGAATCTTTCATTTGGAATCTCTTACCTGATGACACAGAAATTA 600  
QY 607 GCTGTGATGAAACCTGTATGCACTATGATTAAGAGATGATTTTGGTCTGAGGA 666  
DB 601 GCTGTGATGAAACCTGTATGCACTATGATTAAGAGATGATTTTGGTCTGAGGA 660  
QY 667 ATCACAGCCATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726  
DB 661 ATCACAGCCATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
QY 727 GCTCTTCTCTATCTCTGAAACCTCCGCGGAGCTCAAGTCCAAAGTGTAAAG 786  
DB 721 GCTCTTCTCTATCTCTGAAACCTCCGCGGAGCTCAAGTCCAAAGTGTAAAG 780  
QY 787 AAGTTCAATGATCTTCAATGACATGTCATCAAGACTTACCTGAGCGGCCAACG 846  
DB 781 AATTTCAAGTCAATTTATGAGAGCTGTTGTAAAGATCAAGCCAGGACCAAGCA 840  
QY 847 GAGCACTACTGAATTTCTCTCATCCGCGGAGCAAGCCCAAGAGAGAGAGAGAG 906  
DB 841 GAGCACTACTGAATTTCTCTCATCCGCGGAGCAAGCCCAAGAGAGAGAGAGAG 900  
QY 907 CAGCTTAAGAGCAATGATCCGAGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAG 966  
DB 901 CAGCTTAAGAGCAATGATCCGAGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
QY 967 TATGATGATGAG 1026  
DB 961 TATGATGATGAG 1017  
QY 1027 TCCATCATGAAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1086  
DB 1018 TCCATCATGAAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1077  
QY 1087 GAAAAATGAG 1146  
DB 1078 GAAAAATGAG 1131  
QY 1147 GAG 1206  
DB 1132 GAG 1191  
QY 1207 CAGAAAG 1266  
DB 1192 CAGAAAG 1251  
QY 1267 CTGAG 1326  
DB 1252 CAG 1305

QY 1327 GAGCGCGGAG 1386  
DB 1306 GAG 1365  
QY 1387 CAGTCAAG 1446  
DB 1366 CAG 1425  
QY 1447 CAG 1506  
DB 1426 CAG 1455  
QY 1507 AG 1566  
DB 1486 AG 1515  
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DB 1573 CAG 1632  
QY 1678 CAG 1731  
DB 1633 CAG 1692  
QY 1732 CAG 1788  
DB 1693 CAG 1752  
QY 1789 CAG 1848  
DB 1733 CAG 1812  
QY 1849 CAG 1901  
DB 1813 CAG 1872  
QY 1902 CAG 1953  
DB 1873 CAG 1932  
QY 1954 CAG 2013  
DB 1933 CAG 1992  
QY 2014 CAG 2071  
DB 1993 CAG 2052  
QY 2072 CAG 2131  
DB 2053 CAG 2112  
QY 2132 CAG 2187  
DB 2113 CAG 2172  
QY 2188 CAG 2247  
DB 2173 CAG 2232  
QY 2248 CAG 2307  
DB 2233 CAG 2292  
QY 2308 CAG 2367  
DB 2293 CAG 2352  
QY 2368 CAG 2427



Db 2253 CTCGGATTGAAAGAAACAACCGCCCAATGAAAGAGTGAATGATTAATCTCTCTCCAGT 2412  
 Qy 2428 GAGGAGGTGAAAGCAGTGAAGACGACGAGAGGAGGCGAAGCGGCGCAGCAGAGGGG 2487  
 Db 2413 GAGAGTGCAGAAAGTACGCGAAGAGAGAGAGATGAGAGAGAGAACCATGATGGG 2472  
 Qy 2488 A-----GCAAGATACCCCTGGGGCCGACG 2514  
 Db 2473 ACAATGCTGTACGCGACATACCCAGACTGATACCAACAGAGCTCCAGGACGACAG 2532  
 Qy 2515 GATGGGATACAGACAGGCTGACGACCAATGGTGTCCACAGCTGCGAGAGATCACCGGG 2574  
 Db 2533 CAGTACATGTGGGAATGTGGGAGCGATGGGCTGGAGACTCTCAATGCGGACAGTTTC 2592  
 Qy 2575 ACCGAGCCCATATACGGGGGCGGACCAATGGTGTCCAGCGCACCCCTGAAAGAGAGCGG 2634  
 Db 2593 AGCGGCAAGTATTTCAAGAGAGAACTTGATGATTAAGAGAGCGTGGAGAGAAAGAG 2652  
 Qy 2635 AACCTGCTGATGCTGACAGCAATGGT-----ACACAAACCTGCTGACGTGTC 2685  
 Db 2653 CGATCTGGCCACAGTGAAGAGAAATGGCTTGTGGCCACATCACTCCCTGACCTGTGTG 2712  
 Qy 2686 CAGCCAGCCCACTACCCACCGAAGACAGCAAGGCCAAA-----GCCCACTCGAAG 2739  
 Db 2713 CAGCAGAGCCATTCTCCAGCTGGAACCCGACTGAGGAGCTGGGGCGGCTCTCAACCAT 2772  
 Qy 2740 GATGGAGTGTGATCAACAGTCTGCTGGGCTGTGTAAGGCGCCCTGGCAGAGCTCGTTC 2799  
 Db 2773 TCCAGGAGATGATGACTCTGGGACATGATATGGCATGGGAGACAGCACAAAGCCCTCCTC 2832  
 Qy 2800 ACGATGTTTGTGATCTAGGATCTACCAAGCTGAGGCGCATGGGAGACATGCTC----- 2854  
 Db 2833 ACCCCCTTTGTGAGCCCGAAGATACCAAGCTCTCCACTGATGAAGATGAAGAGAT 2892  
 Qy 2855 -----CCATCAAGCCCTAGTGGGTGAAGAGGCGCATCGGCTGACAG-----CTG 2901  
 Db 2893 GAGGATATCATAGCCGCGAGCTCTGTTTACTAGCCAACTTTTGAAGAGAACAGGCCAAA 2952  
 Qy 2902 CAGTACGACGTGAGAGAGGTTCTGTGTCAACGTGAATCCCAACCAACCCGCGGCCAC 2961  
 Db 2953 CTCAATGAAAGCAAGAAAGATTTCCGTGTGTAATGTAATCCCAACCAACATTCGCGCTCAT 3012  
 Qy 2962 AGTGAAGCCCTGAGATCCGGAAGTACAAAGAGATTCACCTCGAGATCTCTGTGCA 3021  
 Db 3013 AGCACAACCAAGAAATACAGAAATACAAAGATTCACCTCAAGAAATCTTTGTGCA 3072  
 Qy 3022 GCCCTTTGGGGGTCAACCTGCTGGTGGGCACGAGAACGGGCTGATGTTCTGGACCGA 3081  
 Db 3073 GCTCTGTGGGTGTAAACCTTGTGGTGGGACTGAAATGGCTGATGCTTTTGAACCGA 3132  
 Qy 3082 AGTGGGAGGCGCAAGTGTATGACTCATTTGGGCGGCGACCTTCCAGCAGATGATGTG 3141  
 Db 3133 AGTGGGCAAGGCAAGTCTATATCTGATCAACCGGAGGCGATTTCAAGCAATGGAATGTG 3192  
 Qy 3142 CTGAGAGGGCTCAACCTGCTCATCACTCAAGGAAAGAAAGAAACAACCTCGGGTGTAT 3201  
 Db 3193 CTAGAGGGAAGTAAATGTCCTTGTGCAATTTCAAGAAAGAAAGAAATAGCTAGATTAC 3252  
 Qy 3202 TACCTGCTGGGCTCCGGAACAAGTTCTGCAACATGACCCAGAGTGGAGAGAGAGAG 3261  
 Db 3253 TATCTTTCATGTATTAAGAAACGAATACTACATTAATGACCCAGAGATGAAAGAAACAA 3312  
 Qy 3262 GGTGAGCAACCGTGGGAGCATGAGGCTGCGGCGCACTACCGTGTGTGAATACAG 3321  
 Db 3313 GGTCTGATCACTGTTGGGAGCTTGGAGGCTGTATATCAATTAAAGTTGTTAAATATGAA 3372  
 Qy 3322 CGAATTAGTCTGTGATGCTCTCAAGAGCTCCGTGAGGCTGTATGCTGGGCGCC 3381  
 Db 3373 AGGATCAAAATTTTGTGATGCTCTTAAAGATGTGTGAAATATATGCTTTGGGCTCT 3432  
 Qy 3382 AAACCTACCAACAATTCATGAGCTTCAAGTCTTTGCGGACTCCCGCCAGCGGCTCTG 3441

Db 3433 AAACGATATCAATTAATTCATGAGCATTAAGTCTTTTGCAGATCTCCAGACAGACCTCTG 3492  
 Qy 3442 CTGCTGACTGACAGATGAGAGAGGCGAGGCTCAAGGCTATGCTCCAGTCT 3501  
 Db 3493 CTAGTATATCTACAGGTAGAGAGATCAAGATTAAGGTTATTTTGTTCACACT 3552  
 Qy 3502 GGTTCATGCTGTGATGATGCTCGGGGAAAGACTATGACATCTACATCCCTGTGAC 3561  
 Db 3553 GATTCCATGATTAATGATGATGATTCAGAAACTTTATGATATCTACATCTCAT 3612  
 Qy 3562 ATCCAGAGCAGATACAGCCCATGACATCTTCTCTCCCAACACGAGCGATGAG 3621  
 Db 3613 ATTCAGGCAATATCACTCCCATGCTATGTCATCTTGCCTTAAACAGATGAAATGAA 3672  
 Qy 3622 ATGCTGCTGTGCTAGAGAGAGAGGCTCTACCTCAACAGTACGGGCGCATATTAA 3681  
 Db 3673 ATGCTGTTGTCTATGAGAGATGAGGGGCTGTATGTAACACTATGACCGGATACAG 3732  
 Qy 3682 GATGTGCTGCTGAGTGGGGGAGATGCTTCTGTGGCTTACATCTGCTCCAACCA 3741  
 Db 3733 GATGTGCTGCTCAATGAGGAGAAATGCCAGCTGTGCTTACATTCATTCATATG 3792  
 Qy 3742 ATATGAGGCTGGGCTGAGAAAGCCATTAAGATCCGCTCTGTGAGAGCGGCACTCGAC 3801  
 Db 3793 ATATGAGGCTGGGCGAGAAAGCTATTAAGATCCGCTGATGAGAAACAGACATTTGAT 3852  
 Qy 3802 GGGGCTTTCATGACAAACGAGCTCAGAGCTCAAGTTCTGTGTGACGGAGATGACAG 3861  
 Db 3853 GAGATATTTATGCAATTAAGCAGAGCTCAAGGTTAAAGTTTCTATGTGAAGAAATGATAG 3912  
 Qy 3862 GTGTTTTTTCCTCAGTCCGCTCGGGGCGAGCCCAAGTTTACTTCATGACTCTGAC 3921  
 Db 3913 GTATTTTGTGATCGGCGCATCTGAGAGAGATGCCAGATGTTTTTCAATGACCTTCAAC 3972  
 Qy 3922 CGTAACTGACATCAATGAACTGTGA 3945  
 Db 3973 AGAAATTCATGATGAATGCTGTAA 3996

RESULT 4  
 US-09-425-324A-2  
 ; Sequence 2, Application US/09425324A  
 ; Patent No. 6562591  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FU, C. Alan  
 ; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AND  
 ; FILE REFERENCE: A-68344/RMS/DHR  
 ; CURRENT APPLICATION NUMBER: US/09/425, 324A  
 ; CURRENT FILING DATE: 1999-10-21  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 3996  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthetic  
 US-09-425-324A-2  
 Query Match 35.6%; Score 1407.2; DB 4; Length 3996;  
 Best Local Similarity 62.5%; Pred. No. 6.4e-285;  
 Matches 2528; Conservative 0; Mismatches 1363; Indels 153; Gaps 15;

Qy 7 ATGGGAGACCAAGCCCGCCGAGCCTGAGACGACATCGACTGCTCGGCTGCGGAGAC 66  
 Db 1 ATGGCGAGCACTCCCGGCTCGAAGCCTGGAATGAATATCTCGGCTGAGGAGAC 60  
 Qy 67 CTTGCTGGATCTTTGACTTGTGAGAGTGTGTGCGCAATGAACTTACGACAGTGTAC 126  
 Db 61 CTGAGAGGATCTTTGATGATGATGAGATCTTGTGAAATGAAATATACATACGGGCAAGTTAT 120  
 Qy 127 AAGGCTGCGATGTCAAGAGGGGCGAGCTGCTGCCATCAAGGTCAATGATGTCAAGAG 186

121 AAGGTCGTCATGTCAAAACGGGCGAGCTTGCAGCATCAAGTTATGATGTCTCACAGG 180  
187 GACGAGGAGGAGAGATCAACAGAGATCAATGTCTGAAAAAGTACTCTCAACACGG 246  
181 GATGAAAGGAGAAATCAACAGAAATTAACATGTGAAAGAAATATCTCATCACGG 240  
247 AACATGCGACCTTACAGGAGCCTTCATCAAGAAAGCCCCGGGAAACGATGACG 306  
241 AATATTGCTACATCTATGTGTCTTTTATCAAAAAGAACCCACAGGCTGATGACCA 300  
307 CTCTGCTGTGTATGAGATTCTGTGTGTCTGTGTCTGATGATGATGATGATGATGAT 366  
301 CTTGTGTGTGTATGAGATTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360  
367 AAGGCAACGCTTGAAGAGAGCTGTATGCTTATATCTGATGAGGAGATCTCTAGGG 426  
361 AAGGTTAACCTTGAAGAGAGATGTATGATCATCTGACAGGGAATCTTACGGGG 420  
427 CTGGCCCATCTCTCATGCCCCAGAGGTGATCATTCGAGATCATGAGGGGAGATGTCT 486  
421 CTGAGTACCTGACCAAGCATTAAGTATTCATCGAGATTTAAAGGGCAAAATGTCTTG 480  
487 CTGACAGAGATGTGAGGTCAAGCTAGTGAATTTTGGGTGAGTGTCTGATGACGG 546  
481 CTGACGAAATATGCAAGATTAACCTAGTGAATTTTGGGTGAGTGTCTGATGACGG 540  
547 ACCGTGGGAGACGGAACCTTTCATTTGGGACTCTCTATCTGATGATGATGATGATG 606  
541 ACAGTGGGAGAGAGATCTTTCATTTGGAATCTCTCTATCTGATGATGATGATGATG 600  
607 GCTGTGATGAGAACCTCTGATGACCTATGATTTACAGAGATGATTTGTGTCTGATGA 666  
601 GCTGTGATGAGAACCTCTGATGACCTATGATTTACAGAGATGATTTGTGTCTGATGA 660  
667 ATCAAGCCATCGAATGAGCAGAGGAGCCCCCTGTGTGACATGACCCCATGCGA 726  
661 ATCAAGCCATCGAATGAGCAGAGGAGCCCCCTGTGTGACATGACCCCATGCGA 720  
727 GCTGTGTGTCTCATTTCTGTGAAACCTCCGCGCAAGCTCAAGTCCAAAGTGTGTAG 786  
721 GCTGTGTGTCTCATTTCTGTGAAACCTCCGCGCAAGCTCAAGTCCAAAGTGTGTAG 780  
787 AAGTTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 846  
781 AATATTCAGTCAATTTATGAGAGCTGTGTGTAAAGATCAACAGCAGGACCAAGACA 840  
847 GAGCAGCTACTGAAGTTTCTCTTCATCCGCGACCAAGCCACGAGCGGAGTCCGATC 906  
841 GAAACAATGATGAGATCATTTTATGAGACCAACCTAATGAGGAGCAGGTCGCAAT 900  
907 CAGCTTAAAGACCAATTTGACCGATCCGGAAGAGCGGGGTGAGAAAGAGACAGAA 966  
901 CAATCTAAGGACCAATTTGATGAAACAAAGAAAGCGAGGAAAGAAATATGACAGAG 960  
967 TATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1026  
961 TATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1017  
1027 TCCATCATGAACTGTGAGAGTGAATCTTACCGCGGAGTTTCTCGGCTCCAGAG 1086  
1018 TCCATCTGAACTGTGAGAGGAGTGAATCTTACCGGAGGAGGAGGAGGAGGAGGAGGAG 1077  
1087 GAAATTAAGAGCACTCAGAGGCTTTAAACAGCAGCAGAGCTGACAGCAGCAGCAG 1146  
1078 GCCAACAGAGAGCTTCTGAGGCGCTA-----CGAGAGCAGAGCTGAGAGCAGCAG 1131  
1147 CGAGAGCCCGAGAGCAGATCAACACCTGTGACCAAGGGAGGCGGCGGCTAAGAGAG 1206  
1132 CGGAGAGATGAGAGAGCAGAGCGGAGCTGTGGCGAGCGTGCAGAGGCGCATCGAGAG 1191  
1207 CAGAAAGAGAGAGCGGCGCGCTGTGAGAGCAACAGCGCGGAGCGGAGCAGCGAGAG 1266

1192 CAGAAAGCAGAGCGGCGGCTGTGAGAGCAACAAAGCGAGAGAGAGCTGCGAGAG 1251  
1267 CTGACAGAGAGAGAGCAGCAGCGGCGCTGTGAGAGCATGACAGCTCTGCGCGGAGAG 1326  
1252 CAGCAGAGAGAGAGAGCAGCAGCGGCGCTGTGAGAG-----AGCAGATGCGCGGAGAG 1305  
1327 GAGCGCGGAGAGCGGAGCGTGTGAGCAGAGATTAACAGCGGAGAGCAGCTGTGAGAGCAG 1386  
1306 GAGAGAGAGCGTGTGAGAGCAGAGATTAAGAGCGCAACAAATTTGAGAGAGCAGAGAG 1365  
1387 CAGTCAAGAGCTCTTCAAGAGCAGCTGTGAGAGAGAGCTGTCTTCAATCTCTGTAG 1446  
1366 CAGCAGAGAGAGCAGCAGAGCAGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1425  
1447 CAGCAGAGAGAGCAGCAGAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1506  
1426 CATCAGCGGAGAGAGAG-----AGGCTGTGTAG 1455  
1507 AGAAGCCCTGTACATTAATGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1566  
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1567 CGAG 1626  
1516 AAG 1572  
1627 AAGCAG 1677  
1573 AAGGTTGAG 1632  
1678 CCCCCAG 1731  
1633 AGTGAAGTTGAG 1692  
1732 ---GAGGAG 1788  
1693 CATCTGT 1752  
1789 GCTTCCATGAG 1848  
1753 CAGCCACAG 1812  
1849 GCTGTCTGAG 1901  
1813 GAGATGAG 1872  
1902 -----GAATCCCCAG 1953  
1873 GAAAGTTTGAACCGAG 1932  
1954 CAG 2013  
1933 CAAAG 1992  
2014 GCGCAG 2071  
1993 GCTGTGAG 2052  
2072 GCGGAG 2131  
2053 ACTGAG 2112  
2132 CCAAG 2187  
2113 AGCAG 2172  
2188 GACAG 2247  
2173 TCCAG 2232  
2248 GCGGTGAG 2307  
2233 CATGAG 2292

QY 2308 AAGCCGACGACACCCGCTCAGGCGCCGCGCCGACGACTTGTGTGTGAAGAAG 2367  
DB 2293 GCTACCTCAAAAAAGCTATAGATGAGATCTGACGGCATTAAGCAAAAGAACTAAGAAA 2352  
QY 2368 CGGACTCTGAGACGAGGCCCTCGGCTCCCAAGAGCCATGATCTACTGTGTGACG 2427  
DB 2353 CTCGGGATTGAAGAAACAAACCGCCCAATGAAGAGGTGATGATTAATCTCTCTCCAGT 2412  
QY 2428 GAGGAGGTGAAAAGCATGAGACGACGAGAGAGGCGCAAGCGGCGCAGCAGAGGGG 2487  
DB 2413 GAGGAGTGAAGAAAGTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2472  
QY 2488 A-----GCAAGATACCTCGGCGGCGCGAC 2514  
DB 2473 ACAGTGCTGTACGAGACATACCAAGCTGATACCAAGAGCTCCAGGCGCAACGAG 2532  
QY 2515 GATGGGATATACAGACAGGCTGACGACATGTGTGTCCAGAGTGAAGAGATCACCGG 2574  
DB 2533 CAGTACATGTGGGAATGTGGGAGCGATGGGCTGGAGACTCTCAATCGGACAGTTTC 2592  
QY 2575 ACCGAGCCCATACGAGGGGCGGCAACATGTGTGTCCAGCGCACCCCTGAAGAGAGCGG 2634  
DB 2593 AGCGGCACTATTTCAGAGAGAGAACTTGAATGAAGAGACGTCTGAGAGAGAAAG 2652  
QY 2635 AACCTGTGCTACGTGACGACGAAATGGGT-----ACAAACCTGTGACGTGTG 2685  
DB 2653 CGATCTGGCCACAGTACGACGAAATGGCTTGTGTGCGCACATCACTCTGACCTGTGTG 2712  
QY 2686 CAGCCACGCACTCACCCAGGAGAAAGCAAAAGGCGCAA-----GCCACCTCGAAG 2739  
DB 2713 CAGGAGACCATTTCTCCAGCTGGAACCCGACTGAGGAGCTGGGGCGGCTCTCAACCAT 2772  
QY 2740 GATGGAGTGTGATCAACAGTCTCTGTGGGCTGTGAAGGCCCTGGGAGAGCTGTTC 2799  
DB 2773 TCCAGAGATGAGACTGTGGGACTGAATATGSCATGGGAGAGACCAAGAGCTCTTC 2832  
QY 2800 ACGATTTTGTGATCTAGGAGCTTACAGCCTGAGGAGAGGTGGGAGACGATCC----- 2854  
DB 2833 ACCCCCTTTGTGAGCCCGAGATATACGAGCTGTCCCATGATGAAGATGAAGAGAT 2892  
QY 2855 -----CCATCAGACCCCTAGTGGGTGAGAGGGGCACTCGGCTGACGAG---CTG 2901  
DB 2893 GAGGATATATAGCCGCGAGCTGTGTTTACTAGCGAACTTTAGCGAAGAAAGGCCAA 2952  
QY 2902 CAGTACGACGTGAGAAAGGTTCTGTGTCAACGTGAATCCCAACCAACCCGCGGCCAC 2961  
DB 2953 CTCATGAAAGCAAGAAAGATTTGGTGTAAATGAATGAACCAACCAACATTCGGCTCAT 3012  
QY 2962 AGTGAACCCCTGAGATCCGAAAGTACAAAGAGGATTCACCTCGAGATCTCTGTGCA 3021  
DB 3013 AGCGACACACGAAATCAGAAATACAAAGAACATTCACCTCAGAAATCTTGTGTCA 3072  
QY 3022 GCCCTTTGGGGGTCAACCTGTGTGTGCGACGAGAAACGGGCTGATTTGTGTGACCGA 3081  
DB 3073 GCTCTGTGGGTGTAACTTCTGTGTGAGACTGAAATGGCTGTATCTTTGACCGA 3132  
QY 3082 AGTGGGCAAGGCAAGGTATAGACTCATTTGGGCGGCGACGCTTCCACAGATGATGTG 3141  
DB 3133 AGTGGGCAAGGCAAGGTATATATGTGATCAACCGAGGCGATTTCAAGATGTGATGTG 3192  
QY 3142 CTGAGAGGCTCAACCTGCTCATCACTTCAGGGAAGAGAAACAACTCGGGGTGTAT 3201  
DB 3193 CTAGAGGAGCTGAATGTCTGTGTGCAATTTCAAGAAAGAAATGAATCAGATTAC 3252  
QY 3202 TACCTGTCTGTGCTCCGGAACAAGATTCTGACATATGACCAAGATGGAAGAGAGAG 3261  
DB 3253 TATCTTATGTGTTAAGAAACGAAATACATATATGACCCAGAGATGAAAGAAACAA 3312  
QY 3262 GGTGAGACCAACCTGTGGGCAATGAGAGGCTGGGCGACTACCTGTGTGAAATACGAG 3321  
DB 3313 GGTGAGTCACTGTTGGGCACTTGAAGGCTGTATATACATTTAAGTTGTTAAATATGA 3372

QY 3322 CGGATTAAGTCTGTGATCGCCCTCAAGAGCTCCGAGAGGTGATGCTTGGGCCCC 3381  
DB 3373 AGGATCAAAATTTTGGTATGTCTTAAAGAAATGTGTGAGAAATATATGCTTGGCTCT 3432  
QY 3382 AAACCTACCAAAATTCATGGCTTCAAGTCTTTTGGCGACCTCCCGACCGGCTCTG 3441  
DB 3433 AAACGATATCAATTAATTCATGGCATTTAAGTCTTTTGGAGATCTCCAGCAAGCTCTG 3492  
QY 3442 CTGTGCACTGACATGAGAGAGGGGCGGCTCAAGGTCTATATGCTTCCAGTCT 3501  
DB 3493 CTAGTGTCTCACGATGAGAGAGGTCAAGATTAAGTTAATTTTGTGTCAACACT 3552  
QY 3502 GGTTCATGTGTGATGTGATCTCGGAGGAAACAGCTATGACATCTACATCCGTGTGAC 3561  
DB 3553 GGTTCATGTATGATGTGATGTGATTCAGAAACTCTTATGATATCTACATACATCTCAT 3612  
QY 3562 ATCCAGGCGCATACGAGCCCATGACATCTTCTCCCAACAGCGAGAGAGAG 3621  
DB 3613 ATTCAGGCGCAATACATCTCTCATGTATGTGATCTTGTCTTAAACAGATGAGTGA 3672  
QY 3622 ATGCTGTGTCTACAGAGAGAGGTGTCTAGCTCAACAGTACGGGCGCATATTAG 3681  
DB 3673 ATGCTTGTGTCTATGAGATGAGAGGAGGTGTATGTAAACCTATGCGGATTAAG 3732  
QY 3682 GATGTGTGTGCAGTGGGAGAGATGCTTCTGTGTGCTATCTGCTCAACGAG 3741  
DB 3733 GATGTGTGTCTCAATGGGAGAGAAATGCGACGTGTGTGCTACATCTTCAATGAG 3792  
QY 3742 ATAAATGGGCTGGGCTGAGAAAGCCATTGAGATCCGCTGTGTGAGAGCGGCGACCTGAC 3801  
DB 3793 ATAAATGGGCTGGGCGAGAAAGCTATTGAGATCCGCTGATGAGAAACAGGATTTGAT 3852  
QY 3802 GGGGCTTTCATGACAAACGAGCTCAAGAGCTCAAGTCTGTGTGAGCGGAATGACAG 3861  
DB 3853 GGAATATTATGATTAAGCGAGCTCAAGGTTAAGTTTATGTGAAAGAAATGATTAAG 3912  
QY 3862 GTGTTTGTGCTGAGTCCGCTGTGGGGGAGAGCCAGGTTTACTCATGACTGTGAC 3921  
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QY 3922 CGTAACTGACATGAACTGTGTA 3945  
DB 3973 AGAATTCATGATGAACTGTGTA 3996

RESULT 5  
US-09-645-791-2  
; Sequence 2, Application US/09645791  
; Patent No. 6569658  
; GENERAL INFORMATION:  
; APPLICANT: Luo, Ying  
; APPLICANT: Fu, Alan C  
; APPLICANT: Shen, Mary  
; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS; COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS OF USE  
; FILE REFERENCE: A-68344-1/RMS/DHR  
; CURRENT FILING DATE: US/09/645, 791  
; PRIOR APPLICATION NUMBER: 2000-08-24  
; PRIOR FILING DATE: 1999-10-21  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 3996  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-09-645-791-2

Query Match 35.6%; Score 1407.2; DB 4; Length 3996;  
Best Local Similarity 62.5%; Pred. No. 6.4e-285;  
Matches 2528; Conservative 0; Mismatches 1363; Indels 153; Gaps 15;

QY 7 ATGGCGAACCCAGCCCCCGCCGACGCTGAGCAATCGACCTGTCCGCTCGCGGGAC 66  
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QY 67 CCTGCTGGGATCTTTGAGCTTGTGAGGAGTGTGCGCAATGGAACCTACGGACAGGTGTAC 126  
Db 61 CTTGACGGGATCTTTGAATTGTGTGGAATGTTGTGGAATGGAACATACGGGCAAGTTTAT 120  
QY 127 AAGGCTCGCATGTCAAGACGGGGCAGCTGCTGCTCATCAAGTCAATGATTTTCACGGAG 186  
Db 121 AAGGCTCGCATGTCAAAAACGGGGCAGCTGCGAGCCATCAAGTTATGATATTCACAGGG 180  
QY 187 GACGAGGAGGAGAGATCAACAGAGAGATCAATGCTGAAAAAGTACTCTACACACCGC 246  
Db 181 GATGAAGAGAGAGAAATCAAAAGAAATTAACATGTTGAAGAAATATTCTCATACCGG 240  
QY 247 AACATCGCACCTACTACGAGCCCTTCATCAAGAAAGCCCCCGGGAAACGATGACGAG 306  
Db 241 AATATTGCTACATACATATGCTCTTTTATCAAAAAGAACCAACGAGGATGATGACCA 300  
QY 307 CTCTGGCTGTGATGAGATTTCTGTGTGTGCTGTTCAATGATCTGATTAAGAACACA 366  
Db 301 CTTTGTTGTGTATGAGATTTTGTGTGTGCTGCTCTGTCACGACCTGATCAAGAACACA 360  
QY 367 AAAAGCAACGCCCTGAGAGGACTGTATCGCTTATCTGACGAGGAGATCCTCAGGGGT 426  
Db 361 AAGGTAACACCTTGAAAGAGAGTGAATTCATACATCTGACGGGAAATCTTACGGGG 420  
QY 427 CTGGCCCATCTTCATATGCCCAAGGTGATCAATGACATCAAGGGGAGATGTGCTG 486  
Db 421 CTGAGTCACTGCAACGACATAAAGTATTCATCGAGATATTAAAGGGCAAAATGTCTTG 480  
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QY 547 ACCGTGGGAGACGGAACTTTTCAATYGGAATCTCCCTACCTGATGAGGCTCAGAGGTATC 606  
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Db 841 GAAACAATTGATGAAGATCATTTTATACGAGACCAACTAATGAGGAGAGGTCCGCAAT 900  
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Db 1813 GAGATGCCACGCAACATCCAGATCCACTCGGAAATCTCTCTTCCCACTGCAATT 1872  
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QY 2072 GCGCGGAGAGGAGGAGCCCAAGGCTCCAGAGGCGCCCTGTGATGAGCCCTGAGCCGCG 2131  
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QY 2132 CCAAGCCTTAATGAATCCCGACCTCAGAGAGAGGACCTGAGCTG---GAACGCTCG 2187

Db 2113 AGCACCCTTACCTCCAGCCAGCTCCAGAGAGGCTCCAGCTGATTCACAGCAGGA 2172  
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 Db 3973 AGAAATTCATGATGAATCTGTGA 3996

RESULT 6  
 US-09-645-456A-6  
 ; Sequence 6, Application US/09645456A  
 ; Patent No. 6562580  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fu, C. Alan  
 ; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AND METHODS OF USE  
 ; FILE REFERENCE: A-68344/RMS/DHR  
 ; CURRENT APPLICATION NUMBER: US/09/645, 456A  
 ; CURRENT FILING DATE: 2000-08-24  
 ; PRIOR APPLICATION NUMBER: US/09/425, 324  
 ; PRIOR FILING DATE: 1999-10-21  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 6  
 ; LENGTH: 3972  
 ; TYPE: DNA



ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: synthetic  
US-09-645-456A-6

Query Match 35.2%; Score 1391.2; DB 4; Length 3972;  
Best Local Similarity 62.7%; Pred. No. 1.4e-281;  
Matches 2533; Conservative 0; Mismatches 1338; Indels 169; Gaps 17;

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RESULT 7  
 US-09-425-324A-6  
 ; Sequence 6, Application US/09425324A  
 ; Patent No. 6562591  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FU, C. Alan  
 ; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AN  
 ; FILE REFERENCE: A-68344/RMS/DHR  
 ; CURRENT APPLICATION NUMBER: US/09/425,324A



QY 1954 CAGAGACCTGATCTATGCGCACTGCGCTTAAACACAGTGGGCGGAGGGTCCCGGCA 2013  
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Db 3953 ATTCCATGATGAATCTGTA 3972

RESULT 8  
US-09-645-791-6  
; Sequence 6, Application US/09645791  
; Patent No. 656958

GENERAL INFORMATION:  
 APPLICANT: Luo, Ying  
 APPLICANT: Pu, Alan C  
 APPLICANT: Shen, Mary  
 TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AND METHODS OF USE  
 FILE REFERENCE: A-68344-1/RMS/DRR  
 CURRENT APPLICATION NUMBER: US/09/645,791  
 PRIOR FILING DATE: 2000-08-24  
 PRIOR APPLICATION NUMBER: US 09/425,324  
 NUMBER OF SEQ ID NOS: 36  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 6  
 LENGTH: 3972  
 TYPE: DNA  
 ORGANISM: Artificial sequence  
 FEATURE:  
 OTHER INFORMATION: synthetic  
 US-09-645-791-6

Query Match 35.2%; Score 1391.2; DB 4; Length 3972;  
 Best Local Similarity 62.7%; Pred. No. 1.4e-281;  
 Matches 2533; Conservative 0; Mismatches 1338; Indels 169; Gaps 17;

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Db 3233 TTTCTATGTTAAGAAACAGAAATCAATATATGACCAAGAGTGAAGAAAGAAAGGCT 3292
Qy 3266 GGAACACGCTGGGGGAGATGAGAGGCTCGGGGCACTACGTTGTGTAATACAGAGCG 3325
Db 3293 GGATCACTGTTGGGAGCTTGAAGGCTGTATATCTTAAGTTGTTAAATTAAGAGGA 3352
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QY      3926 ACTGCATCATGAACCTGGTGA 3945
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DB      3953 ATTCATGATGAAGACTGTAA 3972

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RESULT 9  
11S-09-57

US-09-579-664B-7

; Sequence 7, Application US/09579664B

Patent No. 6514719

GENERAL INFORMATION:

APPLICANT: Immunex Corporation

APPLICANT: Bird, Timothy A.

APPLICANT: Virca, G. Duke

APPLICANT: Martin, Unja

APPLICANT: Anderson, Dirk M.

TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES

FILE REFERENCE: 2923-A

FILE REFERENCE: 2923-A  
CURRENT APPLICATION NUMBER: US/09/579,664E

CURRENT FILING DATE: 2000-05-26

CURRENT FILING DATE: 20  
NUMBER OF SEO ID NOS: 36

NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.1; SOFTWARE: PAC  
: SEQ ID NO 7: SEQ ID NO 7  
: LENGTH: 4083

TYPE: DNA

TYPE: DNA

ORGANISM: HCO<sub>2</sub>;  
NO. OF TUBES: 1

Query Match	34.4%;	Score 1358.6;	DB 4;	Length 4083;
Best Local Similarity	61.7%;	Pred. No. 9.2e-275;		
Matches 2532;	Conservative	0;	Mismatches 1389;	Indels 180;
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 Db 301 CTTTGGTTGTGTATGAGATTGTGTGTGCTGGCTCTGTCAACCACTGATCAAGAACCA 360  
 QY 367 AAAGCGAAGCCCTGAAGGAGAGCTGTATGCTTATATCTGCAGGGAGATCCTCAGGGGT 426  
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 QY 487 CTGACAGAGAAATGCTGAGGTCAAGCTTAAATGATTTTTGGGGTGAATGCTCAAGCTGACCG 546  
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D	b	661	ATCACCGGCATTGAAATGGCAGAAAGGTGCTCCCTCTCTGTGACAGACCCCATGAGA	720
O	y	727	GCCCTTTCCCTCATTCCTCCGGAGCCCTCCGCGCCAGGCTCAAGTCCAAAGATGGTCTAAG	786
D	b	721	GCTCTCTTCTCAATCCCCCGGAATCCAGCGCTCGGTGAAGTCTAAGATGGTGTCAAAA	780
O	y	787	AAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTAACCTGAGCGCCCAACCCAG	846
D	b	781	AAATTCAGTCATTATATTGAGAGCTGTGGTAAAGAAATCACAGCCAGCCAGCAAGCA	840
O	y	847	GAGCAGCTACTGAAGTTTCCCTTATCCGGGACCAAGCCACGAGCGGCAGGTCCGATC	906
D	b	841	GAACTATTGATGAAGACATCCATTTATACGAGACCAACTAATGAGCCACAGTCCGATTT	900
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D	b	901	CACTCTAAGGACCAATTTATATGAAACAAAGAAAGAGAGAGAAAAAGATGAGACAGAG	960
O	y	967	TATGAGTACAGCGGCAGGAGGAGGAAAGTACACCATGAGAGAGAGAGAGCCAAAC	1026
D	b	961	TATGAGTACAGTGAAGTGAAGAAAGAGAGAGAGAGAAAT---GACTCAGGAGAGCCAGC	1017
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D	b	1252	CAGCAGGAGAGGAGAGCAGCGCGCGCACTATGAG-----AGCAGATGCCCGGAGAGAG	1305
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D	b	1366	AGACAGTTAGAGATTTTGCAGCAGCAGCTACTGATGAACAGCTCTACTTCTGGAATAT	1425
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D	b	1426	AAGCGCAAACTATGAGAGAACAGAGCAACAGAAAGACTGCAGAGCAGCTAAACAA	1485
O	y	1473	-----GAAACAGAGAGAGAGAGCGCTCAGCGCTGGGGAAGG	1509
D	b	1486	GAAAGAGACTATAGTTCCCTTCAGATATAGCGGAGAGAGAGCGCTGTGGAAGAG	1545
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D	b	1546	AAGCCACTGTACATTAACAAAGAGAGATGAGTCTTATGAGAGCCAGCATGGGCCAAG	1605
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D	b	1606	GAGGTAGAAGAACGATCAAGGCTCAACCGGCAAAAGTTTCCCTGCTCAGTCTCA---CAAG	1662
O	y	1630	CGAGGACACACGGGGCTGAGCGCCCACTCCCC-----AGGCTCCCAAGGGCCC	1680



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Db 1663 GTTGCACAAGATATCTGACCCCAACCTGCCCCAAGGTGGAGTCTTCAAGATTAGT 1722
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Db 1903 ATGCCAGCCAGAACTCAGATCCCACTCGAATAATCTCTCTCCCACTCGCATTTGAA 1962
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Db 1963 AAGTTGACCGAAGCTCTGTGTTACGACAGAGAGAACATTCCACAAAGGTGCTTCA 2022
Qy 1957 AGGACTCATCTATCGCACTGCGCTTAAACAAGTGGGCGGAGGATCCCGGCAAGC 2016
Db 2023 AGAACAACTTATATCCCAAGCATTAAGCAAAAGATTCTCTGGGAAATGTATGCT 2082
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RESULT 10  
US-09-645-456A-1  
; Sequence 1, Application US/09645456A  
; Patent No. 6562580  
; GENERAL INFORMATION:  
; APPLICANT: FU, C. Alan  
; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AN  
; FILE OF INVENTION: METHODS OF USE  
; FILE REFERENCE: A-68344/RMS/DRR  
; CURRENT APPLICATION NUMBER: US/09/645,456A  
; CURRENT FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US/09/425,324  
; PRIOR FILING DATE: 1999-10-21  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 1  
; LENGTH: 4083  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-09-645-456A-1

Query Match 34.4%; Score 1358.6; DB 4; Length 4083;  
Best Local Similarity 61.7%; Pred. No. 9.2e-275;  
Matches 2532; Conservative 0; Mismatches 1389; Indels 180; Gaps 16;

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1207 CAGAAAGAGAGAGCGGCGCGGCTGAGAGAGCAACAGCGGAGGAGCGGAGAGCGGAGAG 1266  
|||||  
1192 CAGAAAGAGAGAGCGGCGGCTGAGAGAGCAACAGCGGAGGAGAGAGAGCTGCGAGAG 1251  
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1267 CTGACAGAGAGAGAGCAGCAGCGCGGCTGAGAGCATGAGAGCTCTGCGCGGAGAGAG 1326  
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1252 CAGCAGAGAGAGAGAGCAGCGCGGCTGAGAG-----AGCAATGCGCGGAGAGAG 1305  
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1327 GAGCGCGGAGAGCGGAGCGGAGGAGAGATCAAGCGGAGAGAGCT---GAGAGAGAG 1383  
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1306 GAGAGAGAGCGGAGCGGAGAGATCAAGAGAGATCAAGCGGAGAGAGAGAGAGAGAG 1365  
|||||  
1384 CGGAGAGAGAGAGCTCTGAGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1443  
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1366 AGACAGTATGAGAGATTTTCAAGAGAGAGCTATGCAATGAAAGAGCTTCTTCTGAGATAT 1425  
|||||  
1444 CAGCAG 1472  
|||||  
1426 AAGCGCAACAAATTTGAAG 1485  
|||||  
1473 -----GAAACAG 1509  
|||||

D	b	1486	GAAAGAGACTACTT	AGTTTCCCTTCAGCATTCAGCCGACAGAGACAGAGCCCTGTGGAGAG	1545
O	y	1510	AAGCCCTGTACATTA	TGTCGGGACATGAATCCCGCTGACAAACCAAGCTTGAGCCGA	1568
D	b	1546	AAGCCACTGTACATTA	CAAGAAAGAAATGAGTCTTAGTGAGAAACCCAGCATGGGCCAAG	1605
O	y	1570	GAGGTGAAAGAGAA	CAAGATGAAACAAGACGACGAACTCTCCCTTGGCCAAAGACAG	1629
D	b	1606	GAGGTGAAAGAA	CGGTCAAGGCTCAACCGGCAAAAGTTCCCTGCATCTCTCA--CAAG	1662
O	y	1630	CCAGGACACACGGGG	CTGAGGCCCCCCTATCCCC-----AGGCTCCCAAGGGCC	1688
D	b	1663	GTTGCCAACAGGATAT	CTGACCCCAACTGCCCCCAAGTGGAGTCTTTACGACTT	1722
O	y	1681	CCAGGACCCCTTT	CCCAAGCTCTCTCTATGCAAGGCCGTGGAGCCCAAG-----	1731
D	b	1723	GGAATTCAGCGCTG	CTGAACACCCCCATGCTCACAACAGTCGATGCCCAAGTCCCAAT	1782
O	y	1732	GAGGAGCCGACACAGT	CTCTGAGAGCAAGCCCAACCTTGACTGGCTGCTTCCCAACC	1791
D	b	1783	CTGTAGTGTGTAAAT	TCCACAGGACCTGCTTGACCGCTCCCACTCAGTGCACACAGCAG	1842
O	y	1792	TCCCATGACCCGAC	CCCTGAGCATCCCGGCAACCACTGCAAGCCCAAGGCCGAGGAGCT	1851
D	b	1843	CCCAACAAAGGGCT	CTCTTGGGTTTACAGAGGCTTGAAAGTCACTCCACACCGCTGGAG	1902
O	y	1852	GTCATCCGCGCAGAA	ATTACAGACCCCACTCTGAAAGAGCTGGGCCGACGCGA-----	1903
D	b	1903	ATGCAACCCCAAGAA	ATCAGATCCCACTCTGAAAATCTCTCTCTCCCACTCGCATTTGAA	1962
O	y	1904	-----ATCCCCCAG	CTGGGTCCGCCAAGTAAAGAGGCCCAACCCCAAGGTGCTCAG	1956
D	b	1963	AAGTTTGACCGAAG	CTTTGGTTACGACAGGAAGAAAGCATTTCCACCAAGGTGCTCAA	2022
O	y	1957	AGGACCTATATATG	CCACATGCGCTTAAACCACTAGGGGGCCGAGGGTCCCGGCAAGCC	2016
D	b	2023	AGAACATCTTATAT	TCCCAAGCATTAGCCAGAAAGAAATTTCTCTGGGAAATGTAAGTCT	2082
O	y	2017	CAGGACGTCCGTC	AGACCTTCGCAGCACTTCGCAGCAACTCCGCTGGCAATCTATCTGCAAG--GC	2074
D	b	2083	CTGGGACCCACAT	AGATAGATCTTCAACCATTCAGAGGAAACATCCGATCTCGGAGAACT	2142
O	y	2075	GGGCAAGCGGGGCA	CCCCCAAGCTCCAGGGCCCCCTGCTCAGCCCCCTTGACCCGCCCA	2134
D	b	2143	GAGCCCATCTTGG	AGAGCCCCCTTGAGAGGACCCCTTGAGAGGACCAAGCACTGGCAGTTCTTCCAGCTTCAGC	2202
O	y	2135	ACGCTCTATGTA	CCCCCGACCTCAAGAGAGAGAGACCTTCGGCTGG-----GAAGCTCCGAC	2190
D	b	2203	ACCCCTAGCTCC	CAAGCCCAAGCTCCCAAGAGAGGCTCCCAAGCTTGATCAACAGAGATCC	2262
O	y	2191	AGCGTCTTCAG	AGCTCTCAAGGACCTCCACGGGACCTCCCCCAAGGCTGAGCTCATCTGAGAGGAAACGC	2250
D	b	2263	AGTGAACGCA	CCAGATTCGAGCCCAAGCTAGTATCTCAGAAAGATCACTGTGTCTTCCCAT	2322
O	y	2251	GTGGAGGCTCT	CCCAACCTGACACGCTCCCTGTGCTCTCCCTCGGAAATTAAGCCAG	2310
D	b	2323	GAGCTGCGAAG	GTGAAACCAAGATTCAGAGGACATTAACCGGCCAGCTGCACAGCT	2382
O	y	2311	CCCGACGAC	CCGCTCAACGGCCAGGGCCGGCCCGAGACTTTGTGTCTGTGAAGAGCG	2370
D	b	2383	AGCTACAAAAA	AGCTATAGATGAGGATCTGACGGCATTAGCCAAAGAACTAAGAGAACTC	2442
O	y	2371	ACTCTGACG	AGGCCCCCTGAGCTCCCAAGAGGCGCATGACTACTGCTGTCAGCAG	2430
D	b	2443	CGGATTTGA	AAAAACCAACCGCCCAATGAAGAGGTGACTGAATTACTCTCTCCAGTGA	2502
O	y	2431	GAGGTGAAAG	CAGTGAGAGCGACGAGAGGAAGGCGAAGCGGGCCAGCAGAGGGA--	2488
D	b	2503	GAGTCAGAA	ATGAGGAGAAAGAGAGGAAAGTGAAGAGAGAGAACCCATGATGGGACA	2562
O	y	2489	-----G	CAGATTAACCTCTGGGGCCGACAGCAT	2517
D	b	2563	GTGGCTGT	CAAGCATTAACCAAGAGAGGTCCAGGAGGAAAGAGCAG	2622

QY	2518	GGGGATACAGACAGCTTCAGCAACATAGTGGTTCACAGACCTTCAGAGAGATACACGGGAC	2517
Db	2623	TACAAATGCGAAATGATGCGGAGCCCATGCGCTGAGACCTCTCATGCGGACATTTTCACG	2623
QY	2578	CAGCCCCATACCGGGGGCGGACCATGGTGTCTCAGCGCACCCCTGAAAGAGACGGAAC	2637
Db	2663	GGCAGTATTTTCAGAGAAAGAAACCTTGATGATTAGAGAGACGTGTGGAGAGAAAGAGCGA	2742
QY	2638	CTGCTGCATGCTGACAGCAATGGGT-----ACACAAACCTTGCTGACGTGGTCCAG	2688
Db	2743	TCTGGCCCAAGATGACAGCAATAGGCTTTTGCTGGCCACATCAACCTTCGACCTTGGATGAG	2802
QY	2669	CCGAGCCATCTACCCACCGGAGAACAGCAAGAGCCAA-----AGCCCAACCTCGAAGGAT	2742
Db	2803	CAGAGCCATTTTTCAGCTGGAACCCCGACTGAGGAGCTGGGGCGGTCTCAACCACTTCC	2862
QY	2743	GGGAGTGTGACTACAGCTCTGTGGGTGTGTAAGGCCCTCTGCAAGAGCTGTGTCAG	2802
Db	2863	CAGAGATAGACTCTGGGACTGAATATGCGATGGGAGAGCACCAAGAGCTCTCTTCAAC	2922
QY	2803	ATGTTTGTGATCTTAGGATCTTACCAGCTTGGAGGCACT-----GGGAC	2847
Db	2923	CCCTTTTGGACCCCAAGTATACCAAGTCTCCACTGATGAATGAAGAGATGAG	2982
QY	2848	AGCATCCCAATCACAGCCCTAGTGGGTGAGAGGGCACTCGGCTCGACAG---CTGCAG	2904
Db	2993	GATCATACGCCGACAGCTCTGTTTTACTAGGCACTTCTTAGGCAAGACAGCCAACTC	3042
QY	2905	TACGACGTGAGAAAGGTTCTGTGGTCAACGTGAATCCACCAACACCCGGGCCCAAGT	2964
Db	3043	AATAGACGAAAGAAAGATTTCCGTGTGTAATGTAAACCAACCAATTCGGCTCATATGC	3102
QY	2965	GAGACCCCTGATCCGGAGTACAGAAAGGATTCACATCGAGATCCTGTGCGAGCC	3024
Db	3103	GACACACGAAATTCAGAAATACAGAAACGATTCACACTGAAATTACTTTGTGCACT	3162
QY	3025	CTTTGGGGGCTCAACCTGCTGTGGGACCGGAGAACGGGCTGATGTTGCTGGACCGAAT	3084
Db	3163	CTGTGGGGTGTAAACCTTCTGTGGGGCTGAATAATGGCTGATGCTTTTGGACCGAAGT	3222
QY	3085	GGGCGAGGGCAAGGTGTATGACTATATGGCGCGGAGCGCTTCGACGAGATGATGCTG	3144
Db	3223	GGGCAAGGCAAAAGCTTATATCTGATCAACCGGAGGGGATTTACGACAGATGATGTGCTA	3282
QY	3145	GAGGGGCTCAACCTGCTCATATCCATCTCAGGGGAAAGAAACAACCTGCGGGTATATAC	3204
Db	3283	GAGGGACTGAATGTCTTGTGACAAATTTCAAGAAAGAAATAGCTACAGATTTACAT	3342
QY	3205	CTGTCTTGACTCCGGAACAAAGATTTCTGCAATGACCCAGAGTGGAGAGAGCAAGGC	3264
Db	3343	CTTTCAATGTTAAAGAACAGAAATCTCATATATGACCAAGATGAAAGAAACAAGGC	3402
QY	3265	TGGAACACCGTGGGGGACATGGAAGGCTGCGGGGACTACGTTGTGGAAATAGAGCGG	3324
Db	3403	TGGAATCACTGTGGGACTTGGAAAGCTGTATACATTATTAAGTTGTTAAATATGAAGG	3462
QY	3325	ATTAAAGTTCCTGCTATATCGCCCTAGAGGCTCCGTGAGGTGTATGCTCGGCGCCCA	3384
Db	3463	ATCAAAATTTTGTGTGATTTGCTTAAAGATGCTGTGAAATATATGTGTGGGCTCTTAA	3522
QY	3385	CCCTTACCAAAATTCATGGCCTTCAAGTCTTTGCGGACCTTCCCAACCGCTCTGTG	3444
Db	3523	CCGATATCAATAATTCATGGCAATTTTAAGCTTTTTCAGATCTCCAGCAACAGCCTCTGTA	3582
QY	3445	GTGCACCTGACAGTAGAGAGGGGACAGCGCTCAAGGTCATCTATGCTCCAGCTGCTGC	3504
Db	3563	GTTGATCTCAGCGTGAAGAAAGGTCAAAAGATTAAGGTATTTTGTGTACACACTGGT	3642
QY	3505	TTCATAGCTGTGATGTGACTCGGGGAACAGTATGACTTACATCTTCCCTGTGCAATC	3564
Db	3643	TTCATATGAATTTGATGTTGATTCAGAAACCTCTTATGATTTCTACATACATCTCATAAT	3702

Oy		307	CTCTGGCTGGTATGAGATTCTGTGGTCGTGGTTCAAGACTGCCTCGTAAAGAACA	366
Dd		301	CTTGTGTGTATGAGATTGTGTGTCTGTCAACGACTGATCMAAGAACCA	360
Oy		367	AAAGCAACGCCCTGAAGAGACGTATCCGCTAATCTTGACAGGAGATCTCAAGGAT	426
Dd		361	AAAGTAACAACGTTGAAGAGAGTGATGTCATACATCTGCAGGGAATCTTAACGGGGG	420
Oy		427	CTGGCCCATCTCCATGCCCCAAGGTATCCATGAGACATCAAAGGGCACAAATGTGCTG	486
Dd		421	CTGAGTCACCTCACACAGCATTAAGTAGTTCATGAGATATAAAGGGCAAAATGTCTTG	480
Oy		487	CTBACGAGAAATCTGAGGTCAAGTATGATTTTGGGGGAGATGTCACGTGACCGC	546
Dd		481	CTBACTGAAAATGCAAGAACTTAATCTATGTGACCTTGGAGTCAGTGTCTCAGCTTGATCGA	540
Oy		547	ACCGTGGGACAGCGNAACATTTCAATTGGGACCTCCTACTGATGGCTCGACAGGTCATC	606
Dd		541	ACAGTGGGACGAGGAATCTTTCAATTGGAACTCCCTACTGATGGCACAGAAATTAAT	600
Oy		607	GCTGTGATGAGAAACCCTGATGCCACCTATGATTAAGAGATGATTAATTTGGTCTTCAGGA	666
Dd		601	GCTGTGATGAAAAACCAAGATGCCACATATGATTTCAAGAGTGACTGTGTGCTTTTGGGT	660
Oy		667	ATCACAGCCATGGAATGGCANAGGAGACCCCCTCTGTGTGATGACAGCAACCCCATCGA	726
Dd				

Qy	72	GCCTCTTCTCATTCTCTGGAACCTCTCGCCGACAGGCTCAAGTCAAGAAAGTGGTCTAAG	786
Db	721	GCTCTTCTCTCATCCCCGGAATCAACGCTCGGCTGAAAGTCTAAGAAAGTGGTCAAAA	780
Qy	787	AACTTCATTGACTTCATTGACGATGTCTCATCAAGAATTACTGAGCCGCGCCACACG	846
Db	781	AAATTCCAATCATTTTATTGAGAGCTGCTTGGTAAAGATCAACACCACGACCAAGAACAA	840
Qy	847	GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAAGCCACGAGCGGACGTTCCGATC	906
Db	841	GAACAAATTATGAAAGATCCATTTTTAAAGAGCCAACTTAATGAGCGACAGGTTCCGATTT	900
Qy	907	CAGCTTAAGGACCAACATTGACCGATCCCGGAAGAACGGGCTGGAAGAGGAGACAGAA	966
Db	901	CAACTCAAGGACCATTTGATATGAACAAAGAAAGGACGAGAGAAAAAGATGAGACAGAG	966
Qy	967	TATGAGTAAACGGCGACGAGAGGAAATATGACAGCCATGGAAGAGAAAGAGAGCCCAAGC	1020
Db	961	TATGAGTACAGTGAAGTGAAGGAAGAAAGGAGGAGAT--GACTCGAGAGACCCAGC	1010

Db	1018	TCATCCTGATATCTGCACAGGGAGTCGACGCTCGGAGGGACTTTCTGAGGCTCAGCTTG	107
Qy	1087	GAAATATAGCACTCAGAGGCTTTAAACAAGCAGCAGCTGCGACAGCAGCAG	117
Db	1078	GCCAAACAAGAGCGTTCTGAGGCCCTA-----CGAGGCGACAGCTGAGACACACAG	113
Qy	1147	CGAGACCCCGAGCACAACATCAACACTCTGTGCACACGCGACCGCGCATGAGAG	120
Db	1132	CGGAGATATGAGAGCACAAGCGGCGACTGTGGCCGACGTCAGAAAGCGCATGAGAG	119
Qy	1207	CATAAAGAGAGCGCGCGCCGTGGAGAGCAACAAGCGCGGAGCGGAGCAGCGAG	126
Db	1192	CAGAAAGACAGAGGCGCGCTGGAGAGCACAAAGCCAGAGAAAGAGCTCGGAG	125
Qy	1267	CTGCAGAGAGAGCAGCAGCGCGCGCTGAGAGCATGCAAGCTCTCGCGCGGAGAG	132
Db	1252	CAGCAGAGAGGAGCAGCGCGCGCACTATAGG-----AGCAGATGCGCGGAGAG	130
Qy	1327	GACCGCGCAGCGCGAGCGCTGAGAGAGAAATCAAGCGGAGCAGCT---GAGAGACAG	138
Db	1306	GAGAGAGGCGTCCGAGCATACAGGAAATACATCAGGCGACAGTTTAGAGAGAGCAG	136

1384 GGGAGTGAAGACGTCGAGAGGCGAGTGCAGAGACATGCTACCTCAAGTCCTG 1443  
1386 AGACGTTAGAGATTTTCAGAGCAGCTACTGACATGAACAAAGCTCTACTGTGAATAT 1425  
1444 CAGGACGAGCAACAGCAGCAGAGCTTCA----- 1472  
1426 AAGGGCAAAACAAATTGGAAGAACAGACAGAAAAGACTGCAGAGGAGCTAAAGCAA 1485  
1473 -----GAAACAGACGACGACGAGCTCTGCTGGGAGCAG 1509  
1486 GAAAGAGACTACTAGTTTCCCTTCAGCATCAGCGGACAGAGAGGCTGTGGAGAG 1545  
1510 AAGCCCTGATCACTTATGTCGGGGCATGAAATCCCGCTGACAAACGACCTGGGGCCGA 1569  
1546 AAGCCATGTCATTTACAAAGAAAGAAATGAGTCTAGTGAAGCCAGCAATGGGCCAAG 1605  
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1630 CCAAGCAGACAGGGGCTGAGCCCCCATCCCC-----AGGCTCCCAAGGGCCC 1680  
1663 GTTCCCAACAGGATATCTGACCCCAACCTGCCCAAGTGGAGTCCCTTACGACTTATG 1722  
1681 CCAAGACCCCTTCCCAAGCTCTCTATGCAAGGCGGTGGAGCCGAG----- 1731  
1723 GGAATTCAGCTGCTGAAACACCCCAATGCTCAGACCAAGTCGATCCCAATCCCAT 1782  
1732 GAGGACCCGCAAAAGTCCCTCAGAGACAGCCCAACGAAACCTGGCTGCTCCAGACC 1791  
1783 CTGATGATGTTAAATTCAGAGGACCTGCTTGAACCGGCTCCAGTCAAGTCAAGAGAG 1842  
1792 TCCCATGACCCGACCTGCAATCCCGCACCTGCAAGCGCCAGTGGCCCGAGAGCT 1851  
1843 CCCCAAAAGGGGCTCTGCGGTTTCAAGAGGCTGAAAGTGAACCTCCCAACCGGTGAG 1902  
1852 GTCAATCCCGCAATTTGACACCCCACTCTGAAAGACCTGGGCCCAAGCCGA----- 1903  
1903 ATGCGACGCCAAGACTAGATCCCACTCGAATAATCTCTCTCCCACTCGCATTTGAA 1962  
1904 -----ATCCCGAGCTGGGTCGCGCCAGATTAACAGAGCCCAACCAAGTGCCTAG 1956  
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1957 AGGACCTCATATTCGACCACTGCCCCCTTAACCAAGTGGGGCCGAGGGTCCCGGCAACC 2016  
2023 AGAACAACTTCTAATATCCCGACATTAGCCAGAAAGAAATTCCTCGGAATGTAATGCT 2082  
2017 CAGGCAATCCGTGCAGACTTCGACGAACTCCGCTTGGCAATATATCTGCAAG--GC 2074  
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2143 GAGCCCATCTTGGAGAGGCCCCCTTGCAGAGACACAGAGTGCAATTTCTTCCAGCTCCAGC 2202  
2135 ACAGCTCTATGTAACCCCGACCTCAGAGAGAGCAACCTTGGCTG---GAAAGCTCGGAC 2190  
2203 ACCCTTACGCTCCAGCCAGCTCCCAAGAGGCTCCAGCTGATTCACAGAGAGATCC 2262  
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2443 CGGATTTGAAGAAACAAACCCGCCAATGAAGAGTGACTGATTTACTCTCTCCAGTGA 2502  
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2503 GAGTCAAGAAAGTACCGAGAAAGAGAGAGATGAGAGAGCGAGACCATGATATGGGCA 2562  
2489 -----GCAAGATATCCCTGGGGGCGGAGGAT 2517  
2563 GTGGCTGACGCAATATCCAGACTGATACAAACAGAGCTCCAGGACGAAAGAGCAG 2622  
2518 GGGGATACAGACAGCTCAGACCATGATGGTCCACGACGTGAGAGATCACCGGAGCC 2577  
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2683 GGCAGTATTTCAAGAGAAAGAACTTGATGATTAAGAGAGAGTCTGGAGAGAAAGCGA 2742  
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3385 CCTTACACAATTCATGGGCTTCAAGTCCTTTGGCGAGCTCCCGCCAGCGGCTCTGCTG 3444



Db	3523	CCGATATCATTAATTCATGGCATTTAAGTCTTTTGACATCTCCAGACACAGCCTCTGCTA	3582
Qy	3445	GTCCAGCTGACAGTAGAGAGAGGGCAGCGGCTCAAGTGCATCTATGGCTCCAGTGGCC	3504
Db	3583	GTGTATCTCAGCGTAGAAGAAAGTCAAAAGATTAAAGGTATTTTGGTTCACACACTGGT	3642
Qy	3505	TTCCATGCTGTGGAATGTTCGACTCGGGGAAACAGCTATGACATCTACATCCCTGTGACATC	3564
Db	3643	TTCCATGTAATTAATGATTGGATTACAGAAACTCTATAGTATCTACATACCATCTCATATT	3702
Qy	3565	CAGAGCCAGATCAGGCCCATGGCATCATCTTCCGCCCAACACGAGCGATGAGATG	3624
Db	3703	CAGGCGAATATCATCTCTCATGCTATTTGTACTCTTGGCTTAAACAGATGAAATGAAATG	3762
Qy	3625	CTGCTGTGCTACGAGGACGAGGGGTGTACGTCAACAAGTACGGGCGCATCTTAAGAT	3684
Db	3763	CTGTGTGTGCTATGAGAGATGAGGGGTGTATATTAAACACTATGCGCGGATTAACTAAGAT	3822
Qy	3685	GTGCTGCTGCAGTGGGGGAGATGCTACTTCTGTGGCTTACATCTGCTCCACACAGATA	3744
Db	3823	GTGGTGTCTCCATGGGGGAGAAATGCCCACTGTGGGCTTCAATTCATCCAAACAGATA	3882
Qy	3745	ATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGGAGAGCGGGCACCTGAGACGGG	3804
Db	3883	ATGGGCTGGGGGCGAGAAAGCTATTGAGATCCGGTCAAGTGAAGAACAGGACATTTGGATGGA	3942
Qy	3805	GTCCTTCATGACCAACAGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAGGTG	3864
Db	3943	GTATTTATGCAATTAAGCGAGCTCAAAAGTTTAAGTTTCTATGTGAAGAAATGATTAAGTA	4002
Qy	3865	TTTTTTTGCTCAGTCCGCTCTGGGGGACAGCCAAAGTTTACTTCATGACTCTGAACCGT	3924
Db	4003	TTTTTTTGATCCGTCGCACTGTGAGGAAGTAGCCAAAGTGTTTTCATGATGACCTCAACAGA	4062
Qy	3925	AACCTGCATCATGAAGTGGTGA	3945
Db	4063	AATTCATGATGAAGTGGTAA	4083

RESULT 12  
US-09-645-791-1  
; Sequence 1, Application US/09645791

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1  GENERAL INFORMATION:
2  APPLICANT: Luo, Ying
3  APPLICANT: Fu, Alan C
4  APPLICANT: Shen, Mary
5  TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS; COMPOSITIONS AND
6  TITLE OF INVENTION: METHODS OF USE
7  TITLE OF INVENTION: METHODS OF USE
8  FILE REFERENCE: A-68344-1/RMS/DHR
9  CURRENT APPLICATION NUMBER: US/09/645,791
10 CURRENT FILING DATE: 2000-08-24
11 PRIOR APPLICATION NUMBER: US 09/425,324
12 PRIOR FILING DATE: 1999-10-21
13 NUMBER OF SEQ ID NOS: 36
14 SOFTWARE: PatentIn version 3.1
15 SEQ ID NO 1
16 LENGTH: 4083
17 TYPE: DNA
18 ORGANISM: Artificial sequence
19 FEATURE:
20 OTHER INFORMATION: synthetic
21 US-09-645-791-1

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Query Match	34.4%	Score	1358.6	DB	4	Length	4083
Best Local Similarity	61.7%	Pred. No.	9.2e-275				
Matches 2532; Conservative	0	Mismatches	1389	Indels	180	Gaps	16

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QY 3205 CTGCTCGGCTCCGGAACAGATTCTGCAACATGACCCAGAACTGGAGAGAGAGGCGC 3264
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DB 4003 TTTTGTGATCGCTGCTGATCTGAGAGAGTACCAAGTCTTTTTCATGACCTTCAACAGA 4062
QY 3925 AACTGATCATGAACTGTGA 3945
DB 4063 AATTCATGATGAACTGTGA 4083

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RESULT 13
US-09-393-569-1
; Sequence 1, Application US/09393569
; Patent No. 627979
; GENERAL INFORMATION:
; APPLICANT: BINGHAM, SHARON
; APPLICANT: CASE, PATRICK
; APPLICANT: LAWSON, SALLY NEALE
; APPLICANT: NEWTON, RICHARD ANTHONY
; APPLICANT: PIERCE, VALERIE
; APPLICANT: RAUSCH, OLIVER LARS
; APPLICANT: RAVAL, PRAVIN
; APPLICANT: REITH, ALASTAIR DAVID
; APPLICANT: SANGER, GARETH JOHN
; TITLE OF INVENTION: NEW USE
; FILE REFERENCE: P32261
; CURRENT APPLICATION NUMBER: US/09/393,569
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: GB 9907261.3
; EARLIER FILING DATE: 1999-03-29

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; EARLIER APPLICATION NUMBER: GB 9819779-1
; EARLIER FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4181
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-393-569-1

Query Match      34.4%; Score 1358.6; DB 3; Length 4181;
Best Local Similarity 61.7%; Pred. No. 9.3e-275;
Matches 2532; Conservative 0; Mismatches 1389; Indels 180; Gaps 16;

QY 7 ATGGGCGAACCAAGCCCCCGCCGAGCTGTGACGACATGACCTGTCCGCCCTGCGGAGC 66
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Db 1524 AMGGCAG 1583  
Qy 1473 -----GAAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1509  
Db 1584 GAAAGAGACTAATTGTTCCCTTCAGCATCAGCGGAGAGAGAGAGAGAGAGAGAG 1643  
Qy 1510 AAGCCCTGATCACTTATGATCGGAGCAGTGAATCCCGCTGACAAACAGAGCTGAGCCGA 1569  
Db 1644 AMGGCAGCTGATCACTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1703  
Qy 1570 GAGGTAAAG 1629  
Db 1704 GAGGTAAAG 1760  
Qy 1530 CCAAGCAGCAGCGGGCTGAGAGCCCGCATCCCGC-----AGGCTCCCGCAGGGGCC 1680  
Db 1761 GTTGCACAGAGATATCTGACCCCAACCTGCCCCAGAGAGAGAGAGAGAGAGAG 1820  
Qy 1681 CCAAGACCCCTTTCAGAGACTCTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1731  
Db 1821 GGAATTCAGCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1880  
Qy 1732 GAGGAGACGAG 1791  
Db 1881 CTGATGAGCTGTAATATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1940  
Qy 1792 TCCCATGACCGGAG 1851  
Db 1941 CCAAG 2000  
Qy 1852 GTATCCGAG 1903  
Db 2001 ATGCAAG 2060

Qy 1904 -----ATCCCGAGCGTGGGTCCGCCAGATTAACGAGAGAGAGAGAGAGAGAGAG 1956  
Db 2061 AAGTTGACCGAG 2120  
Qy 1957 AGGACCTCATCTATCGCCATCGCCCTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAG 2016  
Db 2121 AGAGCACTTATATATCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2180  
Qy 2017 CAGGACATCGGTGAG 2074  
Db 2181 CTGGAAG 2240  
Qy 2075 GGGCAGAGCGGGGAG 2134  
Db 2241 GAGCCCATCTTGGAG 2300  
Qy 2135 AGCGCTCATGTAACCCGAG 2190  
Db 2301 ACCCTTATGCTCCAG 2360  
Qy 2191 AGCGCTCTTCCAG 2250  
Db 2361 AGTGAAG 2420  
Qy 2251 GTGGAG 2310  
Db 2421 GAGCTGAG 2480  
Qy 2311 CCGAG 2370  
Db 2481 AGCTAAG 2540  
Qy 2371 ACTTGAAG 2430  
Db 2541 CGATTTAAG 2600  
Qy 2431 GAGGTGAAG 2488  
Db 2601 GAGTCAAG 2660  
Qy 2489 -----GCAGAGATACCTTGGGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 2517  
Db 2661 GTGGCTGAG 2720  
Qy 2518 GGGGATTAAG 2577  
Db 2721 TACATGAG 2780  
Qy 2578 CAGCCCCATACGGGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2637  
Db 2781 GGCAGTATTTCAAG 2840  
Qy 2638 CTGCTGATGCTGACAGCAATGAGT-----ACACAACTGCTGAGAGAGAGAGAGAGAG 2688  
Db 2841 TCTGGCAG 2900  
Qy 2689 CCAAGCAGCTCACCCACAG 2742  
Db 2901 CAGAGCAGCTTCTCAGCTGAG 2960  
Qy 2743 GGGAGTGTATCACTGCTGAG 2802  
Db 2961 CAGGAGATGAGCTGTGAG 3020  
Qy 2803 ATGTTGTGATCTAGGAGATCTACAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2847  
Db 3021 CCGTTGTGAG 3080  
Qy 2848 AGCATCCCATCAAG 2904  
Db 3081 GAATCATCAG 3140  
Qy 2905 TACGAGTGAAG 2964

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Db      3141  AATGAGCAAGAAAGATTTCGGTGGTAAATGTAAACCCCAACCAACTTCGGCTCATAGC 3200
Qy      2965  GAGACCCCTGAGATCCGAAATGACAAAGAGCAATTCACGAGATCTCTGTGCAGCC 3024
Db      3201  GACACACCAAGAAATGAAATAACAAAGAAACGATTCACGAAATATCTTGTGCAGT 3260
Qy      3025  CTTTGGGGGGGTCAACCTGTGTGGGCAAGAAACGGCTATGTGTGGACGAAAGT 3084
Db      3261  CTGTGGGGGTAAACCTTCTGTGGGCACTGAAATGGCTGTATGTTTGGACGAACT 3320
Qy      3085  GGGCAAGGCAAGGTGTAGTCACTTGGGCGGCAAGCTTCACAGATGATGTCTG 3144
Db      3321  GGGCAAGGCAAGGTGTATATCTGATCAACCGAGGCGATTCAGAGATGATGTCTA 3380
Qy      3145  GAGGGGCTCAACCTGTCTATCACTCAAGGAAAGAAACAACTGGGGGTATATTC 3204
Db      3381  GAGGACCTGAATGTCTTGTGCAATTTCAAGAAAGAAATTAAGTACGAGTTACTAT 3440
Qy      3205  CTGTCTGTGCTCCGAAACAAGATTTGCACAATGACCCAGAGTGAAGAAAGAGGCG 3264
Db      3441  CTTTATGTGTAAAGAAACGAATCTACATTAATGACCCGAAAGTGAAGAAAGAAAGG 3500
Qy      3265  TGAACCAACCGTGGGAGATGAGAGGCTGCGGCACTACCGTGTGTGAATACGAGCG 3324
Db      3501  TGGATCACTGTTGGGAGCTTGAAGGCTGTATACATTAATTAAGTTGTAAATATGAAG 3560
Qy      3325  ATTTAAGTCTGTGTATCGCCCTCAAGAGCTCCGTGAGAGTGTATGCTGGGCCCCAA 3384
Db      3561  ATCAAAATTTTGTGTATGCTTAAAGATGCTGTGAATATATGTGGGCTCTTAA 3620
Qy      3385  CCTACCAAAATTCATGTGCTTCAAGTCTTTCAGGCTCCGCCACCGCCTCTGCTG 3444
Db      3621  CCGTATCAATTAATCTATGAGCATTTAAGTCTTTTGGAGATCTCAGACAAAGCTCTGCTA 3680
Qy      3445  GTGCACTTGACAGTGAAGAGAGGGGAGCGGCTCAAGGTCACTATGAGTCTCAGTGTGCG 3504
Db      3681  GTTGAATCTCAGCGTGAAGAAAGGTCAAAAGATTAAGTTATTTGGTTCAACACTGTGT 3740
Qy      3505  TTTCATGCTGTGATGTGATCTCGGGGAAACAGTATGATCACTACATCCCTGTGCATTC 3564
Db      3741  TTTCATGTAATGATGTGTATTCAGGAACTCTTATGATATCTACATACCTCACTATTT 3800
Qy      3565  CAGAGCAGATCAACGCCCATGCGCATCTTCTCCCAACCGGACGGCAGTGAAGATG 3624
Db      3801  CAGGCAATATCACTCTCATGTCTATGTCTATCTTGCCTTAAACAGATGAAATGAAATG 3860
Qy      3625  CTGCTGTGCTACGAGGAGCGAGGGGTCTTACGTCAACAGCTACGAGGCGATCTTAAGAT 3684
Db      3861  CTGTTTGTATGAGGATGAGGGGGGTGTATTAACACTATGCGCGGATTAAGAT 3920
Qy      3685  GTGTGTGCTGATGAGGGGAGATGCTACTTCTGTGGCCTATCATCTGCTCAACAGAT 3744
Db      3921  GTGTGTGCTCAATGGGAGAAATGCCCAGGTCTGTGGCCTTACATTCATCAATCAGATA 3980
Qy      3745  ATGGGCTGGGGTGAAGAAACCAATGATCCGCTCTGTGAGAGCGGCGCACTCGACGG 3804
Db      3981  ATGGGCTGGGGCGAAGAACTATGAGATCCGCTGAGTGAAGAGAGAACTTTGATGGA 4040
Qy      3805  GTCTTCATGACAAACGAGCTCAGAGGCTCAAGTTCTGTGTAGCGGAATGACAAAGTG 3864
Db      4041  GTATTATGATCAAGGAGCTCAAAAGTTTCTATGTGAAGAAATGATTAAGATA 4100
Qy      3865  TTTTGTGCTCAGTCCGCTGTGGGAGAGAGCAAGTTTACTCATGACTGTGAACCGT 3924
Db      4101  TTTTGTGATCCGTGTGATCTGAGAGAGTGAAGCAAGTGTTTTCAATGACCTCAACAGA 4160
Qy      3925  AATGATCATGAATGATGTA 3945
Db      4161  AATTCATATGAATCTGTAA 4181

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RESULT 14

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US-09-688-188B-10
; Sequence 10, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLIOMMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; PRIORITY FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 4055
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-688-188B-10

Query Match      34.1%; Score 1345.6; DB 4; Length 4055;
Best Local Similarity 62.2%; Pred. No. 4.8e-272;
Matches 2452; Conservative 0; Mismatches 1339; Indels 153; Gaps 15;

Qy      110  CCTAGGACAGGTGTACAAAGGCTGGCATGTCAAGACGGGGAGCTGGCTGCATCAAG 169
Db      2  CTTTGGGAGGTCTATGAGGGTCTCATGTCAAAACGGGCGAGCTTGAGCCATCAAGG 61
Qy      170  TCATGATGTCAACGAGAGACGAGAGAGATCAACAGAGATCAATGTCTGAAA 229
Db      62  TTATGATGTCAACAGGGATGAGAGAGAAATCAACAGAAATTAACATGTTGAAGA 121
Qy      220  ACTACTTCACACCGCAACATCGCCACTTACTAGAGCTTCACTCAAGAAAGACCCC 289
Db      122  AATATTCATCAACCGGAATATGCTACATCTATGTGTCTTTTCAAAAAGAACCCAC 181
Qy      220  CCGGAAAGATGACAGAGCTGGGCTGTGATGAGAGTCTGTGTGCTGTGAGTCAAG 349
Db      182  CAGGATGATGACCAACTTGTGTGTGATGAGAGTGTGTGTGTGTGTGTGTGTGTGT 241
Qy      350  ACCGTGTAAGAACCAAAAGGCAAGCGCTGAGAGAGAGTGTATCGCTATATCTGCA 409
Db      242  ACTGATCAAGAACCAAAAGGTAAACAGTTGAAAGAGAGTGAATGATCATCTGCA 301
Qy      410  GGGAGATCTCAGGGGTCTGGCCATCTTCATGCCCCAAGGTGATTCATGAGACATCA 469
Db      302  GGGAAATCTTACGGGGGCTGAGTCACTGACACAGCATAAAGTGAATTCATGAGATTA 361
Qy      470  AGGGCAAGATGTGCTGTGACAGAGATGCTGAAGTCAAGTATGATTTTGGGGTGA 529
Db      362  AAGGGCAAAATGTCTTGTGACTGAATATGCAAGAGTTAACTATGTGAATTGAGATCA 421
Qy      530  GTGCTCAGCTGAGACCGACCGTGGGACAGAGCACTTCTATTTGGGACTCCCTCACTGA 589
Db      422  GTGCTCAGCTTGTATGAGCAAGTGGGACAGAGGAATCTTCAATTTGGAATCTCCCTGA 481
Qy      590  TGGCTTCAGAGGTCAATCGCTGTGTGATGAGAAACCTGTATGCCACTTATGATTAAGAGATG 649
Db      482  TGGCAACAGAAATTTATGCTGTGTGATGAAGAACCCAGATGCCCATATGATTTCAAGAGTG 541
Qy      650  AATTTGTGCTCTAGAAATCAAGCATCGAGATGAGAGAGAGAGAGAGAGAGAGAGAG 709
Db      542  ACTTGTGTCTTTGGGTATCAACCGCATTTGAATGAGAGAGAGAGAGAGAGAGAGAG 601
Qy      710  ACATGACCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 769
Db      602  AATGACCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 661
Qy      770  CCAGAGAGTGTCTAAGAAATTCATTTGATGATGATGATGATGATGATGATGATGAT 829

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Dh 662 CTAAGAGTGGTCAAAAAATTCCAGTCATTTATGAGAGCTGTTGGTAAAGATCA 721
Qy 830 TGAAGCCGCCACCCAGGAGCAGCTACTGAGTTTCCCTTCATCCGGGACCAAGCCACGG 889
Db 722 GCCAGCCGACAGAACAAATTTGATGAAAGCATCTTATTAAGAACCAACCTAATG 781
Qy 890 AGCCGAGGTCCGCTTCAGCTTAAAGACCATTTGACCGGATCCGGAAAGAGGGGGTGG 949
Db 782 AGCCGAGGTCCGCTTCATCTCAAGGACCATATTGATGAACAAAGAAAGAGGAGAG 841
Qy 950 AGAAAGAGAGACAGAAATATGATGACAGCGGACGGAGAGAGATGACAGCCATGAG 1009
Db 842 AAAAAGATGAGACAGATATGATGACATGAGAGTGAAGAGAGAGAGAGAT---G 898
Qy 1010 AGAAAGAGAGCCAAAGTTCATCATGAAAGTCCCTGAGAGTTCGACTTACGCCGGAGT 1069
Db 899 ACTAGAGAGAGCCCGCTCCATCTCGAAATCTGCCAAGGAGATCGACGCTCGAGGGACT 958
Qy 1070 TTCTCCGCTCCAGAGGAAAAATTAAGACAACTCAGAGGCTTTAAACAGCAGCAGCAGC 1129
Db 959 TTCTGAGCTGAGCTGGCCAAACAGAGACGTTCTGAGGCCCTA-----CGAGGACAGC 1012
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Qy 1250 AGCCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1309
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Qy 1310 CTCTGCGCGGAGAGAGAGCGCGCGCAGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1369
Db 1187 AGATGCGCGGAGAGAGAGAGAGAGCGCTGCGAGCAGTGAACAGGAATTAAGCCCAAC 1246
Qy 1370 AGCTGAGAGAGCAGCGGAGTCAAGACCTCTTCAGAGCAGCTGAGCAGAGAGAGAGCT 1429
Db 1247 AATTGAAAGAACAGAGCAGACAGAAAGATGACAGGCACTAAAGCAGAAAGAGAGACT 1306
Qy 1430 ACCTCAAGTCCCTGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1489
Db 1307 ACTAGTTTCCCTTCAGATCAGCGGACAGCAGCAG----- 1343
Qy 1490 AGCTCTGCTGAGGAGCAGAAAGCCCTGTACCATTTATGTCGAGGAGATGATCCCGCTG 1549
Db 1344 -----GCTGTGAGAGAGAGAGCAGCTGTACATTTACAAAGAGAGATGATGATG 1396
Qy 1550 ACAAAACAGCTGAGCGCCGAGAGGTGAAGAGAGAAACAAGATGAAACAAGCAGCAGAACT 1609
Db 1397 AGAAGCCGATGAGGCGCAAGAGGTGAAGAAACGATCAAGGCTCAACCGGCAAAAGTTCC 1456
Qy 1610 CTCTCTTGGCCAAAGAGCAGCAGCAGCAGCGGGCTGAGAGCCCTCCCATCTCCCTC----- 1663
Db 1457 CTGCGATATGCTCA---CAAGGTTCACACAGATATTCGACCCCAACCTGCGCCCAAGT 1513
Qy 1664 ---AGGCTCTCCCAAGGGCCCAAGGACCCCTTTCCCAAGCTCTCTATGAGAGAGCGGG 1720
Db 1514 CGGAGTCTTTAGCATTTAGTGAAGTTCAAGCTGTGACAGACCCCTCATGTCTCAGACAG 1573
Qy 1721 TGAAGCCCGCAGAGAGAGCAGCAGATCCCTGACAGACAGCCCAACCCGAAACCTGAGCTG 1780
Db 1574 TCGATCCCAAGATCCCAATCTGTAAGTGTAAATTCACAGGACCTGCTTGAACCGCT 1633
Qy 1781 CTTTCCCAAGCTCCCATATACCCG-----ACCTGCAATCCCGCAGCCCATCTGCA 1831
Db 1634 CCGAGTCAAGTCAAGAGCAGCCCAAGAGGCGCTCTGAGGTTTCAGAGAGCTCTGAAG 1693
Qy 1832 CGCCCAAGTCCCGAGAGAGCTGTCAATCGCCAGAAATTCAGACCCCACTCTGAGAGAGCTG 1891
Db 1694 TGACCTCCCAACCGGTGAGATGCCACCGCAGAACTCAGATCCCACTCTGAGAAATCTCTC 1753

Qy 1892 GCCCAGGCC-----GAATCCCCAGCGCTGGGTCCGCCAGATTAAGAG 1936
Db 1754 CTCTCCCACTCGCATTTAAAAAGTTTGAACGAAGCTCTTGTTAGCAGAGAGAGACA 1813
Qy 1937 CCCCACCAAGGTCTCTCAGAGAGCCTCATCTATCGCACTGAGCCCTTAACAACAGTGGGG 1996
Db 1814 TTCCACCAAGGTCTCTCAAGAGACCACTTATATCCCGAGCATTAAGCCAGAAAGATT 1873
Qy 1997 CCGAGAGGTCCCGGACAGCCAGGAGTCCGTGCCAAGCTTCGACAGCATTCGCTGGC 2056
Db 1874 CTCTGGGAAATGTATGTCTCTGGGAGCCAGACTATGATCTCAACCCATCAGAGACAGCA 1933
Qy 2057 AAATCTATCTGC-----AAAGCGGGCAGAGAGGGGGCAGCCCAAGCTCCAGGGCCCCCT 2112
Db 1934 ACCCTGATCTCCGAGAACTGAGCCCATCTTGGAGAGCCCTTTCAGAGAGACAGAGTG 1993
Qy 2113 GCTCAGCCCTCTGAGCCGCGCAACGCTCTATGTAACCCCGACTCAGAGAGAG--CGAGC 2170
Db 1994 GCAATTCCTCAGCTCCAGCAGCAGCCCTAGCTCCAGCCAGCTCCCAAGAGAGGCTCCAGC 2053
Qy 2171 CTGAGTGGAAAGCTCGAGCAGGCTCTTCCAGCTCTCAGCGGCACTCCCAAGCTG 2230
Db 2054 CTGATCACAAGCAGAGATCCAGTGAACGACACAGAGTTCCAGCAACAGTAACTCAGAG 2113
Qy 2231 GCTCACTGAGAGGGAACCGCTGGAGAGCTCTCCAACTGGAACAGCTCCCTGTGCTCT 2290
Db 2114 GATCACTGTGCTCTCCCATGAGCTGCAAGGTGAACCGAAAGAAATTCAGAGACATTA 2173
Qy 2291 CCCCTGGGAATPAAGCCMAAGCCGACGACACCGCTCAAGCGCAGCGCGCCGCAACT 2350
Db 2174 CCGGCGCAGTGCAGACAGCTAGCTACAAAAAGCTATAGATGAGATTTGACGGCATTAG 2233
Qy 2351 TTGTGTCTGAAAAGAGCGACTTGACGAGAGGCCCTCTGGCTCTCCAAAGGCCATG 2410
Db 2234 CCAAAAGAACTPAAGAACTCCGAGTTGAAGAAACAAACCGCCATGAAGAGGATGACTG 2293
Qy 2411 ACTACTGTGCTCCAGCAGAGAGGTGAAGACATGTAGACAGAGAGAGAGAGAGCCAG 2470
Db 2294 ATTACTCTCTCTCCAGTGAAGAGTCAAGAAATGACGAGAAAGAGAGAGATGAGAG 2353
Qy 2471 GCGGCGCAGCAGAGGGAGC-----AGAGATA 2497
Db 2354 GCGAGACCATGATGGAGCAAGTGTCTGACGACATTAACCAAGTATACCAACAGAG 2413
Qy 2498 CCCCTGGAGGCGCCGACGATGGGATACAGACAGCTCAAGCAGATGATGATCAAGAG 2557
Db 2414 CTCAGAGCAGCAACGAGAGTACATGTGGAAATGTGGGAGCGCATGGGCTGAGAGCT 2473
Qy 2558 TCGAGAGATCACCGGAGCCAGGCCCATACGGGGCGGACCATGTGTGTCAGAGCA 2617
Db 2474 CTCAATGGGACAGTTTCAAGCGGAGTATTTCAAGAGAGAACTTGATGATTAAGAGA 2533
Qy 2618 CCCCTGAAGAGAGCGGAACTGCTGATGCTGACAGCAATGGT-----ACACAA 2668
Db 2534 GCTTGAAGAGAGAGAGAGATCTGAGCAGTGAAGCAATGCTTTGTGCTGAGCCATCA 2593
Qy 2669 ACTGCTGAGTGTGATCAGGCCAGCCATCAACCAAGAGAAAGCAAGAGGCCAA----- 2724
Db 2594 ACTGCTGAGTGTGATGAGAGAGCAATTTCTCAGCTGGAACCCGACTGAGGAGACTGG 2653
Qy 2725 --AGCCCACTCTGAGAGAGAGTGTGATCTACAGTCTCGTGGGCTGTTAAAGGCC 2782
Db 2654 GGCAGCTCTCAACCATTTCCAGAGAGATGACTCTGGAGACTGAATATGCAATGGGAGCA 2713
Qy 2783 CTGCAAGAGAGTGTGATCAGATGTTTGTGATCTAAGAGATTTACAGCTTGAAGAGCA 2842
Db 2714 GCACCAAGAGCTCTTCAACCCCTTTGTGAGCCCAAGATTAACAGACGCTCTCCACTG 2773
Qy 2843 GGAAGAGC-----ATCCCAATCAAGCCCTTATGAGTGTGAGAGAGGCACTC 2887
Db 2774 ATGAAGATGAAGAGATGAGGAATCATCAGCGGAGCTGTGTTAATGCGGAACTTCTTA 2833
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QY	830	1GAGCCGCGCCACCCACGGAGCGACTGAAATTTCCCTTACCTCCGGACACGAGCCACGG	889
Db	722	GCCAGCGACACGAACAAGAAACATTGATGAAACATCTATTATACAGACCAACTTAATG	781
QY	890	AGCGCAGATCCGCATCCAGCTTAAAGACCAATTTGACCGATCCCGAAGAACCGGGGTG	949
Db	782	AGCGCAGATCCGCATTCATCTCAAGGACCAATTTGATGAAACAAGAAAGAACGACAGAG	841
QY	950	AGAAAGAGAGACAGAAATTGAGTACAGCGGCAGCGAGAGAGAAATGACCCCTGGAG	1005
Db	842	AAAAAGATGAGACAGATGATGATGATCACTGGAAAGTGAAGAAAGAGAGAGAAAT---G	898
QY	1010	AGGAAGAGAGAGCAAGCTCCATCAAGAAAGTACCTGAGAGAGTGACTTACGCGCGGAGT	1065
Db	899	ACTCAGAGAGAGCCAGCTTCATCTGAAATCTGCAGAGGAGTGCAGCTGCGGAGGACT	958
QY	1070	TTCTCCGCGCTCCAGCAGGAAAAATGAAGCACTCAGAGCTTTAAACACAGACAGCAGC	11225
Db	959	TTCTGAGGCTCAGCTGGCCAAACAGAGACGTTTGAAGGCCCTTA---CGAGAGGACAGC	1012
QY	1130	TGCAGACACACAGAGAGAGACCCCCGAGCACATCAAAACCTTGCTGCACACGCGC	11875
Db	1013	AGCTGAGACACAGACGCGGGAATGAGAGACAAAGCGGAGCTGCTGCGCGAGCGCTC	10775
QY	1190	AGCGCGCATAGAGAGACGAAGAGAGAGACGCGCGCGCTGAGAGAGACAAACGCGCGG	12445
Db	1073	AGAGCGCATGAGAGAGACGAAGAAAGACAGAGCGCGCGCTGAGAGAGACAAAGCGCAG	11325
QY	1250	AGCGGAGACAGCGGAAGCTGCAGAGAAAGAGACAGAGCGCGCGCTGAGAGACATGCAG	13075
Db	1133	AGAAAGAGACTCGGAAGACGACGAGAGAGGAGACACGCGCGCATATGAGT---AGC	11865
QY	1310	CTGCGCGCGGAGAGAGAGCGCGCGGACGCGGAGCGTGAAGAGAAATTAAGCGGAGAC	13675
Db	1187	AGATGCGCGGAGAGAGAGAGAGCGCTGCGGACATGAACAGAAATTTAGCCCAAC	12445
QY	1370	AGCTGAGAGACAGCGGACGTCAGAACGTTCTCAGAGGACGCTGCAGAGAGCATGCGCT	14225
Db	1247	AATTGGAAGAACAGAGACAGAGCAAAACCTTCAGAGGACGCTTAAAGCAAGAAAGACT	13065
QY	1430	ACCTCAAGTCCCTGACAGACAGACAAACAGACGACACTTCAGAAACAGACGACGACG	14875
Db	1307	ACTTATGTTCTCTTACATCAAGCGGACGAGACAG--------	13435
QY	1490	AGCTCTGCTCTGAGGACAGAAAGCCCTGTACATTATGTCGAGGACATGATCCCGTG	15445
Db	1344	-----GCTGTGGAAGAAAGACCACTGTACATTACAAAGAAAGATGATCTTAAGT	13975
QY	1550	ACAAACCAAGCTTGAGCGCCGAGAGGTAGAAAGAGAAACAAGATGAACAGACGACAACT	16095
Db	1397	AGAAAGCCAGATGAGGACCAAGGAGGTAGAAAGAACGCTCAAGGCTCAACCGGCAAAATTC	14565
QY	1610	CTCCCTGGCCAAAGAGCCAGGACACAGCGGCGCTGAGCGCGCCCAATCCCGC-----	16655
Db	1457	CTGCAATCTCA---CAAGGTTCACACAGATATTTGACCCCAACTGCGCCCAAGT	15135
QY	1664	---AGGCTCTCCCAAGGAGCGCCCGAGAGCCCTTTCCCAACTCTCTTATGACAGAGCCGG	17205
Db	1514	CGGAGTCTTACAGATTATGAGAGTTTACGCTGCTGAACACCCCGCATGTCAACAG	15725
QY	1721	TGAGAGCCCAAGAGGAGACCGCAAGTCCCTGCAGAACACAGCCCAACCGAAACTTGGCTG	17875
Db	1574	TGATATCCCAATCCCAATCTGTGATGTGTAATAATCCCAAGGACTTCACTTGAACGGCT	16335
QY	1781	CCCTTCCAGCTTCCCATGACCCCG-----ACCTGCAATCCCGCACCCCATGCGCA	18315
Db	1634	CCCAATGATGACAGAGACGCCCAAAAGGCGCTCTCTGAGTTTACGAGAGGCTGTGAACG	16975
QY	1832	CGCCCATGTCGCCAGAGAGCTGTATTCGCGCAGAATTCAGACCCCACTTGAAGACCTG	18915
Db	1694	TGACCTTCCACCGCGTGAAGATGCAACGCGCAAGATTCAGATCCCACTTGAAGAAATCTCT	17535

QY	1892	GGCCCAAGCC-----GAATCCCCAGCCTGGGTCCGCCAATATACGAG	1935
Db	1754	CTCTCCCACTCGCATTTGAAAGTTTGACCGAAGCTCTTGGATTACGAGGAAGAAGCA	1813
QY	1937	CCCCACCMAAGTGTCTCAGAGACCTCATCTATCGCACCTGACCCTTAAACCAATGGGG	1996
Db	1814	TTCCACCAAAAGTGTCTTAAAGAACACTTCTATCTCCCAAGCATTAAGCCAGAAAGATT	1873
QY	1997	CCGAGGGTCCCGCCAGCCCAAGCAGTCCGTGCCAAGCCTCGAGCAACTCCGCTGGC	2056
Db	1874	CTCCTGGGAATGTGTAGTCTCTGGGAGCCCACTATGAGATCTCAACCCATCAGACAAAGCA	1933
QY	2057	AAATTTATCTG---AAAGCGGCGAAGCGGGACACCCMAAGCCTCCAGGGCCCCCT	2112
Db	1934	ACCTGATCTCTCGAGGAACCTAGGCCCACTTTGGAGAGGCCCTTTCAGAGACAGCAAGTGT	1993
QY	2113	GCTAGCCCCCTGGGCGGCGCCCAAGCCCTCTAGTAAACCCCGACCTCAGAGAGAG---CGAC	2170
Db	1994	GCAGTCTCTCAAGCTCCAGCAACCCCTAGCTCCCAAGCCCAAGCTCCMAAGAGGCTCCAGC	2053
QY	2171	CTGGCTGGAAACGCTCGAGCAGCGTCTTTCAGCCTTCAAGGACACTCCCAAGCTG	2230
Db	2054	CTGATTCACAAAGAGATCCAGTGAAGCAACAGAGTTTCAGCCAAAGTAAATGACAGAG	2113
QY	2231	GCTCACTGAGCGGAACCGCGTGGAGCTCTCTCCAAATGAGACACTCCCTGTGCTCT	2290
Db	2114	GATCACTGTGTCTCCCATGAGCCTGCAAGTGAACCAAGAAATCCAGGACATTA	2173
QY	2231	CCCCGGGAATTAAGCCAAAGCCCAAGCAACCGCTCAAGCCGAGGCGGCGCCAGACT	2356
Db	2174	CCCGGCCAGTCAGCAGCTAGCTACAAAAGCTATGATGAGAGATCTGACGCAATTAG	2233
QY	2351	TTGTGTTCTGTAAGAAGCGGAGACTCTGAGCAGAGCGCCCTCGGCTCTCCAGAAAGCCATGTG	2410
Db	2234	CCAAAGACTTAAGGAATCTCCGATTGAAGAAACAAACGCCCAATAGAAAGGTGACTG	2293
QY	2411	ACTACTGTCGTCCAGCGAGAGGTGAAACAGTGAAGACGACGAGAGAGAGCGAAG	2470
Db	2294	ATTACTCTCTCCCTCAGTAGAGAGTCAGAAAGTACGAGAGAGAGAGAGATGAGAGAG	2353
QY	2471	GGGGCCAGCAGAGGGGAGC-----AGAGATA	2497
Db	2354	GGGAGCCCATGATGAGGACAGTGCCTGCAGCGACATACCAGACTGATACAAACAGAG	2413
QY	2498	CCCCCTGGGGCGGAGCGATGGGATACAGACAGCTCAGACCAATGATGATCCACAGC	2557
Db	2414	CTCCAGGAGCAACGACAGATACATGTGGGAATGTGGGAGCCCATGGGCTGGAGACT	2473
QY	2558	TCGAGAGATCACCGGAGCCAGCCCAATACGGGGGCGCACCATGATGTCCAGCGCA	2617
Db	2474	CTCATGGCGGACAGTTTTCAGCGGAGTATTTCAAGAGAAAGAACTTGATGATTAGAGAG	2533
QY	2618	CCCCGTAAGAGAGACGGAACCTGCTGCATGCTGACAGCAATGGGT-----ACACAA	2668
Db	2534	CGTCTGAGAGAAAGAGGATCTGGCCACAGTGCACCAATAGGCTTTTGTCTGGCCACATCA	2593
QY	2669	ACCTGCTCAGATGGTCCAGCCCAAGCACTCAACCCACGAGAACAGCAAAAGGCCAA-----	2724
Db	2594	ACCTCTCAGACTGGTGCAGAGACCAATTTCTCAGCTGGAACCCCGACTGAGGGAATGG	2653
QY	2725	--AGCCCACTCGAAGAGATGGAGTGGTGACTACAGTCTCTGTGGCTGGTAAAGGCC	2782
Db	2654	GGCGGTCTCAACCAATTTCCAGAGATGAGCTGTGGGACTGAATATGGCATGGGAGCA	2713
QY	2783	CTGGCMAAGCTGTTCAAGATGTTTGTGATCTAAGGATCTTACAGCTGAGAGGCAAGT	2842
Db	2714	GCAACCAAGCTCTCTTACCCCTTTGTGAGACCCCAAGATATACAAACGCTTCCCACTG	2773
QY	2843	GGGACAGC-----ATCCCAATCAAGGCTTATGTTGGTGGAGAGGGCACTC	2887
Db	2774	ATGAAGATGAAGAGATGAGGATATCATACCGCAGCTCTGTTTACTGGGCACTTTTA	2833
QY	2888	GGCTTCAGCAG---CTGCAATGACAGTGAAGAGGGTTCTGTGCTCAACGTGATATCCA	2944

Job time : 336 secs

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Db 2834 GGCAAGAACAGGCCAACTCAATGAGCAGAAATTCGGTGTAAATGTAACCCAA 2893
QY 2945 CCACACCCCGGGCCCAAGTAGACCCCTGAGATCCGGAGATGACAAAGGAGTTCAACT 3004
Db 2894 CCACATTCGGCTCTATAGCAGACACAGAAATCAGAAATACAGAAACGATTCACACT 2953
QY 3005 CCGAGATCCTCTGTGTCAGCCCTTTGGGGGGTCAACCTGCTGGTGGCACGAGAACGGGC 3064
Db 2954 CAGAAATCTTTGTGACACTCTGTGGGGTGTAACTTCTGGTGGGACTGAAAAATGGCC 3013
QY 3065 TGATGTTGCTGAGCCGAAAGTGGGAGGGCAAGGTGATGACTCATTTGGGGGGCGACCT 3124
Db 3014 TGATGCTTTTGGACCGAAGTGGGCAAGGCAAAAGTCTAATCTGATCAACCGAGGCCAT 3073
QY 3125 TCCAGCAGATGATGTGCTGAGGGGGCTCAACCTGCTCATACCATCTCAGGAAAGGA 3184
Db 3074 TTCAGCAGATGATGTGCTGAGGGGACTGAATGTCCTGTGACAAATTCAGGAAAGGA 3133
QY 3185 ACAAACCTGCGGGGTATTAACCTGCTGCTCGGACCAAGATTCGCAATGACCCAG 3244
Db 3134 ATTAGCTACGAGTTACTATCTTTATGTTAAGAAAGAAATCTACATATGACCCAG 3193
QY 3245 AAGTGAAGAGAGAGGAGGCTGAGACCAACGTTGGGAGCAATGAGGGCTGGCGCACTACC 3304
Db 3194 AAGTAGAAAGAGAAACAGAGCTGATCACTGTGGGGACTTGGAGGCTGTATACATTATA 3253
QY 3305 GTGTTGTGAATACAGAGGAGTTAAGTTCCTGTGCTCATGCGCTCAAGAGCTCCGTGAGG 3364
Db 3254 AAGTTGTAAATATATAGAAAGATCAAAATTTTGTGTATGCTTAAAGAAATGCTGTGAAA 3313
QY 3365 TGTATGCTGGGCCCCCAACCTTACCAATTCATGGCTTCAAGTCTTTGCCGACC 3424
Db 3314 TATATGCTTTGGCTCTTAACCTGATCATTAATTCATGSCATTTAAAGTCTTTGCAAGATC 3373
QY 3425 TCCCCACCGCCCTGTGCTGTGATGACCTGACAGTAGAGAGGGGCAAGCGCTCAAGGTCA 3484
Db 3374 TCCAGCAGACAGCTCTGCTAGTTGATCTCACGCTAGAAAGAGTCAAGATTAAGGTTA 3433
QY 3485 TCTATGCTCCAGTGTGCTGCTTCATGCTGTGATGTGATCTGCGGGAAACAGCTATGACA 3544
Db 3434 TTTTGTGTTCAACACTGTTCTTCATGTATTAATGATGTATTCAGGAAATCTTTATGATA 3493
QY 3545 TCTATATCCCTGTGACATCCAGAGCAGATCAGCGCCCATGCAATCTTCTGCCCA 3604
Db 3494 TCTACACACCATCTCATATTCAAGGCAATATCACTCTCATGCTATTTGCACTTGCCCTA 3553
QY 3605 ACACCGACGAGATGAGATGCTGTGTGCTACAGAGACGAGGGTGTCTACGTCAACACGT 3664
Db 3554 AAAACAGATGAGATGAGAAATGCTTTGTTGCTATAGAGGATGAGGGGGTGTATTAACACT 3613
QY 3665 ACGGCGGATCATTAAGATGTGTGTGCTGCAAGTGGGGGAGATGCTTCTGTGGCCT 3724
Db 3614 ATGGCCGGATTAATAAGATGTGTGTGCTCAATGGGGAGAAATGCCACGTCTGTGGCCT 3673
QY 3725 ACATCTGCTCCAAACAGATAATGGGCTGGGGTGAAGAAAGCATTAAGATCCGCTGTGG 3784
Db 3674 ACATTCATTCCAAATCAGATAATGGGCTGGGGGAGAAAGCTATGAGATCCGCTCAGTGG 3733
QY 3785 AGACGGGCGACCTCGACGGGGTCTTTCATGCAACAAAGAGCTCAGAGCTCAAGTTCTGT 3844
Db 3734 AAAACAGACATTTGATGAGATTTATGCAATAGCAGACTCAAGGTTAAAGTTCTAAT 3793
QY 3845 GTAGCGGAATGACAAAGTGTGTTTTCCTCAGTCCGCTCTGGGGGAGAGCAAGATT 3904
Db 3794 GTGAAGAAATGATTAAGTATTTTGTGATCCGTGCAATCTGAGGAAAGTACCAAGTGT 3853
QY 3905 ACTTATGATCTTGAACCGTAACTGATCATGAATCTGTGAAAG 3948
Db 3854 TTTTCAATGACCTCAACAGAAATTCATGATGAATGTGAACAG 3897
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Db	181	ACGGAGAGAGAGAGAGATCAACAGAGATCAATGCTGAAAAATCTTCAC	240
OY	241	CACCCCAATGCGCACTTACTACGAGGCTTTCATCAAGAGCCCCCGGAAACAT	300
Db	241	CACCGCAACATGGCCACTTACGGAAGCTTTCATCAAGAGCCCCCGGAAACAT	300
OY	301	GACCAAGCTCTGGCTGTGTATGAGTTCTGTGGTGTCTGTTCACTGATCACTTGGTAAG	360
Db	301	GACCAAGCTCTGGCTGTGTATGAGTTCTGTGGTGTCTGTTCACTGATCACTTGGTAAG	360
OY	361	AACAACAAAGGACAGCCCTGAAGAGGACTGTATGCTATATCTGACGGAGATCCCTC	420
Db	361	AACAACAAAGGACAGCCCTGAAGAGGACTGTATGCTATATCTGACGGAGATCCCTC	420
OY	421	AGGGGTCTGGCCCATCTCCATGCCCCACAAGGTATCATCGACATCAAGGGGCAAGAT	480
Db	421	AGGGGTCTGGCCCATCTCCATGCCCCACAAGGTATCATCGACATCAAGGGGCAAGAT	480
OY	481	GTCGTCTGTACAGAGATGTCTGAGGTCAAGCTAGTGAATTTTGGGGTGAAGTCTACGCTG	540
Db	481	GTCGTCTGTACAGAGATGTCTGAGGTCAAGCTAGTGAATTTTGGGGTGAAGTCTACGCTG	540
OY	541	GACCGCACCGTGGGAGAGAGCAACTTTCATTTGGGACTCCCTACGTAGATGGCTCCAGAG	600
Db	541	GACCGCACCGTGGGAGAGAGCAACTTTCATTTGGGACTCCCTACGTAGATGGCTCCAGAG	600
OY	601	GTGATCGCCTGTATGAGAACCTGTATGCACTATGATTAAGAGATGATATTGGTCT	660
Db	601	GTGATCGCCTGTATGAGAACCTGTATGCACTATGATTAAGAGATGATATTGGTCT	660
OY	661	CTAGGAATTCACAGCCATCGAGATGGACAGAGAGAGCCCCCTCTGTGTACATGACACCC	720
Db	661	CTAGGAATTCACAGCCATCGAGATGGACAGAGAGAGCCCCCTCTGTGTACATGACACCC	720
OY	721	ATGCGAGCCCTCTTCCCTCATTTCTCGGAACCCCTCGGCGCAGGCTCAAGTCCAAAGAGTGG	780
Db	721	ATGCGAGCCCTCTTCCCTCATTTCTCGGAACCCCTCGGCGCAGGCTCAAGTCCAAAGAGTGG	780
OY	781	TCTAAGAAAGTTCATTGACTTTCATTGACATGATGTCTTCATCAAGCTTACCTGAGCCGCCA	840
Db	781	TCTAAGAAAGTTCATTGACTTTCATTGACATGATGTCTTCATCAAGCTTACCTGAGCCGCCA	840
OY	841	CCCAAGGACAGCTTACTGAAGTTTCCCTTCATCCGGGACACGCCCAACGAGGCGGAGTTC	900
Db	841	CCCAAGGACAGCTTACTGAAGTTTCCCTTCATCCGGGACACGCCCAACGAGGCGGAGTTC	900
OY	901	CGCATCTCAGCTTAAAGACCACTTGCACGATCCCGGAAACAGGGGTGAGAAAGAGAG	960
Db	901	CGCATCTCAGCTTAAAGACCACTTGCACGATCCCGGAAACAGGGGTGAGAAAGAGAG	960
OY	961	ACAGAAATGAGTACAGCGGACGCGAGGAGAGAGATGACAGCCATGAGAGAGAGAGAG	1020
Db	961	ACAGAAATGAGTACAGCGGACGCGAGGAGAGAGATGACAGCCATGAGAGAGAGAGAG	1020
OY	1021	CCAACTCCATATATGAACGTGCTGTGAGATGACCTTACGCGCGGAGTTTCTCGGCTTC	1080
Db	1021	CCAACTCCATATATGAACGTGCTGTGAGATGACCTTACGCGCGGAGTTTCTCGGCTTC	1080
OY	1081	CAGCAGGAAAAATTAAGCAACTCAGAGGCTTTTAAAAACAGCAGCAGCAGCTGACAGCAG	1144
Db	1081	CAGCAGGAAAAATTAAGCAACTCAGAGGCTTTTAAAAACAGCAGCAGCAGCTGACAGCAG	1144
OY	1141	CAGCAGCAGAGACCCCGAGGCAACATCAAAACCTGTGCAACGCGGCAAGCGGCGCATAT	1200
Db	1141	CAGCAGCAGAGACCCCGAGGCAACATCAAAACCTGTGCAACGCGGCAAGCGGCGCATAT	1200
OY	1201	GAGGAGCAGAAAGAGAGAGCGGCGCGGTGAGAGAGCAACAGCGGCGGAGAGCGGAGCAG	1266
Db	1201	GAGGAGCAGAAAGAGAGAGCGGCGCGGTGAGAGAGCAACAGCGGCGGAGAGCGGAGCAG	1266
OY	1261	CGGAAGCTGCAGAGAAAGAGCAGCAGCGCGGCTGTGAGAGCATGCAAGCTCTGCGGCGG	1322

Db	1261	CGAAGCTCGACAGAGAAAGAGACAGACACGGGGCGCTGGAGGACATATGACAGGCTCTGGGGCGG	1320
QY	1321	GAGGAGGAGCGGGCGGCACGGCGGAGCGTGTAGCAGGAATTAACAAGCGGAAGCAGCTTGGAGGAG	1380
Db	1321	GAGGAGGAGCGGGCGGCACGGCGGAGCGTGTAGCAGGAATTAACAAGCGGAAGCAGCTTGGAGGAG	1380
QY	1381	CAGGGGCAAGTCAGAACCTCTCCAGAGGCACTGTAGAGGAGGACATGCTCTCAATCTCC	1440
Db	1381	CAGGGGCAAGTCAGAACCTCTCCAGAGGCACTGTAGAGGAGGACATGCTCTCAATCTCC	1440
QY	1441	CTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCAGCTCTGCT	1500
Db	1441	CTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCAGCTCTGCT	1500
QY	1501	GGGGACAGGAAGCCCTCTGTACCATTAATGATGTGGGGACATGAATCCGCTGACAAACAGCC	1560
Db	1501	GGGGACAGGAAGCCCTCTGTACCATTAATGATGTGGGGACATGAATCCGCTGACAAACAGCC	1560
QY	1561	TGGGCCCCGAGAGGTAGAAAGAGAAACAAAGATGAACAAAGACAGAACTCTCCCTTGGCC	1620
Db	1561	TGGGCCCCGAGAGGTAGAAAGAGAAACAAAGATGAACAAAGACAGAACTCTCTCTTGGCC	1620
QY	1621	AAGACGAAGCCAGGACAGCAGGAGCCCTGAGCCCCCATCTCCCGAGCCTCCCGAGGCCC	1680
Db	1621	AAGACGAAGCCAGGACAGCAGGAGCCCTGAGCCCCCATCTCCCGAGCCTCCCGAGGCCC	1680
QY	1681	CCAGGACCCCTTTTCCAGACATCTCTCTTAATGACAGAGCGGTGTGAGACCCCGAGAGGACCG	1740
Db	1681	CCAGGACCCCTTTTCCAGACATCTCTCTTAATGACAGAGCGGTGTGAGACCCCGAGAGGACCG	1740
QY	1741	CACAAAGTCCCTGTGAGAGCAGAGCCCAACCCCTGACTGCTCCCTCCAGCCTCCCAAGAC	1800
Db	1741	CACAAAGTCCCTGTGAGAGCAGAGCCCAACCCCTGACTGCTCCCTCCAGCCTCCCAAGAC	1800
QY	1801	CCCGACCCCTGCAATCCCCCGACACCCACTGACAGCCCGACAGTCCCGAGGAGCTGTCAATCGC	1860
Db	1801	CCCGACCCCTGCAATCCCCCGACACCCACTGACAGCCCGACAGTCCCGAGGAGCTGTCAATCGC	1860
QY	1861	CAGAAATTCAGACCCCACTCTGAAAGGACCTGTGCCCCAGCCCGAATCCCGACGCTTGGATC	1920
Db	1861	CAGAAATTCAGACCCCACTCTGAAAGGACCTGTGCCCCAGCCCGAATCCCGACGCTTGGATC	1920
QY	1921	CGCCCAAGTAAACAGAGGCCCCCAACCAAGATGCTCAGAGGACCTCATCTATGSCACATGSC	1980
Db	1921	CGCCCAAGTAAACAGAGGCCCCCAACCAAGATGCTCAGAGGACCTCATCTATGSCACATGSC	1980
QY	1981	CTTAAACAACAGTGGGGCCGAGGGGTCCCGGACAGCCAGGCAAGTCCGTGCGACAGCTTCGC	2040
Db	1981	CTTAAACAACAGTGGGGCCGAGGGGTCCCGGACAGCCAGGCAAGTCCGTGCGACAGCTTCGC	2040
QY	2041	AGCAACTCCGCTGTGGCAAAATCTATCTGTCAAAAGGGGGCACAAGCGGGGCAACCCCAAACT	2100
Db	2041	AGCAACTCCGCTGTGGCAAAATCTATCTGTCAAAAGGGGGCACAAGCGGGGCAACCCCAAACT	2100
QY	2101	CCAGGAGCCCCCTGTCAAGCCCCCTGTGGCCCGGCCCAACCGCTCTAGTAACCCCGACTCAGG	2160
Db	2101	CCAGGAGCCCCCTGTCAAGCCCCCTGTGGCCCGGCCCAACCGCTCTAGTAACCCCGACTCAGG	2160
QY	2161	AGGAGCGACCCCTGGCTGGGAAACGCTCGGACAGCGTCTCTTCACGCTCTCAACGGGCACTC	2220
Db	2161	AGGAGCGACCCCTGGCTGGGAAACGCTCGGACAGCGTCTCTTCACAGGCTCTCAACGGGCACTC	2220
QY	2221	CCCCAGGCTGTGCTACTCTGAGCGGAAACCGGTGGGAACCTCTCTCAAACTGGAACGCTCC	2280
Db	2221	CCCCAGGCTGTGCTACTCTGAGCGGAAACCGGTGGGAACCTCTCTCAAACTGGAACGCTCC	2280
QY	2281	CCTGTGCTCTCCCTGTGGGAATTAAGCCCAAGCCCGACAGCACACGCTCAGCGGCGCAGGCGG	2340
Db	2281	CCTGTGCTCTCCCTGTGGGAATTAAGCCCAAGCCCGACAGCACACGCTCAGCGGCGGCGG	2340
QY	2341	CCCGCAGACTTTGTGTGTGTAAGAGAGCGGACCTCTGACAGAGCCCTCTGAGCTCCCAAG	2400
Db	2341	CCCGCAGACTTTGTGTGTGTAAGAGAGCGGACCTCTGACAGAGGCGCCTCTGAGCTCCCAAG	2400

QY 2401 AAGCCATGACTACTCTGCTCCAGCGAGAGGTGAAAGCATGTGAGACGACGAGAG 2460  
 DB 2401 AAGCCATGACTACTCTGCTCCAGCGAGAGGTGAAAGCATGTGAGACGACGAGAG 2460  
 QY 2461 GAAGCGGAAGCGGGCCAGCAGAGAGGAGCAGAGATACCCCTGGGGGGCCGAGCGATGG 2520  
 DB 2461 GAAGCGGAAGCGGGCCAGCAGAGAGGAGCAGAGATACCCCTGGGGGGCCGAGCGATGG 2520  
 QY 2521 GATACAGACAGCGTCAGACCATGTGTGTCCACGACGTGAGAGAGATCACCGGAGCCGAG 2580  
 DB 2521 GATACAGACAGCGTCAGACCATGTGTGTCCACGACGTGAGAGAGATCACCGGAGCCGAG 2580  
 QY 2581 CCCCCATACGGGGGGCGGACCATGTGTGTCCAGCGACCCCTGGAAGAGAGACCGAACTTG 2640  
 DB 2581 CCCCCATACGGGGGGCGGACCATGTGTGTCCAGCGACCCCTGGAAGAGAGACCGAACTTG 2640  
 QY 2641 CTGCAATGTGACAGCAATGGGGTACCAAACTGCTGAGGTGTCAGCCGACCACTCA 2700  
 DB 2641 CTGCAATGTGACAGCAATGGGGTACCAAACTGCTGAGGTGTCAGCCGACCACTCA 2700  
 QY 2701 CCCACCGAAGACAGCAAAAGCCCAAGCCCTTCGAAGAGATGGAGTGTGACTTACGAG 2760  
 DB 2701 CCCACCGAAGACAGCAAAAGCCCAAGCCCTTCGAAGAGATGGAGTGTGACTTACGAG 2760  
 QY 2761 TCTGTGGGCTGTGTAAGAGCCCTGTGGCAAGCTGTGTCAAGATGTTGTGTGATCTAGGG 2820  
 DB 2761 TCTGTGGGCTGTGTAAGAGCCCTGTGGCAAGCTGTGTCAAGATGTTGTGTGATCTAGGG 2820  
 QY 2821 ATCTACCAAGCCTGAGAGGAGTGGGGGACAGCATCCCATCACAGCCCTGATGGGTGAGAG 2880  
 DB 2821 ATCTACCAAGCCTGAGAGGAGTGGGGGACAGCATCCCATCACAGCCCTGATGGGTGAGAG 2880  
 QY 2881 GGCACTCGGCTGACCAAGCTGACAGTACGAGTGAAGAGGGTTCGTGTGTCAACGTGAT 2940  
 DB 2881 GGCACTCGGCTGACCAAGCTGACAGTACGAGTGAAGAGGGTTCGTGTGTCAACGTGAT 2940  
 QY 2941 CCCACCAACACCCGGGGCCCAAGTGAAGACCCCTGAGATCCGGAAGTACAAAGAGCATTC 3000  
 DB 2941 CCCACCAACACCCGGGGCCCAAGTGAAGACCCCTGAGATCCGGAAGTACAAAGAGCATTC 3000  
 QY 3001 AACCTCCGAGATCTCTGTGACGCCCTTGGGGGGGCAACCTGTGTGTGGGACCGAGAAC 3060  
 DB 3001 AACCTCCGAGATCTCTGTGACGCCCTTGGGGGGGCAACCTGTGTGTGGGACCGAGAAC 3060  
 QY 3061 GGGCTGATGTGTGACCAAGTGGGACGAGGCAAGTGTATGACTGATTTGGGCGGCGA 3120  
 DB 3061 GGGCTGATGTGTGACCAAGTGGGACGAGGCAAGTGTATGACTGATTTGGGCGGCGA 3120  
 QY 3121 CGCTTCCAGACAGATGTGTGTGAGGGGGCTCAACTGTCTCATCACTCAGGGGAAA 3180  
 DB 3121 CGCTTCCAGACAGATGTGTGTGAGGGGGCTCAACTGTCTCATCACTCAGGGGAAA 3180  
 QY 3181 AGGAACAAACCTGCGGGGTATTAACCTGTCTGTGCTCCGGAACAAAGTCTCTCAACAATGAC 3240  
 DB 3181 AGGAACAAACCTGCGGGGTATTAACCTGTCTGTGCTCCGGAACAAAGTCTCTCAACAATGAC 3240  
 QY 3241 CCAAGAGTGAAGAAAGCAAGGCTGACCAACCGTGGGGGACATGAGAGGCTGCGGGAC 3300  
 DB 3241 CCAAGAGTGAAGAAAGCAAGGCTGACCAACCGTGGGGGACATGAGAGGCTGCGGGAC 3300  
 QY 3301 TACCGTGTGTGAATAACGAGCGGATTAAGTTCTGTGATTCGCTCAAGAGCTCCGTG 3360  
 DB 3301 TACCGTGTGTGAATAACGAGCGGATTAAGTTCTGTGATTCGCTCAAGAGCTCCGTG 3360  
 QY 3361 GAGGTGTATGTGCTGGGGCCCAAAACCTTACCAAAATTCATAGGCTCTTGAGCC 3420  
 DB 3361 GAGGTGTATGTGCTGGGGCCCAAAACCTTACCAAAATTCATAGGCTCTTGAGCC 3420  
 QY 3421 GACCTCCCGCAACCGGCTCTGTGTGTGACCTGACAGTGAAGAGGGGACGCGCTCAAG 3480  
 DB 3421 GACCTCCCGCAACCGGCTCTGTGTGTGACCTGACAGTGAAGAGGGGACGCGCTCAAG 3480

QY 3481 GTCACTATGAGCTCCAGGCTGAGCTTCGATCTGTGATGATGCACTCGGGAAAGACTAT 3540  
 DB 3481 GTCACTATGAGCTCCAGGCTGAGCTTCGATCTGTGATGATGCACTCGGGAAAGACTAT 3540  
 QY 3541 GACATCTAATCCCTGTGACATTCAGAGCCAGATCAAGCCCATTCATCTTCTC 3600  
 DB 3541 GACATCTAATCCCTGTGACATTCAGAGCCAGATCAAGCCCATTCATCTTCTC 3600  
 QY 3601 CCCAACCCGACGATGAGATGCTGTGTCTACAGAGACAGAGGTGTCTAGTCAAC 3660  
 DB 3601 CCCAACCCGACGATGAGATGCTGTGTCTACAGAGACAGAGGTGTCTAGTCAAC 3660  
 QY 3661 ACGTACGGGGCGCATTAAGATGTGTGTGTGACAGTGGGGGAGATGCTTCTGTG 3720  
 DB 3661 ACGTACGGGGCGCATTAAGATGTGTGTGTGACAGTGGGGGAGATGCTTCTGTG 3720  
 QY 3721 GCTTACATCTGCTCAACCAAGATTAAGGCTGGGGTGAAGAAAGCATTAAGATCCGCTCT 3780  
 DB 3721 GCTTACATCTGCTCAACCAAGATTAAGGCTGGGGTGAAGAAAGCATTAAGATCCGCTCT 3780  
 QY 3781 GTGAGACGGGGCCACTCTGACAGGGGTCTTCAATGACAAAGAGCTCAGAGCTCAAGTTC 3840  
 DB 3781 GTGAGACGGGGCCACTCTGACAGGGGTCTTCAATGACAAAGAGCTCAGAGCTCAAGTTC 3840  
 QY 3841 CTGTGTAGGGGATGACAAAGGTGTTTTTGGCTCAGTCCGCTGTGGGGGACGAGCCAA 3900  
 DB 3841 CTGTGTAGGGGATGACAAAGGTGTTTTTGGCTCAGTCCGCTGTGGGGGACGAGCCAA 3900  
 QY 3901 GTTACTTCACTGACTGTGAACCGTACATGATCATGAACTGTGAAAGGGC 3951  
 DB 3901 GTTACTTCACTGACTGTGAACCGTACATGATCATGAACTGTGAAAGGGC 3951

## RESULT 2

US-10-029-115-5

Sequence 5, Application US/10029115

Publication No. US20030077597A1

GENERAL INFORMATION:

APPLICANT: Luo, Ying

APPLICANT: Fu, Alan C

APPLICANT: Shen, Mary

TITLE OF INVENTION: No. US20030077597A1e1 Germinal Center Kinase Cell Cycle Proteins,

TITLE OF INVENTION: Methods of Use

FILE REFERENCE: A-70229/RMS/DHR

CURRENT FILING DATE: US/10-029-115

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn version 3.1

SEQ ID NO 5

LENGTH: 4033

TYPE: DNA

ORGANISM: Homo sapiens

US-10-029-115-5

Query Match 96.0%; Score 3792.8; DB 14; Length 4033;

Best Local Similarity .96.4%; Pred. No. 0; Mismatches 2; Indels 63; Gaps 2;

Matches 3877; Conservative 0;

QY 64 GACCTGCTGGGATCTTGTAGAGCTTGTGAGGTGTGCGCAATGGAACCTACGACAGGTG 123  
 DB 95 GACCTGCTGGGATCTTGTAGAGCTTGTGAGGTGTGCGCAATGGAACCTACGACAGGTG 154  
 QY 124 TACAAGGTGTGGCATGTCAAGCGGGCAAGTGGCTCCATCAAGTCAATGATGTCAAG 183  
 DB 155 TACAAGGTGTGGCATGTCAAGCGGGCAAGTGGCTCCATCAAGTCAATGATGTCAAG 214  
 QY 184 GAGGACGAGAGGAAGATGAACAGAGATGAACATGCTGAAAAGTACTCACAC 243  
 DB 215 GAGGACGAGAGGAAGATGAACAGAGATGAACATGCTGAAAAGTACTCACAC 274  
 QY 244 CGCAACATCGGCACCTTACGAGAGCTTCAAGAGAGAGCCCGGGGAAAGATGAC 303  
 DB 275 CGCAACATCGGCACCTTACGAGAGCTTCAAGAGAGAGCCCGGGGAAAGATGAC 334

OY	304	CAGCCTCTGGCTGGTATGGAGATTCTGTGGTGTGGCTGTTCAGTGACATGCACTCGGTAAAGAAC	363
Db	335	CAGCTCTGGCTGTGTAGTGAAGTTCTGTGGTGTGGTTCAGTGTACTGACCTGGTAAAGAAC	394
OY	364	ACAAAGGCAAGCCCTGAAAGGAGACTGTATCGCCTATATCTGCAGAGAGATCCTCAGG	423
Db	395	ACAAAGGCAAGCCCTGAAAGGAGACTGTATCGCCTATATCTGCAGAGAGATCCTCAGG	454
OY	424	GGTCTGGCCCATCTCATATCCCAACAAGTGAATCATTCAGACATCAAGGGGCAAGATGTG	483
Db	455	GGTCTGGCCCATCTCATATCCCAACAAGTGAATCATTCAGACATCAAGGGGCAAGATGTG	514
OY	484	CTGCTGACAGAGATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAAGTCTCAGCTGCAC	543
Db	515	CTGCTGACAGAGATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAAGTCTCAGCTGCAC	574
OY	544	CGCACCGTGGGAGACGGAAACCTTCATTGGGAGCTCCCTACGTAGTGGCTCCAGAGTTC	603
Db	575	CGCACCGTGGGAGACGGAAACCTTCATTGGGAGCTCCCTACGTAGTGGCTCCAGAGTTC	634
OY	604	ATCGCCTGTGATGAGAACCCCTGATCGCACTATGATTAAGAGATGATATTGTGCTCTA	663
Db	635	ATCGCCTGTGATGAGAACCCCTGATCGCACTATGATTAAGAGATGATATTGTGCTCTA	694
OY	664	GGAAATCACAGCCATCGAGATGTCAGAGGGAGGCCCCCTCTGTGTGACATGCAACCCATG	723
Db	695	GGAAATCACAGCCATCGAGATGTCAGAGGGAGGCCCCCTCTGTGTGACATGCAACCCATG	754
OY	724	CGAGCCCTCTTCTCTCATTTCTCTGGAACTCTCCGCCCAAGGCTCAAGTCCAAAGATGCTCT	783
Db	755	CGAGCCCTCTTCTCTCATTTCTCTGGAACTCTCCGCCCAAGGCTCAAGTCCAAAGATGCTCT	814
OY	784	AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAMAAGTTACTCTGAGCGGCCACCC	843
Db	815	AAGAAGTTCATTGACTTCATTGACACATGTCTCATCAMAAGTTACTCTGAGCGGCCACCC	874
OY	844	ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAAGCCCAAGGAGCGGCAAGTCCGC	903
Db	875	ACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAAGCCCAAGGAGCGGCAAGTCCGC	934
OY	904	ATCCAGCTTAAAGAACCAATTGACCGGATCCCGGGAAGAAGCGGGGTGAGAAAGAGAGACA	963
Db	935	ATCCAGCTTAAAGAACCAATTGACCGGATCCCGGGAAGAAGCGGGGTGAGAAAGAGAGACA	994
OY	964	GAATATGAGTACAGCGGCGACGAGAGAGAGAGATGACAGCATGAGAGAGAGAGAGAGCCA	1023
Db	995	GAATATGAGTACAGCGGCGACGAGAGAGAGAGATGACAGCATGAGAGAGAGAGAGAGCCA	1054
OY	1024	AGCTTCATCATGAAAGTGCTGCTTGGAGAGTGACTTACGCCGGGAGTTTCTCCGGCTCCAG	1083
Db	1055	AGCTTCATCATGAAAGTGCTGCTTGGAGAGTGACTTACGCCGGGAGTTTCTCCGGCTCCAG	1114
OY	1084	CAGAAAAATTAAGACACTCAGAGGCTTTAAAAACAGCAGACAGCACTGACAGCAGCAGCAG	1144
Db	1115	CAGAAAAATTAAGACACTCAGAGGCTTTAAAAACAGCAGCAGCAGCACTGACAGCAGCAGCAG	1175
OY	1144	CAGCAGACCCCGAGGACACATCAAAACACTTGCTGCACCAAGCGGACCGGCGCATGAGAG	1204
Db	1175	CAGCAGACCCCGAGGACACATCAAAACACTTGCTGCACCAAGCGGACCGGCGCATGAGAG	1235
OY	1204	GAGCAGAAAGGAGAGCGCGCGCGCTGTGAGAGAGCAACACCGCGGGAGAGGGGAGCAGCGG	1264
Db	1235	GAGCAGAAAGGAGAGCGCGCGCGCTGTGAGAGAGCAACACCGCGGGAGAGGGGAGCAGCGG	1295
OY	1264	AAGCTTGCAGAGAGAGAGCAGCAGCGCGGCTGTGAGAGATGCAAGGCTCTGCGGCGGGAG	1332
Db	1295	AAGCTTGCAGAGAGAGAGCAGCAGCGCGGCTGTGAGAGATGCAAGGCTCTGCGGCGGGAG	1363
OY	1324	CAGGAGCCGGCGGACGCGGAGCGTGTAGCAGGAATTAACAAGGAAAGCACTGAGAGAGCAG	1383
Db	1355	CAGGAGCCGGCGGACGCGGAGCGTGTAGCAGGAATTAACAAGGAAAGCACTGAGAGAGCAG	1414

QY	1384	AGGAGAGTCAGAAAGCTCTCCAGAGGACCTGGACAGGAGATGGCTTACCTCAAGTCCCTG	1443
Db	1415	CGGCAGTCAGAAAGCTCTCCAGAGGACCTGGACAGGAGATGGCTTACCTCAAGTCCCTG	1474
QY	1444	CAGCAGCAGCAACAGCAGCAGCAGCTTCCAGAAACAGCAGCAGCAGCAGCTTCCCTGGG	1503
Db	1475	CAGCAGCAGCAACAGCAGCAGCAGCTTCCAGAAACAGCAGCAGCAGCAGCTTCCCTGGG	1534
QY	1504	GACAGGAAAGCCCTGTACATTATGTGTGGGGCATGAAATCCCTGTGACAAACAGCCTGG	1563
Db	1535	GACAGGAAAGCCCTGTACATTATGTGTGGGGCATGAAATCCCTGTGACAAACAGCCTGG	1594
QY	1564	GCCCCGAGAGTAAAGAGAAACAAGGATGAAACAAGCAGAACTCTCCCTTGGGCCAAG	1623
Db	1595	GCCCCGAGAGTAAAGAGAAACAAGGATGAAACAAGCAGAACTCTCCCTTGGGCCAAG	1654
QY	1624	AGCAAGCCAGGACACACGAGGGCTGAGACCCCTCATCCCGAGGCTCCCGAGGGCCCA	1683
Db	1655	AGCAAGCCAGGACACACGAGGGCTGAGACCCCTCATCCCGAGGCTCCCGAGGGCCCA	1714
QY	1684	GGAACCCCTTTCCAGACTCTCTTATGACAGAGCGGTGAGAGCCCGAGAGGACGCGAC	1743
Db	1715	GGAACCCCTTTCCAGACTCTCTTATGACAGAGCGGTGAGAGCCCGAGAGGACGCGAC	1774
QY	1744	A-----	1744
Db	1775	AAGAGCCTGTGGACACACGGGCTCCACTGAAAGCATATGACAGACTGTACCCCGATCC	1834
QY	1745	-AGTCCCTGCAGACACAGCCACCCGAAACTGTGCTCCTTCCAGCCTCCCATGACCC	1803
Db	1835	CAGTCTCCGCAGACACAGCCACCCGAAACTGTGCTCCTTCCAGCCTCCCATGACCC	1894
QY	1804	GACCCTGCAATCCCGCACCCACTGACACGCGCCAGTSCCGAGGAGCTGTATCCGACAG	1863
Db	1895	GACCCTGCAATCCCGCACCCACTGACACGCGCCAGTSCCGAGGAGCTGTATCCGACAG	1954
QY	1864	AATTCAAGACCCCACTCTGAAAGGACCTGTGCCCCGAAATCCCGACGCTGGGTCCGC	1923
Db	1955	AATTCAAGACCCCACTCTGAAAGGACCTGTGCCCCGAAATCCCGACGCTGGGTCCGC	2014
QY	1924	CCAGATTAACGAGGCCCAACCCCAAGGTGCTCAGAGGACCTCATATATGCGACCTG	1983
Db	2015	CCAGATTAACGAGGCCCAACCCCAAGGTGCTCAGAGGACCTCATATATGCGACCTG	2074
QY	1984	AACAACAGTGGGGCGGAGGGTCCCGGCAAGCCAGGACGTCCGTGCAGACCTCGAGC	2043
Db	2075	AACAACAGTGGGGCGGAGGGTCCCGGCAAGCCAGGACGTCCGTGCAGACCTCGAGC	2134
QY	2044	AACCTCGCTGGCAAAATATATCTGCAAAAGCGGGCAGAGCGGGCACCCCAAGCTTCCA	2103
Db	2135	AACCTCGCTGGCAAAATATATCTGCAAAAGCGGGCAGAGCGGGCACCCCAAGCTTCCA	2194
QY	2104	GGGCCCCCTGTCAGCCCCCTGTGGGCCGCGCCCAAGGCTCTAGTAAACCCCGACTCAGAGG	2163
Db	2195	GGGCCCCCTGTCAGCCCCCTGTGGGCCGCGCCCAAGGCTCTAGTAAACCCCGACTCAGAGG	2254
QY	2164	AGCAGCCCTGTGGGAAACGCTCGGACAGGCTCTTTCAGGCTTCAACGCGCACCTTCCC	2223
Db	2255	AGCAGCCCTGTGGGAAACGCTCGGACAGGCTCTTTCAGGCTTCAACGCGCACCTTCCC	2314
QY	2224	CAGGCTGGCTCACTGAGCGGAAACCGCGTGGAGACTCTTCCAAACCTGAAACAGTCCCT	2283
Db	2315	CAGGCTGGCTCACTGAGCGGAAACCGCGTGGAGACTCTTCCAAACCTGAAACAGTCCCT	2374
QY	2284	GTGCTCTTCCCTGGGAAATTAAGCCCAAGCCCGACGACCTTCAACGCGCACGCGGCC	2343
Db	2375	GTGCTCTTCCCTGGGAAATTAAGCCCAAGCCCGACGACCTTCAACGCGCACGCGGCC	2434
QY	2344	GCAGACTTTGTGTGTGTAAGAGACCGGACTCTGACAGAGGCCCTCGGCTCCCAAGAG	2403
Db	2435	GCAGACTTTGTGTGTGTAAGAGACCGGACTCTGACAGAGGCCCTCGGCTCCCAAGAG	2494
QY	2404	GCCATGACCTACTGTCGTCTCCAGGAGAGGTGAAAGCAGTGAAGACAGAGAGAA	2463



Db	2495	GCATAGCACTACTCGTCTGTCACGACGAGGGTGGAAAGCATGAGGACACACGAGAGGAA	255
OY	2494	GGCGAAGCGGCGCCACAGAGGGGGACAGAGATTAACCCCTGGGGGGCGCAGCAGTGGAGAT	252
Db	2555	GGCGAAGCGGCGCCACGAGAGGGGAGCAGAGATTACCCCTGGGGGGC---GCCATGGGAT	261
OY	2554	ACAGACAGCGTCAGACCACTGGTGTCTCAACGACGTTCGAGAGATCAACGGGACCAAGCCC	258
Db	2612	ACAGACAGCGTTCAGACCACTGGTGTCTCAACGACGTTCGAGAGATCAACGGGACCAAGCCC	267
OY	2584	CCATACGGGGGGGGGACCACTGGTGTCTCAACGACCCCTCGAAGAGAGAGCGGAACTGGCTG	264
Db	2672	CCATACGGGGGGGGGACCACTGGTGTCTCAACGACCCCTCGAAGAGAGAGAGCGGAACTGGCTG	273
OY	2644	CATGCTGCACAGCAATAGGGTACACAAACCTGACGTGTCTCAGCCAGCCACCTCAACCC	270
Db	2732	CATGCTGCACAGCAATAGGGTACACAAACCTGACGTGTCTCAGCCAGCCACCTCAACCC	279
OY	2704	ACCGAAGAACGAAAGGCGCAAGGCCCACTTCGAAAGATGGGAGTGGTGACTTACCAAGTCT	276
Db	2792	ACCGAAGAACGAAAGGCGCAAGGCCCACTTCGAAAGATGGGAGTGGTGACTTACCAAGTCT	285
OY	2784	CGTGGGCTGTGTTAAAGGCCCTTGGCAAGACTGTTCACGATGTTTGTGATCTTAAGGATTC	282
Db	2852	CGTGGGCTGTGTTAAAGGCCCTTGGCAAGACTGTTCACGATGTTTGTGATCTTAAGGATTC	291
OY	2834	TACCAAGCTTGAGGAGTGGGGACAGCATCCCATCAACAGCCCTTAGTGGTGGAGAGGAC	288
Db	2912	TACCAAGCTTGAGGAGTGGGGACAGCATCCCATCAACAGCCCTTAGTGGTGGAGAGGAC	297
OY	2884	ACTCGGCTTCGACAGCTGCAGTACGACGTTGAGAAAGGTTCTGTGTCTCAACGTGAATCCC	294
Db	2972	ACTCGGCTTCGACAGCTGCAGTACGACGTTGAGAAAGGTTCTGTGTCTCAACGTGAATCCC	303
OY	2944	ACCAACACCCCGGGCCCAACGTGAGAACCCCTGAGATTCGGAGATCAAGAAAGGATTTCAAC	300
Db	3032	ACCAACACCCCGGGCCCAACGTGAGAACCCCTGAGATTCGGAGATCAAGAAAGGATTTCAAC	309
OY	3004	TCCGAGATCTCTGTGTCAAGCCCTTTGGGGGGGTCAACTGTCTGTGGGACGGAGAACGGG	306
Db	3082	TCCGAGATCTCTGTGTCAAGCCCTTTGGGGGGGTCAACTGTCTGTGGGACGGAGAACGGG	315
OY	3064	CTGATGTGTTCGACCGAAGTGGGCAAGGGCAAGGTGTATGACTATTGGGCGGCGAAGC	312
Db	3152	CTGATGTGTTCGACCGAAGTGGGCAAGGGCAAGGTGTATGACTATTGGGCGGCGAAGC	321
OY	3124	TTCCAGCAGATGAGATGTCTGAGGGGGCTCAACTGTCTCATCAACATTCAGGGAAAGG	318
Db	3212	TTCCAGCAGATGAGATGTCTGAGGGGGCTCAACTGTCTCATCAACATTCAGGGAAAGG	327
OY	3184	AACAAACCTGGGGGTTAATTAACTGTCTGTGGGCTCCGGAAACAATTTCTGACAAATGACCA	324
Db	3272	AACAAACCTGGGGGTTAATTAACTGTCTGTGGGCTCCGGAAACAATTTCTGACAAATGACCA	333
OY	3244	GAAGTGAGAAAGAACAGGGCTGGAACAACGTGGGGGACATGAGAGGGCTGCGGGCACTAC	330
Db	3332	GAAGTGAGAAAGAACAGGGCTGGAACAACGTGGGGGACATGAGAGGGCTGCGGGCACTAC	339
OY	3304	CGTGTGTGAAATACGAGCGGATTAAGTTCTGTGTCTATCGCCCTCAAGAGCTCCGTGAG	336
Db	3392	CGTGTGTGAAATACGAGCGGATTAAGTTCTGTGTCTATCGCCCTCAAGAGCTCCGTGAG	345
OY	3364	GGTATGCTGGGGCCCCCAAAACCTTACACCAAAATTCATGGGCTTCAAGTCCCTTTCGAC	342
Db	3452	GGTATGCTGGGGCCCCCAAAACCTTACACCAAAATTCATGGGCTTCAAGTCCCTTTCGAC	351
OY	3424	CTCCCCCAACCGCTCTGTGTGTCACTTGAACAGTATGAGAGGGGACAGCGGCTCAAGGTC	348
Db	3512	CTCCCCCAACCGCTCTGTGTGTCACTTGAACAGTATGAGAGGGGACAGCGGCTCAAGGTC	357
OY	3484	ATCTATGGCTCAAGTGTGGCTTCAATGCTGTGATGTTCGACTCGGGGACAGCTATGAC	354

Db	3572	ATCTATGGCTCCAGTGCCTGCTTCCATGTCGTGGAGATGTCCAGTCGTGGGAAACAGCTATGAC	3631
QY	3544	ATCTACATCCCTGTGTCACATCCAGAGCCAGATCAAGCCCAATGCATCATCTTCTCTCCG	3603
Db	3632	ATCTACATCCCTGTGTGCATCATCAGAGCCAGATCAAGCCCAATGCATCATCTTCTCTCCG	3691
QY	3604	AAACCCGACGGGCATGAGAGATGCTGCTGTGCTACAGAGACGAGGGTGTCTACGTCAACACG	3663
Db	3692	AAACCCGACGGGCATGAGAGATGCTGCTGTGCTACAGAGACGAGGGTGTCTACGTCAACACG	3751
QY	3664	TACGGGGCCATCATTTAAGAGATGTGTGTGTGACGTGGGGGGAGATGCTTACTTCTGTGTGCC	3723
Db	3752	TACGGGGCCATCATTTAAGAGATGTGTGTGTGACGTGGGGGGAGATGCTTACTTCTGTGTGCC	3811
QY	3724	TACATCTGCTCCAAACAGATTAATGGGCTGGGGGTGAGAAAGCATTTGAGATCCGCTCTGTG	3783
Db	3812	TACATCTGCTCCAAACAGATTAATGGGCTGGGGGTGAGAAAGCATTTGAGATCCGCTCTGTG	3871
QY	3784	GAGACGGGGCCACTTCGACGGGGTCTTATATGACAAGAGCTCAGAGGCTCAAGTTCCGTG	3843
Db	3872	GAGACGGGGCCACTTCGACGGGGTCTTATATGACAAGAGCTCAGAGGCTCAAGTTCCGTG	3931
QY	3844	TGTGACGGGATGACAAAGGTGTTTTTTTGCCCTCAGTCCGCTCTGGGGGGACGACGCAAGTT	3903
Db	3932	TGTGACGGGATGACAAAGGTGTTTTTTTGCCCTCAGTCCGCTCTGGGGGGACGACGCAAGTT	3991
QY	3904	TACTTCATGACTCGAACCCTGATCTGCATCTGAACATGATGTGA	3945
Db	3992	TACTTCATGACTCGAACCCTGATCTGCATCTGAACATGATGTGTGA	4033

RESULT 3  
US-09-291-417-11

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? Sequence 11, Application US/09291417A
? Publication No. US20030050230A1
? GENERAL INFORMATION:
? APPLICANT: PLOMMAN, GREGORY
? APPLICANT: MARTINEZ, RICARDO
? APPLICANT: WHYTE, DAVID
? TITLE OF INVENTION: STR20-RELATED PROTEIN
? FILE REFERENCE: 240/300
? CURRENT APPLICATION NUMBER: US/09/291,417M
? CURRENT FILING DATE: 1999-04-13
? EARLIER APPLICATION NUMBER: US 60/081,784
? EARLIER FILING DATE: 1998-04-14
? NUMBER OF SEQ ID NOS: 147
? SOFTWARE: FASTSEQ for Windows Version 3.0
? SEQ ID NO 11
? LENGTH: 4133
? TYPE: DNA
? ORGANISM: Mammalian (Human) ZC3
? US-09-291-417-11

```

Query Match	92.0%	Score 3635;	DB 10;	Length 4133;
Best Local Similarity	95.9%	Pred. No. 0;		
Matches 3824; Conservative	0;	Mismatches 15;	Indels 150;	Gaps 3

QY	110	CCTACGACAGGTGTACAAAGGGTCGCGCATGTCAAGA	CGGGGACGCTGGCTGCCATC	AGG	169
Db	2	CATTGGGGAGGTGTATGAGGGTCGGCANTGTCAAG <td>CGGGGACGCTGGCTGCCATC <td>AGG</td> <td>61</td> </td>	CGGGGACGCTGGCTGCCATC <td>AGG</td> <td>61</td>	AGG	61
QY	170	TCATGATGTCCGAGNGACGAGGAGGAAGATCAAC <td>GAGATCAACATCTG <td>AAAA</td> <td>229</td> </td>	GAGATCAACATCTG <td>AAAA</td> <td>229</td>	AAAA	229
Db	62	TCATGATGTCCGAGNGACGAGGAGGAAGATCAAC <td>GAGATCAACATCTG <td>AAAA</td> <td>121</td> </td>	GAGATCAACATCTG <td>AAAA</td> <td>121</td>	AAAA	121
QY	230	AGTACTTCCACCCGCAACATCCGACCTTAC <td>TACGGAACCTTCATCAAG <td>ANAGCCCC</td> <td>289</td> </td>	TACGGAACCTTCATCAAG <td>ANAGCCCC</td> <td>289</td>	ANAGCCCC	289
Db	122	AGTACTTCCACCCGCAACATCCGACCTTAC <td>TACGGAACCTTCATCAAG <td>ANAGCCCC</td> <td>181</td> </td>	TACGGAACCTTCATCAAG <td>ANAGCCCC</td> <td>181</td>	ANAGCCCC	181
QY	290	CGGGAACGATGACCGAGCTCTGGCTGATGAGAGTCTGTGGTGTG <td>GTTCAGTACTG</td> <td></td> <td>349</td>	GTTCAGTACTG		349
Db	182	CGGGAACGATGACCGAGCTCTGGCTGATGAGAGTCTGTGGTGTG <td>GTTCAGTACTG</td> <td></td> <td>241</td>	GTTCAGTACTG		241

OY	350	ACCTGCTAAACAACAAGGCAACGCCCTGAAAGAGACCTGTAATGCCCTAATCTGCA	409
Db	242	ACCTGCTAAAGAACAAAGGCAACGCCCTGAAAGAGACCTGTAATGCCCTAATCTGCA	301
OY	410	GGAGATCCTCAGGGGCTTGCCCATCTCCATGCGCCAAAGGTGATCATGACATCA	469
Db	302	GGAGATCCTCAGGGGCTTGCCCATCTCCATGCGCCAAAGGTGATCATGACATCA	361
OY	470	AGGGGAGAAATGTGCTGCTGAACAGAAATGCTGAGTCAAGCTATGTGATTTTGGGGTGA	529
Db	362	AGGGGAGAAATGTGCTGCTGAACAGAAATGCTGAGTCAAGCTATGTGATTTTGGGGTGA	421
OY	530	GTGCTCAGCTGGACCGGCAACCGGGGCAACGGAAACATTTATTTGGGACTCCCTACTGGA	589
Db	422	GTGCTCAGCTGGACCGGCAACCGGGGCAACGGAAACATTTATTTGGGACTCCCTACTGGA	481
OY	590	TGCTCCAGAGGTCAATCGCTGTGTGTAAGAACCCCTGATGCGACCTATATTAAGAGTGTG	649
Db	482	TGCTCCAGAGGTCAATCGCTGTGTGTAAGAACCCCTGATGCGACCTATATTAAGAGTGTG	541
OY	650	ATATTGGGTCTCTTAGAAATCAACAGCCATCGAGATGGCAGAGGAGACCCCTCTGTGTG	709
Db	542	ATATTGGGTCTCTTAGAAATCAACAGCCATCGAGATGGCAGAGGAGACCCCTCTGTGTG	601
OY	710	ACATGCAACCCCATGGAGCCCTCTTCCTCATTTCCCGGAAACCTCCCGCCAGGCGTCAAGT	769
Db	602	ACATGCAACCCCATGGAGCCCTCTTCCTCATTTCCCGGAAACCTCCCGCCAGGCGTCAAGT	661
OY	770	CCAAGAAATGTGCTTAAGAAAGTTCAATTTGACTTATTCATGACATGTCATCAAGACTTAAC	829
Db	662	CCAAGAAATGTGCTTAAGAAAGTTCAATTTGACTTATTCATGACATGTCATCAAGACTTAAC	721
OY	830	TGAGCGCGCCACCCACGGAGCAGCTACTGAAGTTTCCTTCAATCCGGGACCAAGCCACAG	889
Db	722	TGAGCGCGCCACCCACGGAGCAGCTACTGAAGTTTCCTTCAATCCGGGACCAAGCCACAG	781
OY	890	AGCGGCAAGTCCGCAATCCAGCTTAAAGACCAATTGACCGATCCCGGAAAGCGGGGTG	949
Db	782	AGCGGCAAGTCCGCAATCCAGCTTAAAGACCAATTGACCGATCCCGGAAAGCGGGGTG	841
OY	950	AGAAAGAGAGACAGAAATATGAGTACAGCGGACGGAGAGAGAAATGACAGCCATGGAG	1009
Db	842	AGAAAGAGAGACAGAAATATGAGTACAGCGGACGGAGAGAGAAATGACAGCCATGGAG	901
OY	1010	AGGAAGAGAGCCCAAGCTTCCATCATGAAACGTGCTTGGAGAGTCCACTTACGCCGGAGT	1069
Db	902	AGGAAGAGAGCCCAAGCTTCCATCATGAAACGTGCTTGGAGAGTCCACTTACGCCGGAGT	961
OY	1070	TTCTCCGAGCTCCAGCAGGAAAAATAGACCACTCAGAGGCTTTTAAAACAGCAGCAGCAGC	1129
Db	962	TTCTCCGAGCTCCAGCAGGAAAAATAGACCACTCAGAGGCTTTTAAAACAGCAGCAGCAGC	1021
OY	1130	TGCAGCAGCAGCAGCAGCAGGACCCCGAGGACACATCAAAACCTCTGTGACCAAGCGGC	1189
Db	1022	TGCAGCAGCAGCAGCAGCAGGACCCCGAGGACACATCAAAACCTCTGTGACCAAGCGGC	1081
OY	1190	AGCGGCGCATTAGAGAGCAAGAAAGGAGCGGCGCGCTGTGAGAGCAACAAGCGGCGGG	1249
Db	1082	AGCGGCGCATTAGAGAGCAAGAAAGGAGCGGCGCGCTGTGAGAGCAACAAGCGGCGGG	1141
OY	1250	AGCGGAGCAGCGGAAAGCTGCGAGAGAGAGCAGCAGCGCGCTGTGAGAGCAATGCAAG	1309
Db	1142	AGCGGAGCAGCGGAAAGCTGCGAGAGAGAGCAGCAGCGCGCTGTGAGAGCAATGCAAG	1201
OY	1310	CTTCTGCGCGGAGAGAGCGGCGGACGCGGAGCGTGAGCA-----	1352
Db	1202	CTTCTGCGCGGAGAGAGCGGCGGACGCGGAGCGGAGCGTGAGCAATATTGCTCACA	1261
OY	1353	-----GGATTACAAAGCGGAAGCAAGCTGAGAGAGCAGCGGCAAGTCAAGACGTCTCC	1402

Db	1322	CCCTGCTGCTGGAATACAGCGGAAAGACGCTGGAGAGACCGGACGTCAGAACTCTCC	1361
Qy	1403	AGAAGCAGCTGACAGAGAGCATGCTTAACCTCAAGTCCCTGACAGACAGCAACAGACG	1462
Db	1382	AGAGGACAGCTCAGACAGGAGCATGCTTAACCTCAAGTCCCTGACAGACAGCAACAGACG	1441
Qy	1433	AGCGCTTCAGAAACAGCAGAGAGAGAGAGCTCCGCTGGGGAGACGAAAGCCCTGTACC	1522
Db	1442	AGCAGCTTCAGAAACAGCAGAGAGAGAGAGCTCCGCTGGGGAGACGAAAGCCCTGTACC	1501
Qy	1523	ATTATGCTCGGGGAGATGATCCCGCTGCAAAACAGGCTGGGCCCGAGAGGTAGAAGAGA	1582
Db	1502	ATTATGCTCGGGGAGATGATCCCGCTGCAAAACAGGCTGGGCCCGAGAGGTAGAAGAGA	1561
Qy	1563	GAACAGAGATGAAACAGCAGCAGAACTCTCCCTTTGGCCAGAGCAAGCAGGCGACACGG	1642
Db	1562	GAACAGAGATGAAACAGCAGCAGAACTCTCCCTTTGGCCAGAGCAAGCAGGCGACACGG	1621
Qy	1643	GGCCGACAGCCCCCATCCCCCAGGCGCTCCCCAGGGGGCCCCAGAGACCCCTTTCCAGATC	1702
Db	1622	GGCCGACAGCCCCCATCCCCCAGGCGCTCCCCAGGGGGCCCCAGAGACCCCTTTCCAGATC	1681
Qy	1703	CTCCTATGACAGAGCCGGTGGAGGCCCGCAGAGGAGACGCGACA-----	1744
Db	1682	CTCCTATGACAGAGCCGGTGGAGGCCCGCAGAGGAGACGCGACA-----	1741
Qy	1745	-----AATCCTTCGAGAGCCAGC	1762
Db	1742	GGGTCCCACTGAAGCCATATGACAGACCTGTACCCGATCCCAATCCCTGACAGACAGC	1801
Qy	1763	CCACCCGAAACCTGGCTGCTTCCGAGGCTCCCATGACCCCGGACCCGAGCCCTGCGAC	1822
Db	1802	CCACCCGAAACCTGGCTGCTTCCGAGGCTCCCATGACCCCGGACCCCTGCGAC	1861
Qy	1823	CCACTGCGACGCGCAGGTGCGCAGAGAGCTGTCACTCGCAGAAATTCAGACCCCACTCTG	1882
Db	1862	CCACTGCGACGCGCAGGTGCGCAGAGAGCTGTCACTCGCAGAAATTCAGACCCCACTCTG	1921
Qy	1883	AAAGACCTGGCCCCCAGCCCCGAAATCCCCCAGGCTGGGTCCGCCAGATTAAGAGGCCCCAC	1942
Db	1922	AAAGACCTGGCCCCCAGCCCCGAAATCCCCCAGGCTGGGTCCGCCAGATTAAGAGGCCCCAC	1981
Qy	1943	CCAAAGTGCCTCAGAGGACCTCATCTATCGSCATGCGCCTTAAACAGCAGTGGGCCGGAG	2002
Db	1982	CCAAAGTGCCTCAGAGGACCTCATCTATCGSCATGCGCCTTAAACAGCAGTGGGCCGGAG	2041
Qy	2003	GGTCCCGGACGAGCCAGGCAAGTCCGTGCAGACCTCGCAGCAACTCCGCTGGCAATCT	2062
Db	2042	GGTCCCGGACGAGCCAGGCAAGTCCGTGCAGACCTCGCAGCAACTCCGCTGGCAATCT	2101
Qy	2063	ATCTGCAAAAGCGGGCAGAGCGGGGCAACCCAAAGCTCCAGGGCCCCCTGCTCAAGCCCC	2122
Db	2102	ATCTGCAAAAGCGGGCAGAGCGGGGCAACCCAAAGCTCCAGGGCCCCCTGCTCAAGCCCC	2161
Qy	2123	CTGGCGCGCCCAACGCTCTAGTAAACCCCGACCTCAGAGAGAGGAGACCTTGCTGGGAAAC	2182
Db	2162	CTGGCGCGCCCAACGCTCTAGTAAACCCCGACCTCAGAGAGAGGAGACCTTGCTGGGAAAC	2221
Qy	2183	GCTCGGACAGGCTCTTTCAGGCTCTCAAGGAGCACTTCCCGCAGGCTGGTCACTGAGAC	2242
Db	2222	GCTCGGACAGGCTCTTTCAGGCTCTCAAGGAGCACTTCCCGCAGGCTGGTCACTGAGAC	2281
Qy	2243	GGAAACCGGTGGAGCTCTTTCAGAACTGGGACAGCTCCCTGTGCTCTCCCTGGGAATA	2302
Db	2282	GGAAACCGGTGGAGCTCTTTCAGAACTGGGACAGCTCCCTGTGCTCTCCCTGGGAATA	2341
Qy	2303	AAAGCAAGCCGAGACGACCAACGCTCAAGGCGAGGCGCGGACGCGACATTTGTGTGCTGA	2362
Db	2342	AAAGCAAGCCGAGACGACCAACGCTCAAGGCGAGGCGCGGACGCGACATTTGTGTGCTGA	2401
Qy	2363	AAAGACGAGACTCTGACAGAGGCCCTCGGCTCTCCAAAGAGGCATGAGCTACTGCTGT	2422

2402 AAGAGCGGACTGTGACGAGGCGCCCTGGGCGCTCCCAAGAGGCCATGGAATTACTGTGT 2461  
2423 CCAGCGAGAGGTGGAAGCAGTGAAGCAGACGAGAGGAAAGGCGAGCGGCGCAGAG 2482  
2462 CCACGAGAGGTGGAAGCAGTGAAGCAGACGAGAGGAAAGGCGAGCGGCGCAGAG 2521  
2483 AGGGAGAGAGATATCCCTGGGGGCGGCGAGATGGGGATATACAGACGCGTACAGACA 2542  
2522 AGGGAGAGAGATATCCCTGGGGGCGGCGAGATGGGGATATACAGACGCGTACAGACA 2578  
2543 TGTGTGTCAAGACGTTCGAGAGATCAACCGGAGCCGAGCCCATATCCGGGGCGGACA 2602  
2579 TGTGTGTCAAGACGTTCGAGAGATCAACCGGAGCCGAGCCCATATCCGGGGCGGACA 2638  
2603 TGTGTGTCAAGACGTTCGAGAGATCAACCGGAGCCGAGCCCATATCCGGGGCGGACA 2662  
2639 TGTGTGTCAAGACGTTCGAGAGATCAACCGGAGCCGAGCCCATATCCGGGGCGGACA 2698  
2663 AACAAACCTGCGTGAAGTGTCCAGCCGAGCACTCAACCGAGAAACGAAAGGCG 2722  
2699 ACACAAACCTGCGTGAAGTGTCCAGCCGAGCACTCAACCGAGAAACGAAAGGCG 2758  
2723 AAAGCCCACTTCGAGAGATGGAGTGTGACTACAGTCTGTGGCTGTGTAAGGCC 2782  
2759 AAAGCCCACTTCGAGAGATGGAGTGTGACTACAGTCTGTGGCTGTGTAAGGCC 2818  
2783 CTGGCAAGAGTCTGTTACAGATGTTTGTGATCTAGGATCTACAGCTGTGAGGCA 2842  
2819 CTGGCAAGAGTCTGTTACAGATGTTTGTGATCTAGGATCTACAGCTGTGAGGCA 2878  
2843 GGGACAGATTCCTCATCAAGCCCTAGGGGTGAGAGAGGCACTCGGGTCCAGCAAGCTG 2902  
2879 GGGACAGATTCCTCATCAAGCCCTAGGGGTGAGAGAGGCACTCGGGTCCAGCAAGCTG 2938  
2903 AGTACGAGTGAAGAGGGTCTGTGTCTCAACGTGAATCCCAACCAACCCGGGCCACA 2962  
2939 AGTACGAGTGAAGAGGGTCTGTGTCTCAACGTGAATCCCAACCAACCCGGGCCACA 2998  
2963 GTGAGACCTCTGAGATCCGGAAGTACAGAAAGCATCACTCCGAGATCTCTGTGAG 3022  
2999 GTGAGACCTCTGAGATCCGGAAGTACAGAAAGCATCACTCCGAGATCTCTGTGAG 3058  
3023 CCCCTTGGGGGTGCAACCTGTGTGTGGGACGAGAAAGGGCTGATGTTGCTGAGACG 3082  
3059 CCCCTTGGGGGTGCAACCTGTGTGTGGGACGAGAAAGGGCTGATGTTGCTGAGACG 3118  
3083 GTGGGACAGGGAGGTATGATCACTATTGGGCGGCGAGCTTCCAGAGATGATGTGC 3142  
3119 GTGGGACAGGGAGGTATGATCACTATTGGGCGGCGAGCTTCCAGAGATGATGTGC 3178  
3143 TGAAGGGCTCAACCTGTCTATCACTATCAAGGAAAGAAACAACTGGGGGTGAT 3202  
3179 TGAAGGGCTCAACCTGTCTATCACTATCAAGGAAAGAAACAACTGGGGGTGAT 3238  
3203 ACCTGTCTGTGCTCGGAGCAAGATCTGCAATAGACCCAGAGTGGAGAAAGAGCAG 3262  
3239 ACTGTCTGTGCTCGGAGCAAGATCTGCAATAGACCCAGAGTGGAGAAAGAGCAG 3298  
3263 GCTGACACCGTGGGGGACATGAGAGGCTCGGGGCACTACCGTGTGTGAATACGAGC 3322  
3299 GCTGACACCGTGGGGGACATGAGAGGCTCGGGGCACTACCGTGTGTGAATACGAGC 3358  
3323 GGATTAAGTTCGTGTATCGCCCTCAAGAGCTCGTGAAGTGTATGCTGTGGGCCCA 3382  
3359 GGATTAAGTTCGTGTATCGCCCTCAAGAGCTCGTGAAGTGTATGCTGTGGGCCCA 3418  
3383 AACCTTACCAAAATTCATGAGCTTCAAGTCTTTTGGCGAGCTCCCGACCGGCTTGC 3442  
3419 AACCTTACCAAAATTCATGAGCTTCAAGTCTTTTGGCGAGCTCCCGACCGGCTTGC 3478  
3443 TGTGTGACCTGACATGAGAGAGGGGACGAGCTCAAGTATCTATGAGCTCAAGTGTG 3502  
3479 TGTGTGACCTGACATGAGAGAGGGGACGAGCTCAAGTATCTATGAGCTCAAGTGTG 3538

3503 GCTTCAATGCTGTGATGTGACCTGGGGAAACAGCTATGACATCAATCCCTGAGACA 3562  
3539 GCTTCAATGCTGTGATGTGACCTGGGGAAACAGCTATGACATCAATCCCTGAGACA 3598  
3563 TCCAGAGCAGATACCGCCCATGCTCACTCTTCCCAACAGCGGACGAGTGA 3622  
3599 TCCAGAGCAGATACCGCCCATGCTCACTCTTCCCAACAGCGGACGAGTGA 3658  
3623 TGTGTGTGTCAAGAGAGAGGTGTCTAGTCAACAGTACGAGGCGCATTTAAG 3682  
3659 TGTGTGTGTCAAGAGAGAGGTGTCTAGTCAACAGTACGAGGCGCATTTAAG 3718  
3683 ATGTGTGTGTCAAGAGAGAGGTGTCTAGTCAACAGTACGAGGCGCATTTAAG 3742  
3719 ATGTGTGTGTCAAGAGAGAGGTGTCTAGTCAACAGTACGAGGCGCATTTAAG 3778  
3743 TAATGGGCTGGGGTGAAGAAAGCATTTGAGATCCGCTGTGAGAGAGCGGCCACTGAG 3802  
3779 TAATGGGCTGGGGTGAAGAAAGCATTTGAGATCCGCTGTGAGAGAGCGGCCACTGAG 3838  
3803 GGTGTCTCATGACAAACAGACTCAAGGCTCAAGTCTGTGTGTGAGCGGATGACAG 3862  
3839 GGTGTCTCATGACAAACAGACTCAAGGCTCAAGTCTGTGTGTGAGCGGATGACAG 3898  
3863 TGT 3922  
3899 TGT 3958  
3923 GTAACGATCATGATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3951  
3959 GTAACGATCATGATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3987

RESULT 4  
US-10-441-281-30  
; Sequence 30, Application US/10441281  
; Publication No. US20030228618A1  
; GENERAL INFORMATION:  
; APPLICANT: Levanon Erez, et al.  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR IDENTIFYING NATURALLY OCCURRING ANTISENSE  
; FILE REFERENCE: 02/26133  
; CURRENT APPLICATION NUMBER: US/10/441,281.  
; PRIOR FILING DATE: 2003-05-20  
; PRIOR APPLICATION NUMBER: US 09/718,407  
; PRIOR FILING DATE: 2000-11-24  
; PRIOR APPLICATION NUMBER: US 09/732,938  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/785,439  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: US 09/907,923  
; PRIOR FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: US 009/993,398  
; PRIOR FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: US 10/201,605  
; PRIOR FILING DATE: 2002-07-24  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 30  
; LENGTH: 4863  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-441-281-30

Query Match 91.1%; Score 3601; DB 15; Length 4863;  
Best Local Similarity 95.0%; Pred. No. 0;  
Matches 3829; Conservative 0; Mismatches 5; Indels 195; Gaps 3;  
7 ATGGGACACCAAGCCCGCCGAGCGTGAAGACATGACCTGTCCGCCCTGCGGAGC 66  
185 ATGGGACACCAAGCCCGCCGAGCGTGAAGACATGACCTGTCCGCCCTGCGGAGC 244

OY	6	CTGTGTGGGATCTTTGACCTTGTGAGGTGTGGCGAATGGAACTTACCGGACAGTGTAC	126
Db	245	CCTGTGTGGGATCTTTGACCTTGTGAGGTGTGTGGCAATGGAACTTACCGGACAGTGTAC	304
OY	127	AAGGATCGGCAATGTCAAGACGGGGGAGGTGGCTGGCATCAAGTCAATGATGTACAGGAG	186
Db	305	AAAGGTCCGGCATGTCAAGACGGGGGAGCTGGCTGGCATCAAGTCAATGATGTACAGGAG	364
OY	187	GACGAGGAGGAAGAGATCAAAACAGGAGTCAACATGCTGAATAAAGTACTTCCACACGC	246
Db	365	GACGAGGAGGAAGAGATCAAAACAGGAGTCAACATGCTGAATAAAGTACTTCCACACGC	424
OY	247	AACTATCGGCACTTCTACGGAGCCTTCAAGAAAGACCCCCCGGGGAAAGATGACAG	306
Db	425	AACTATCGGCACTTCTACGGAGCCTTCAAGAAAGACCCCCCGGGGAAAGATGACAG	484
OY	307	CTTGTGCTGTGATGAGATTCTGTGGTCTGTGGTCAAGTCACTGACTTGTAAAGACA	366
Db	485	CTTGTGCTGTGATGAGATTCTGTGGTCTGTGGTCAAGTCACTGACTTGTAAAGACA	544
OY	367	AAAGGCAACGCTTGAGAGAGACTGTATGCGCTATATCTGCAAGGAGATCTCAAGGCT	426
Db	545	AAAGGCAACGCTTGAGAGAGACTGTATGCGCTATATCTGCAAGGAGATCTCAAGGCT	604
OY	427	CTGGGCCCATCTCCANTGCCCAAGGTGATCCATGAGACATCAAGAGGGGCAAAATGTCTG	486
Db	605	CTGGGCCCATCTCCANTGCCCAAGGTGATCCATGAGACATCAAGAGGGGCAAAATGTCTG	664
OY	487	CTGACAGAGAAATGCTGAGGTCAAGCTAGTGAATTTTGGGGTGAAGTCTCACTGGAACGC	546
Db	665	CTGACAGAGAAATGCTGAGGTCAAGCTAGTGAATTTTGGGGTGAAGTCTCACTGGAACGC	724
OY	547	ACCGTGGGCAACGGAAACATTTCAATTGGGAATCCCTCATCTGATGTGCTCAAGAGTCAATC	606
Db	725	ACCGTGGGCAACGGAAACATTTCAATTGGGAATCCCTCATCTGATGTGCTCAAGAGTCAATC	784
OY	607	GGCTGTGATGGAACCCGTGATGCCACCTATATTAACAGAGTGAATTTGGTCTCTTGA	666
Db	785	GGCTGTGATGGAACCCGTGATGCCACCTATATTAACAGAGTGAATTTGGTCTCTTGA	844
OY	667	ATCAGAGCATTCAGAGATGGCAGAGGGAGCCCCCTCTGTGTGACATGCACCCCATGCGA	726
Db	845	ATCAGAGCATTCAGAGATGGCAGAGGGAGCCCCCTCTGTGTGACATGCACCCCATGCGA	904
OY	727	GCCCTCTTCTCATTTCTTCGGAAACCTTCGCGCCAGGCTCAAGTCCAAAGATGTGTCTAAG	786
Db	905	GCCCTCTTCTCATTTCTTCGGAAACCTTCGCGCCAGGCTCAAGTCCAAAGATGTGTCTAAG	964
OY	787	AAAGTTCATTTGACTTCATTTGACACANTGTCTCAACAACTTACCTTACGCGGCCCAACGAG	846
Db	965	AAAGTTCATTTGACTTCATTTGACACANTGTCTCAACAACTTACCTTACGCGGCCCAACGAG	1024
OY	847	GAGCAGCTACTGAAGTTTCCCTTCATCCGGACACGACCACGAGCGGCAAGTCCGCAATC	906
Db	1025	GAGCAGCTACTGAAGTTTCCCTTCATCCGGACACGACCACGAGCGGCAAGTCCGCAATC	1084
OY	907	CAGCTTAAAGAACACATTTGACCGATCCCGGAAGAAACCGGGGTGAAGAAAGAGAGACAA	966
Db	1085	CAGCTTAAAGAACACATTTGACCGATCCCGGAAGAAACCGGGGTGAAGAAAGAGAGACAA	1144
OY	967	TATAGATCACCGGAGGAGGAGGABAATGACGCCATGAGAGGAAAGAGAGACCAAGC	1026
Db	1145	TATAGATCACCGGAGGAGGAGGABAATGACGCCATGAGAGGAAAGAGAGACCAAGC	1204
OY	1027	TTCATCATGAAGCTGTGAGAGTGCATCAAGCCGAGAGTTTCTCCGCTCCAGAG	1086
Db	1205	TTCATCATGAAGCTGTGAGAGTGCATCAAGCCGAGAGTTTCTCCGCTCCAGAG	1264
OY	1087	GAATAATAAGCAACTCAGAGGCTTTAAACACGACGACAGCTGACAGCAGCAGCAG	1146
Db	1265	GAATAATAAGCAACTCAGAGGCTTTAAACACGACGACAGCTGACAGCAGCAGCAGCAG	1324
OY	1147	CGAGACCCCGAGGACACATCAAAACCTGCTGCACACGCGGACGCGGCGCATAGAGAG	1206

Db	1325	CGAAGCCCCGAGGACACATCTCAACACCTCTGCAACAGCGGACAGCGGCCCATATGAGGAG	1384
QY	1207	CAGAAGAGAGCGGCGCCCGCTGTGAGAGCAACAGCGGCGGAGCGGAGCGAGCGGAG	1266
Db	1385	CAGAAGGAGGACGGCGCCCGGTGTGAGAGCAACAGCGGCGGAGCGGAGCGAGCGGAG	1444
QY	1287	CTGCAGAGGAAGAGAGCAGAGCGGCGGCTGTAGAGCAATGCAAGCTCTGCGCGGAGAGAG	1326
Db	1445	CTGCAGAGGAAGAGAGCAGAGCGGCGGCTGTAGAGCAATGCAAGCTCTGCGCGGAGAGAG	1504
QY	1327	GAGCGGCGGACGAGCGGAGCGCTGAGCAGAAATACAAAGCGAAGCAGCTGAGAGCAGCGG	1386
Db	1505	GAGCGGCGGACGAGCGGAGCGGAGCGGAGAAATACAAAGCGAAGCAGCTGAGAGAGCAGCGG	1564
QY	1387	CAGTCAGAACGTCTCCAGAGGACGCTGACAGAGAGCATGCGCTTACCTCAAGTCCCTGACG	1446
Db	1565	CAGTCAGAACGTCTCCAGAGGACGCTGACAGAGAGCATGCGCTTACCTCAAGTCCCTGACG	1624
QY	1447	CAGCAGCAACAGCAGCAGCAGCCTTCABAACAGAGAGAGCAGAGCCTCCGCTGGGAGAG	1506
Db	1625	CAGCAGCAACAGCAGCAGCAGCCTTCABAACAGAGAGAGCAGAGCCTCCGCTGGGAGAG	1684
QY	1507	AGGAAGCCCCCTGTACCATTAATGTCTGGGAGCATGAATCCGCTGCACAAACGAGCTGGGCG	1566
Db	1685	AGGAAGCCCCCTGTACCATTAATGTCTGGGAGCATGAATCCGCTGCACAAACGAGCTGGGCGC	1744
QY	1567	CGAGAGGTAGAGAGAGAACAGAGATGAACAGCAGCAGAACTTCTCCCTTGGCCAGAGC	1626
Db	1745	CGAGAGGTAGAGAGAGAACAGAGATGAACAGCAGCAGAACTTCTCCCTTGGCCAGAGC	1804
QY	1627	AAAGCAGAGCAGCAAGGAGGCGCTGAGGCGGCCCATATCCCGAGGCGCTCCCGAGGAGCCCGCAG	1686
Db	1805	AAAGCAGAGCAGCAAGGAGGCGCTGAGGCGGCCCATATCCCGAGGCGCTCCCGAGGAGCCCGCAG	1864
QY	1687	CCGCTTTTCCAGACTCTCTCTATATCAGAGGCGGAGTGAGGCGCCAGAGAGGAGCGCACA--	1744
Db	1865	CCGCTTTTCCAGACTCTCTCTATATCAGAGGCGGAGTGAGGCGCCAGAGAGGAGCGCACAAG	1924
QY	1745	-----AG 1746	
Db	1925	AGCCTGTGTGCACACCGGGATCCCATGAAGCATATGACAGACCTGTATACCCGATCCGAC	1984
QY	1747	TCCCTGCAAGACCAAGCCCAACCTGGCTGCGCTCCCAAGCTCCCAATGAGCCGAC	1806
Db	1985	TCCCTGCAAGACCAAGCCCAACCTGGCTGCGCTCCCAAGCTCCCAATGAGCCGAC	2044
QY	1807	CCTGCATATCCCGACCACTGACAGCCGCAAGTGCCTCGAGAGAGCTGTCAATCCGCAAAAT	1866
Db	2045	CCTGCATATCCCGACCACTGACAGCCGCAAGTGCCTCGAGAGAGCTGTCAATCCGCAAAAT	2104
QY	1867	TCAGACCCCACTCTGAAAGACCTTGGCCCGACCGGAATCCCGACGCTTGGGTCCGCCA	1926
Db	2105	TCAGACCCCACTCTGAAAGACCTTGGCCCGACCGGAATCCCGACGCTTGGGTCCGCCA	2164
QY	1927	GATTAACGAGGCGCCACCAAGGTGCTCAGAGACCTCACTATGCGCACTGCGCCTTAAC	1986
Db	2165	GATTAACGAGGCGCCACCAAGGTGCTCAGAGACCTCACTATGCGCACTGCGCCTTAAC	2224
QY	1987	ACCAAGTGGGAGCGAGAGGTCCCGGACAGCCAGCAGTCTGCTGCAGAACTCGCAGCAAC	2046
Db	2225	ACCAAGTGGGAGCGAGAGGTCCCGGACAGCCAGCAGTCTGCTGCAGAACTCGCTGC-----	2269
QY	2047	TCGCGCTGGCAAAATCTATCTGCAAAAGCGGCAAGCGGAGCACCCAAAGCTCCAGGG	2106
Db	2270	-----2269	
QY	2107	CCCCCTGTACAGCCCCCTGAGCCCGCCCAACGCTCTATAGTAACCCCGACCTCAGAGGAGC	2166
Db	2270	-----AGTAACCCCGACCTCAGAGGAGC 2293	
QY	2167	GACCCTGGCTGGAAAGCGTCGAGCAGGCTCTTCAGACCTCTCAAGGAGCACTCCCGAC	2226

D	2254	GAACCTGGCTGGGAACGCTCGGACAGCGCTCTTCCAGCTCTCAACGGGCACTCCCCAC	2353
O	2227	GCTGGCTCACTGGAGCGGAAACCGCGTGGAGCGCTCTTCCAACTGGACAGCTCCCTGTG	2286
D	2354	GCTGGCTCACTGGAGCGGAAACCGCGTGGAGCTCTCTCCAAACCGGACAGCTCCCTGTG	2413
O	2287	CTCTCCCTGGGAAATTAAGCCAGGCCGACCAACCGCTCAACGGCCAGGCCGCCGCA	2346
D	2414	CTCTCCCTGGGAAATTAAGCCAGGCCGACCAACCGCTCAACGGCCAGGCCGCCGCA	2473
O	2347	-----GACTTGTGTGCTGAAGAGCGGACTCTGGACGAG	2382
D	2474	AGCTAATAAGCGAGCAATTGTGAGGACTTTGTGTGCTGAAGAGCGGACTCTGGACGAG	2533
O	2383	GCCCTCGGCGCTCCCAAGAGGCCATGACCTTGTGCTCGACGAGAGGTGGAAGC	2442
D	2534	GCCCTCGGCGCTCCCAAGAGGCCATGACCTTGTGCTCGACGAGAGGTGGAAGC	2593
O	2443	AGTAGAGACGACGAGAGAGGAAGGCGAAGCGGCGCAGCAGAGGGGACAGAGATACCTCT	2502
D	2594	AGTAGAGACGACGAGAGAGGAAGGCGAAGCGGCGCAGCAGAGGGGACAGAGATACCTCT	2653
O	2503	GGGGGCGCGACGATGGGGGATACAGACAGCGTCAGCACATGTGTGTCAAGAGGTGAG	2562
D	2654	GGGGGCGCGACGATGGGGGATACAGACAGCGTCAGCACATGTGTGTCAAGAGGTGAG	2713
O	2563	GAGATCAACCGGGAACCCAGCGCCCATACGGGGCGGCACTATGTGTGTCAACGCAACCTT	2622
D	2714	GAGATCAACCGGGAACCCAGCGCCCATACGGGGCGGCACTATGTGTGTCAACGCAACCTT	2773
O	2623	GAAAGAGAGCGGAACCTGCTGCAATCTGACAGCAATGGGTACACAACTTGCCTGACGTG	2682
D	2774	GAAAGAGAGCGGAACCTGCTGCAATCTGACAGCAATGGGTACACAACTTGCCTGACGTG	2833
O	2683	GTCCAGCCCAACCACTCAACCGACGAGAACAGCAAAAGGCCAAAGGCCAACCCTCGAAGGAT	2742
D	2834	GTCCAGCCCAACCACTCAACCGACGAGAACAGCAAAAGGCCAAGGCCAACCCTCGAAGGAT	2893
O	2743	GGAGATGGTGACTACCACTCTCGTGGCGTGGTAAAGGCCCTCGGCAAGACTCGTTACG	2802
D	2894	GGAGATGGTGACTACCACTCTCGTGGCGTGGTAAAGGCCCTCGGCAAGACTCGTTACG	2953
O	2803	ATGTTTGTGATCTTAGGGATCTTACGAGCTTGAGAGGCACTGGGAGACAGATCCCATCA	2862
D	2954	ATGTTTGTGATCTTAGGGATCTTACGAGCTTGAGAGGCACTGGGAGACAGATCCCATCA	3013
O	2863	GCCCTAGTGGGTGGAGAGGGCACTGGCTCGACACGCTGCAGTACAGAGTATAGAGGAAGGT	2922
D	3014	GCCCTAGTGGGTGGAGAGGGCACTGGCTCGACACGCTGCAGTACAGAGTATAGAGGAAGGT	3073
O	2923	TCTGTGGGTCAACGTGAATCCCAACCAACCGGGGCCCACTGTGAAGCCCTGAGATCCGG	2982
D	3074	TCTGTGGGTCAACGTGAATCCCAACCAACCGGGGCCCACTGTGAAGCCCTGAGATCCGG	3133
O	2983	AAGTACAAAGAGCGATTCACATCTCCGAGATCTCTGTGTGCAAGCCTTTTGGGGGTCAACCTG	3042
D	3134	AAGTACAAAGAGCGATTCACATCTCCGAGATCTCTGTGTGCAAGCCTTTTGGGGGTCAACCTG	3193
O	3043	CTGTGGGCAACGAGAACCGGCTGATGTTGCTGGAACCGAAGTGGCAAGGCAAGTGTAT	3102
D	3194	CTGTGGGCAACGAGAACCGGCTGATGTTGCTGGAACCGAAGTGGCAAGGCAAGTGTAT	3253
O	3103	GGAATCAATGGGCGGCGAGCGCTCCAGAGATGGAATGTGCTGGAGAGGGCTCAACTGTGTC	3162
D	3254	GGAATCAATGGGCGGCGAGCGCTCCAGAGATGGAATGTGCTGGAGAGGGCTCAACTGTGTC	3313
O	3163	ATCAACCATCTCAGGGAAAAAGAACAAACTGGCGGTGTATTAACCTGTCTCTGCTCCGAAAC	3222
D	3314	ATCAACCATCTCAGGGAAAAAGAACAAACTGGCGGTGTATTAACCTGTCTCTGCTCCGAAAC	3373
O	3223	AAGATTCTGCACATGACCCAGAGTGGAGAAAGACAGGCTGGACCACTGTGGGGGAC	3282
D	3374	AAGATTCTGCACATGACCCAGAGTGGAGAAAGACAGGCTGGACCACTGTGGGGGAC	3433

QY	3283	ATGAGAGGCTGCGGGACACTACCGGTGTGTGAATAAGAGCGGATTAACTTCGTGATC	3342
Db	3434	ATGAGAGGCTGCGGGACACTACCGGTGTGTGAATAAGAGCGGATTAACTTCGTGATC	3493
QY	3343	GCCCTCAAGACCTCGATGAGGTTATGCGCTGGGCCCCAAACCTTACCAAAATTCATG	3402
Db	3494	GCCCTCAAGACCTCGATGAGGTTATGCGCTGGGCCCCAAACCTTACCAAAATTCATG	3553
QY	3403	GCTTCAAGTCTTTTGCCGACCTTCCCAACCGGCTCTGTGTCGACCTTGACATGAG	3462
Db	3554	GCTTCAAGTCTTTTGCCGACCTTCCCAACCGGCTCTGTGTCGACCTTGACATGAG	3613
QY	3463	GAGGGGGACGGGCTCAAGTTCATTTATGAGCTGCGCTGGCTTCATGCTGAGGATGTC	3522
Db	3614	GAGGGGGACGGGCTCAAGTTCATTTATGAGCTGCGCTGGCTTCATGCTGAGGATGTC	3673
QY	3523	GACTCGGGGAAACAGCTATGACATCTACATCCCTGTGCAATCCAGAGCCAGATACGCC	3582
Db	3674	GACTCGGGGAAACAGCTATGACATCTACATCCCTGTGCAATCCAGAGCCAGATACGCC	3733
QY	3583	CATGCCATCATCTTCTTCCCAACACGACCGGATGAGATGCTGTGTCTACGAGAC	3642
Db	3734	CATGCCATCATCTTCTTCCCAACACGACCGGATGAGATGCTGTGTCTACGAGAC	3793
QY	3643	GAGGTTGTTTACCTTCACACAGTACGGGCGCATCTTAAAGATGTGTGCTGCAATGGGG	3702
Db	3794	GAGGTTGTTTACCTTCACACAGTACGGGCGCATCTTAAAGATGTGTGCTGCAATGGGG	3853
QY	3703	GAGATGCTTACTTCTGTGAGCCTTACATCTGCTCAACAGATTAATGGGCTGGGTGAGAA	3762
Db	3854	GAGATGCTTACTTCTGTGAGCCTTACATCTGCTCAACAGATTAATGGGCTGGGTGAGAA	3913
QY	3763	GCCATTGATCGCCTCTGTGAGACGGGCGCACTCGACGGGGTCTTCATGCAAAACGA	3822
Db	3914	GCCATTGATCGCCTCTGTGAGACGGGCGCACTCGACGGGGTCTTCATGCAAAACGA	3973
QY	3823	GCTGAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTTTGTGCTCAGTCGCG	3882
Db	3974	GCTGAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTTTGTGCTCAGTCGCG	4033
QY	3883	TCTGGGGGACAGACCCAAATTACTTATGACTCTGAAACCGTAACTGCATCATGAATCG	3942
Db	4034	TCTGGGGGACAGACCCAAATTACTTATGACTCTGAAACCGTAACTGCATCATGAATCG	4093
QY	3943	TGAAAGGCGC 3951	
Db	4094	TGACGGGGC 4102	
RESULT 5			
US-09-789-390-8			
; Sequence 8, Application US/09789390			
; Publication No. US20030059768A1			
GENERAL INFORMATION:			
APPLICANT: Vernet, Corine			
APPLICANT: Fernandes, Elma			
APPLICANT: MacDougall, John			
APPLICANT: Shimkels, Richard A			
APPLICANT: Spaderna, Steven K			
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME			
FILE REFERENCE: 15966-692			
CURRENT APPLICATION NUMBER: US/09/789,390			
CURRENT FILING DATE: 2001-02-23			
PRIOR APPLICATION NUMBER: 60/185,548			
PRIOR FILING DATE: 2000-02-28			
PRIOR APPLICATION NUMBER: 60/199,957			
PRIOR FILING DATE: 2000-04-27			
PRIOR APPLICATION NUMBER: 60/184,951			
PRIOR FILING DATE: 2000-02-25			
PRIOR APPLICATION NUMBER: 60/185,967			
PRIOR FILING DATE: 2000-03-01			
PRIOR APPLICATION NUMBER: 60/197,723			







Db 1921 TCAGACCCACACTCTGAAAGACCTGGCCCAAGCCGAAATCCCCAGACCTGGGGTCCGCCA 1980  
Qy 1927 GATATACAGAGGCCCAACCAAGGTGCTCAAGAGACCTCATCTATGCGCATGCCCCCTTAAC 1986  
Db 1981 GATATACAGAGGCCCAACCAAGGTGCTCAAGAGACCTCATCTATGCGCATGCCCCCTTAAC 2040  
Qy 1987 ACCAGTGGGGCCGAGGGGTCCCGGCACGCCAGGACGATCCGGGCCAGACCTCGACGAAAC 2046  
Db 2041 ACCAGTGGGGCCGAGGGGTCCCGGCACGCCAGGACGATCCGGGCC----- 2085  
Qy 2047 TCCGCTGGCAAAATCTATCTGCAAAAGGCGGCGAGAGCGGGGCAACCCCAAGCCTTCAGAGG 2106  
Db 2086 ----- 2085  
Qy 2107 CCCCCCTGCTAGCCCCCTTGCGCCGCAACGCTCTAGTAACCCCGACCTTGAAGAGAGC 2166  
Db 2086 -----AGTAAACCCCGACCTTGAAGAGAGC 2109  
Qy 2167 GACCCCTGGCTGGGAACGCTCGGAGACGGTCCCTCCAGCTCTCAAGGGGCACTCCGCCAG 2226  
Db 2110 GACCCCTGGCTGGGAACGCTCGGAGACGGTCCCTCCAGCTCTCAAGGGGCACTCCGCCAG 2169  
Qy 2227 GCTGCTCACTGAGCGGAAACCGCTGGGAGCTCTCTCAAACTGAGCAGCTCCCTGTG 2286  
Db 2170 GCTGCTCACTGAGCGGAAACCGCTGGGAGCTCTCTCAAAACGAGCAGCTCCCTGTG 2229  
Qy 2287 CTCTCCCTGGGAAATAAGCCAGACCGGACGACCAACGCTCAAGGCGAGCGCGCCGCA 2346  
Db 2230 CTCTCCCTGGGAAATAAGCCAGACCGGACGACCAACGCTCAAGGCGAGCGCGCCGCA 2289  
Qy 2347 -----GACTTGTGTGCTGAAAGAGCGGACCTTGAAGAG 2382  
Db 2290 AGCTATAAGCGAGCAATTTGTGAGGACTTGTGTGTGCTGAAAGAGCGGACCTTGAAGAG 2349  
Qy 2283 GCCCTCGGCTCTCCCAAGAAAGCCATGGACTACTGCTGCTCAAGGAGAGAGTGGAAAGC 2442  
Db 2250 GCCCTCGGCTCTCCCAAGAAAGCCATGGACTACTGCTGCTCAAGGAGAGAGTGGAAAGC 2409  
Qy 2443 AGTAGAGACGACGAGAGAGAGCGGAGCGGCGCCAGAGAGGGGAGAGATACCTCT 2502  
Db 2410 AGTAGAGACGACGAGAGAGAGCGGAGCGGCGCCAGAGAGGGGAGAGATACCTCT 2469  
Qy 2503 GGGGGCCGACAGATGGGGATACAGACAGCGTCAAGCAATAGTGTCTCAAGAGCTGAG 2562  
Db 2470 GGGGGCCGACAGATGGGGATACAGACAGCGTCAAGCAATAGTGTCTCAAGAGCTGAG 2529  
Qy 2563 GAGATCAACCGGAGCCAGACCCCATACGAGGGGCGGACCATGTGTGCTCAAGCGACCT 2622  
Db 2530 GAGATCAACCGGAGCCAGACCCCATACGAGGGGCGGACCATGTGTGCTCAAGCGACCT 2589  
Qy 2623 GAAGAGAGCGGAACTGTGCTGATGCTGACAGCAATGGGTACACAAACCTTGCTGACGTG 2682  
Db 2590 GAAGAGAGCGGAACTGTGCTGATGCTGACAGCAATGGGTACACAAACCTTGCTGACGTG 2649  
Qy 2683 GTCCAGGCCAGACCACTCAACCGAGAAACAGCAAAAGGCCCAACCTCTCGAAGAT 2742  
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Db 2770 ATGTTTGTGATCTAGGATCTACAGCTGAGGAGCACTGGGAGCAAGATCCCATCA 2829  
Qy 2863 GCCCTAGTGGGTGAGAGAGGCACTGCGCTCGACCAAGCTGCACTACAGTGAAGAGGCT 2922  
Db 2830 GCCCTAGTGGGTGAGAGAGGCACTGCGCTCGACCAAGCTGCACTACAGTGAAGAGGCT 2889  
Qy 2923 TCTGTGCTCAAGTGAATCCAGCAACACCGGGGCCCAAGTGAAGACCCCTGAGATCCGG 2982  
Db 2890 TCTGTGCTCAAGTGAATCCAGCAACACCGGGGCCCAAGTGAAGACCCCTGAGATCCGG 2949

Qy 2983 AAGTACAGAGCGGATTCATCCGAGATCCCTCTGTGAGGCGCTTTGGGGGGTCAACCTG 3042  
Db 2950 AAGTACAGAGCGGATTCATCCGAGATCCCTCTGTGAGGCGCTTTGGGGGGTCAACCTG 3009  
Qy 3043 CTGTGGGGCACGAGAAACGGGCTGATGTGCTGACGAAATGGGGCAGGGGCAAGGTAT 3102  
Db 3010 CTGTGGGGCACGAGAAACGGGCTGATGTGCTGACGAAATGGGGCAGGGGCAAGGTAT 3069  
Qy 3103 GGAATCATTTGGGCGGAGACGCTTCACAGATGATGTGCTGAGGGGCTCAACCTGCTC 3162  
Db 3070 GGAATCATTTGGGCGGAGACGCTTCACAGATGATGTGCTGAGGGGCTCAACCTGCTC 3129  
Qy 3163 ATCAACATTCAGGAGAAAGAAACAACTGGGGTATTAACCTGCTCGGAC 3222  
Db 3130 ATCAACATTCAGGAGAAAGAAACAACTGGGGTATTAACCTGCTCGGAC 3189  
Qy 3223 AAGATTCGACATGACCCAGAGTGAAGAGAGAGGGCTGACCAACCTGAGGAGC 3282  
Db 3190 AAGATTCGACATGACCCAGAGTGAAGAGAGAGGGCTGACCAACCTGAGGAGC 3249  
Qy 3283 ATGAGAGGCTGCGGGCACTACCGTGTGTGAATAAGAGCGGATTAAGTCTGTGTCATC 3342  
Db 3250 ATGAGAGGCTGCGGGCACTACCGTGTGTGAATAAGAGCGGATTAAGTCTGTGTCATC 3309  
Qy 3343 GCCCTCAAGAGCTCCGTGAGGTGTATGCTGGGCCCCCAAAACCTTACCAAAATTGATG 3402  
Db 3310 GCCCTCAAGAGCTCCGTGAGGTGTATGCTGGGCCCCCAAAACCTTACCAAAATTGATG 3369  
Qy 3403 GCCTTCAAGTCTTTGCGGACCTCCCAACCGGCTCTGCTGTGACAGCTGACAGTGAAG 3462  
Db 3370 GCCTTCAAGTCTTTGCGGACCTCCCAACCGGCTCTGCTGTGACAGCTGACAGTGAAG 3429  
Qy 3463 GAGGGGAGCGGCTCAAGGATCATATGCTCAAGTCTGCGCTTCAATGCTGTGATGTC 3522  
Db 3430 GAGGGGAGCGGCTCAAGGATCATATGCTCAAGTCTGCGCTTCAATGCTGTGATGTC 3489  
Qy 3523 GACTCGGGAAACAGCTATGACATCTTACATCCCTGTGACATCCAGAGCCAGATCAAGCCC 3582  
Db 3490 GACTCGGGAAACAGCTATGACATCTTACATCCCTGTGACATCCAGAGCCAGATCAAGCCC 3549  
Qy 3583 CATGCAATCATCTTCTCCCAACCGGAGCGGAGTGAAGATGCTGTGCTACAGAGAC 3642  
Db 3550 CATGCAATCATCTTCTCCCAACCGGAGCGGAGTGAAGATGCTGTGCTACAGAGAC 3609  
Qy 3643 GAGGGTGTCTAAGTCAACAGTACGAGCGGATCAATTAAGATGTGTGCTGCACTGAGG 3702  
Db 3610 GAGGGTGTCTAAGTCAACAGTACGAGCGGATCAATTAAGATGTGTGCTGCACTGAGG 3669  
Qy 3703 GAGATGCTTACTTGTGGCTTACATCTGCTCCAAACGATTAATGGGCTGGGTGAAGAA 3762  
Db 3670 GAGATGCTTACTTGTGGCTTACATCTGCTCCAAACGATTAATGGGCTGGGTGAAGAA 3729  
Qy 3763 GCCATTAAGATCCGCTGTGAGAGAGGGGCAACCTGACGGGGCTTCATGCAAAAGCA 3822  
Db 3730 GCCATTAAGATCCGCTGTGAGAGAGGGGCAACCTGACGGGGCTTCATGCAAAAGCA 3789  
Qy 3823 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAAATGACAAAGTGTGCTTGGCTCAGTCCG 3882  
Db 3790 GCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAAATGACAAAGTGTGCTTGGCTCAGTCCG 3849  
Qy 3883 TCTGGGGGACAGCGCAAGTTACTTATGATCTCTGAACGTTAATGATCATATGAATCG 3942  
Db 3850 TCTGGGGGACAGCGCAAGTTACTTATGATCTCTGAACGTTAATGATCATATGAATCG 3909  
Qy 3943 TGA 3945  
Db 3910 TGA 3912

RESULT 6  
US-09-789-390-6  
; Sequence 6, Application US/09789390



Db 1621 AATCCGCTGACAAACAGCCTGGGCCCCAGAGGTAGAGAGAAACAAGATGAAACAAG 1680  
Qy 1600 CAGCAGAACTCTCCCTTGGCCAAAGAGCAAGCCAGGACAGCGGGGCTGAGCCCCCAATC 1659  
Db 1681 CAGCAGAACTCTCCCTTGGCCAAAGAGCAAGCCAGGACAGCGGGGCTGAGCCCCCAATC 1740  
Qy 1660 CCCGAGGCTCTCCAGGGGCCCCAGAGCCCTTTCCAGACTCTCTATGAGAGGCGG 1719  
Db 1741 CCCGAGGCTCTCCAGGGGCCCCAGAGCCCTTTCCAGACTCTCTATGAGAGGCGG 1800  
Qy 1720 GTGAGCCCCAGAGGAGCCGACCA----- 1744  
Db 1801 GTGAGCCCCAGAGGAGCCGACCAAGAGCTGTGGACACCGGGTCCCATGAAAGCCA 1860  
Qy 1745 -----AGTCCCTGACGAGACAGCCCACTGGCT 1779  
Db 1861 TATCAGACACTGTATCCCGATCCCAAGTCCCTGACAGACAGCCCACTGGCT 1920  
Qy 1780 GCGTTCACAGGCTCCCATGACCCCGAGCCCTGCAATCCCGGACCCCATGCGACCGCAGT 1839  
Db 1921 GCGTTCACAGGCTCCCATGACCCCGAGCCCTGCAATCCCGGACCCCATGCGACCGCAGT 1980  
Qy 1840 GCCCGAGAGGCTGTATCCGCGCAGAAATTCAGACCCCACTGTGAAGAGACTGGCCCCAGC 1899  
Db 1981 GCCCGAGAGGCTGTATCCGCGCAGAAATTCAGACCCCACTGTGAAGAGACTGGCCCCAGC 2040  
Qy 1900 CCGAATCCCGAGGCTGGGTCCGCGCAGATTAAGAGGCCCAACCGAGGTGCTCAGAGG 1959  
Db 2041 CCGAATCCCGAGGCTGGGTCCGCGCAGATTAAGAGGCCCAACCGAGGTGCTCAGAGG 2100  
Qy 1960 ACCCTATATATGCACTGCGCTTAAACAGTGGGGGCGAGGGTCCCGGCAAGCCAG 2019  
Db 2101 ACCCTATATATGCACTGCGCTTAAACAGTGGGGGCGAGGGTCCCGGCAAGCCAG 2160  
Qy 2020 GCACTCCGTGCGAGACTCGAGCAACTCGGCTGGCAAAATCTATCTGCAAAAGGCGGCA 2079  
Db 2161 GCACTCCGTGCG----- 2172  
Qy 2080 GAGCGGGGACCCCAAGCTTCAGAGGGCCCCCTGCTACGCCCTGCGCCCGCCACGCGC 2139  
Db 2173 ----- 2172  
Qy 2140 TCTAGTAAACCCGACCTCAGAGAGAGGAGCCCTGGCTGGAAACGCTCGGACAGGCTCTT 2139  
Db 2173 ---AGTAAACCCGACCTCAGAGAGAGGAGCCCTGGCTGGAAACGCTCGGACAGGCTCTT 2229  
Qy 2200 CCAAGCTCTCAAGGAGCACTCCCGAGGCTGGCTCACTGAGCGGAAACCGGCTGGAGACC 2259  
Db 2230 CCAAGCTCTCAAGGAGCACTCCCGAGGCTGGCTCACTGAGCGGAAACCGGCTGGAGACC 2289  
Qy 2260 TCTCTCAAACTGAGCAGCTCCCTGTGTCTTCCCTGGAAATTAAGCCAGCCCGACGAC 2319  
Db 2290 TCTCTCAAAACGGGACAGCTCCCTGTGTCTTCCCTGGAAATTAAGCCAGCCCGACGAC 2349  
Qy 2320 CACCGCTCAAGGAGCGGAGCGGCGCGCA-----GACTTTGTG 2355  
Db 2350 CACCGCTCAAGGAGCGGAGCGGCGCGCAAGCTTAAGCAGCAATTTGTGAGGACTTTGTG 2409  
Qy 2356 TTGCTGAAAGAGCGGACTCTGAGACAGGCGCTCGGCTCCCAAGAAAGCCATGACTAC 2415  
Db 2410 TTGCTGAAAGAGCGGACTCTGAGACAGGCGCTCGGCTCCCAAGAAAGCCATGACTAC 2469  
Qy 2416 TCGTGTTCAGCGAGAGAGGTGAAAGCAGTGAAGACGACGAGAGAGAAAGCGAAAGCGGG 2475  
Db 2476 TCGTGTTCAGCGAGAGAGGTGAAAGCAGTGAAGACGACGAGAGAGAAAGCGAAAGCGGG 2529  
Qy 2476 CCAAGAGAGGAGAGAGATACCCCTGGGGGCGGCAACGATGGGGATACAGACAGGCTC 2535  
Db 2530 CCAAGAGAGGAGAGAGATACCCCTGGGGGCGGCAACGATGGGGATACAGACAGGCTC 2589  
Qy 2536 AGCAGCAATGTGTCTCAAGAGTCAACCGGAGCCAGCCCGCTTACCGGGGC 2595  
Db 2590 AGCAGCAATGTGTCTCAAGAGTCAACCGGAGCCAGCCCGCTTACCGGGGC 2649

Qy 2596 GGCAACAATGTGTCTCAAGCGGACCCCTGAAGAGAGCGGAACTGTCTGATCTGACAGC 2655  
Db 2650 GGCAACAATGTGTCTCAAGCGGACCCCTGAAGAGAGCGGAACTGTCTGATCTGACAGC 2709  
Qy 2656 AATGGGTACACAAACCTGCTGAGGTGTCCAGCCCACTGACCCACGAGAAACAGC 2715  
Db 2710 AATGGGTACACAAACCTGCTGAGGTGTCCAGCCCACTGACCCACGAGAAACAGC 2769  
Qy 2716 AAAGGCCAAAGCCCACTCTGAGAGATGGAGTGTGTCTACAGTCTCTGTGGCTGTGTA 2775  
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Qy 2896 CAGCTGACATACAGCTGAGAGAGGTTCTGTGTCAAGTGAATCCCAACACACCTGG 2955  
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Qy 2956 GCCCAAGTGAAGACCCCTGAGATCCGGAAGTAAAGAGGATTCACCTCGGATCTCTC 3015  
Db 3010 GCCCAAGTGAAGACCCCTGAGATCCGGAAGTAAAGAGGATTCACCTCGGATCTCTC 3069  
Qy 3016 TGTGACAGCCCTTTGGGGGCTCAACCTGCTGTGTGGGCAACGAGAACGGGCTGATGTGCTG 3075  
Db 3070 TGTGACAGCCCTTTGGGGGCTCAACCTGCTGTGTGGGCAACGAGAACGGGCTGATGTGCTG 3129  
Qy 3076 GACCGAAGTGGGCAAGGCAAGTGTATGACTCAATTGGGCGGCAACGCTTCACAGCATG 3135  
Db 3130 GACCGAAGTGGGCAAGGCAAGTGTATGACTCAATTGGGCGGCAACGCTTCACAGCATG 3189  
Qy 3136 GATGTGCTGAGAGGGGCTCAACCTGCTCATACCAATTCAGGGAAAGAGAACAACTGGGG 3195  
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Db 3250 GTGTATTACCTGCTCTGCTCCGAAACAAGATTCTGACAAATGACAGAGTGAAGAG 3309  
Qy 3256 AAGCAGGAGCTGAGACCAACGTGGGGGACATGAGGGCTGGCGGCACTACCTGTTGTGAA 3315  
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Qy 3316 TACGAGGAGATTAAAGTTCGTGTGATGAGCTCCAGAGCTCCGTGAGAGGTATGCTTGG 3375  
Db 3370 TACGAGGAGATTAAAGTTCGTGTGATGAGCTCCAGAGCTCCGTGAGAGGTATGCTTGG 3429  
Qy 3376 GCGCCCAAAACCTTACCAAAATTCATGAGCTTCAAGTCTTTTGGCGACCTCCCAACGCG 3435  
Db 3430 GCGCCCAAAACCTTACCAAAATTCATGAGCTTCAAGTCTTTTGGCGACCTCCCAACGCG 3489  
Qy 3436 CCTCTGTGTGTGACCTTGAAGTGAAGAGAGGAGCGGCTCAAGGTCTATGAGCTCC 3495  
Db 3490 CCTCTGTGTGTGACCTTGAAGTGAAGAGAGGAGCGGCTCAAGGTCTATGAGCTCC 3549  
Qy 3496 AGTGTGTGTCTTCAATGTGTGTGATGAGCTCGGGGAAACAGTATGATTAATCCCT 3555  
Db 3550 AGTGTGTGTCTTCAATGTGTGTGATGAGCTCGGGGAAACAGTATGATTAATCCCT 3609  
Qy 3556 GTGCAATCCAGAGCAGATACCGCCCATGSCATCATCTTCTCCCAACAACGAGCGG 3615  
Db 3610 GTGCAATCCAGAGCAGATACCGCCCATGSCATCATCTTCTCCCAACAACGAGCGG 3669  
Qy 3616 ATGAGATGTCTGTGTCTTACAGAGCAGAGGTTCTACGTCAACAGTACGAGCGCATC 3675  
Db 3670 ATGAGATGTCTGTGTCTTACAGAGCAGAGGTTCTACGTCAACAGTACGAGCGCATC 3729

QY 3676 ATTAAGATGTGTGTGTCGATGGGGGAGATGCCATCTTGTGTGGCTTACATCTGCTCC 3735  
DB 3730 ATTAAGATGTGTGTGTCGATGGGGGAGATGCCATCTTGTGTGGCTTACATCTGCTCC 3789  
QY 3736 AACCGATATATGGGCTGGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGAGACGGGCCG 3795  
DB 3790 AACCGATATATGGGCTGGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGAGACGGGCCG 3849  
QY 3796 CTCGACGGGGCTCTTCATGCAAAACGAGCTCAGAGGCTCAAGTTCCTGTGTAGCGGAAAT 3855  
DB 3850 CTCGACGGGGCTCTTCATGCAAAACGAGCTCAGAGGCTCAAGTTCCTGTGTAGCGGAAAT 3909  
QY 3856 GACAAAGTGTGTGTGTGCTCAGTCCGCTCTGGGGGAGACAGCCAAATTTACTTCACTACT 3915  
DB 3910 GACAAAGTGTGTGTGTGCTCAGTCCGCTCTGGGGGAGACAGCCAAATTTACTTCACTACT 3969  
QY 3916 CTGAACCGTAACTGCTCATGAACTGTGA 3945  
DB 3970 CTGAACCGTAACTGCTCATGAACTGTGA 3999

## RESULT 7

US-10-029-115-3  
; Sequence 3, Application US/10029115  
; Publication No. US20030077597A1  
; GENERAL INFORMATION:  
; APPLICANT: Luo, Ying  
; APPLICANT: Fu, Alan C  
; APPLICANT: Shen, Mary  
; TITLE OF INVENTION: No. US20030077597A1 Germlinal Center Kinase Cell Cycle Proteins,  
; TITLE OF INVENTION: Methods of Use  
; FILE REFERENCE: A-70229/RMS/DHR  
; CURRENT APPLICATION NUMBER: US/10/029,115  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 3  
; LENGTH: 4414  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-029-115-3

Query Match 87.0%; Score 3437.2; DB 14; Length 4414;  
Best Local Similarity 90.1%; Pred. No. 0;  
Matches 3885; Conservative 0; Mismatches 3; Indels 426; Gaps 2;  
QY 64 GACCTGCTGGGATCTTTGAGCTTGTGAGGTGTGCGGATGGAACCTTACGAGCAGGTG 123  
DB 101 GACCTGCTGGGATCTTTGAGCTTGTGAGGTGTGCGGATGGAACCTTACGAGCAGGTG 160  
QY 124 TCAAGAGGTGCGGATGTCAGAGACGGGGCAGTGGCTGCCATCAAGGTCAATGATGTCAG 183  
DB 161 TCAAGAGGTGCGGATGTCAGAGACGGGGCAGTGGCTGCCATCAAGGTCAATGATGTCAG 220  
QY 184 GAGGACGAGAGAGAGATCAAAACAGAGATCAACATGCTGAAAAAGTACTCTCAAC 243  
DB 221 GAGGACGAGAGAGAGATCAAAACAGAGATCAACATGCTGAAAAAGTACTCTCAAC 280  
QY 244 CGCAATGTCGCACTTCACTACGAGGCTTCTCATCAAGAAAGAGCCCGGGAAACATGAC 303  
DB 281 CGCAATGTCGCACTTCACTACGAGGCTTCTCATCAAGAAAGAGCCCGGGAAACATGAC 340  
QY 304 CAGCTGTGCTGATGATGAGTCTGTGGGCTGTTCACTGATGCTGACCTGTTAAAGAAC 363  
DB 341 CAGCTGTGCTGATGATGAGTCTGTGGGCTGTTCACTGATGCTGACCTGTTAAAGAAC 400  
QY 364 AAAAAAGGCAAGCCCTGAAGAGACTGTATGCTTATATCTGACGAGAGATCTCTCAG 423  
DB 401 AAAAAAGGCAAGCCCTGAAGAGACTGTATGCTTATATCTGACGAGAGATCTCTCAG 460  
QY 424 GGTGTGGCCATCTCATGCCCCCAAGAGGTGATCATGAGACATCAAGGGGAGAAATGTG 483  
DB 461 GGTGTGGCCATCTCATGCCCCCAAGAGGTGATCATGAGACATCAAGGGGAGAAATGTG 520

QY 484 CTGCTGACAGAGATGCTGAGGTCAAGCTATGATTTTGGGGTGAATGCTCACTGAC 543  
DB 521 CTGCTGACAGAGATGCTGAGGTCAAGCTATGATTTTGGGGTGAATGCTCACTGAC 580  
QY 544 CGCACTGTGGGCAAGCACTTCTCATGAGAGTCCCTTACTGATATGGCTCCAGAGTTC 603  
DB 581 CGCACTGTGGGCAAGCACTTCTCATGAGAGTCCCTTACTGATATGGCTCCAGAGTTC 640  
QY 604 ATGCTGTGATGAGAACCTTGAATGCACTATGATTAAGAGATATTTGTGTCTTA 663  
DB 641 ATGCTGTGATGAGAACCTTGAATGCACTATGATTAAGAGATATTTGTGTCTTA 700  
QY 664 GGAATCAGAGCCATGAGATGAGCAGAGGAGACCCCTCTGTGTGATGATGACCCATG 723  
DB 701 GGAATCAGAGCCATGAGATGAGCAGAGGAGACCCCTCTGTGTGATGATGACCCATG 760  
QY 724 CGAGCCCTCTTCTCATTTCTGGAACCTTCCGCTCAGAGCTTCAAGTCCAAAGTGTCT 783  
DB 761 CGAGCCCTCTTCTCATTTCTGGAACCTTCCGCTCAGAGCTTCAAGTCCAAAGTGTCT 820  
QY 784 AAGAATTCATTGACTTATGACATGTCTCATCAAGACTTACCTGAGCCGCCACCC 843  
DB 821 AAGAATTCATTGACTTATGACATGTCTCATCAAGACTTACCTGAGCCGCCACCC 880  
QY 844 ACGGACGACTACTGAGTTCCTTCAATCCGGGACCAAGCCAGAGCCGAGGCTCCGC 903  
DB 881 ACGGACGACTACTGAGTTCCTTCAATCCGGGACCAAGCCAGAGCCGAGGCTCCGC 940  
QY 904 ATCCGCTTAAAGACCAATGACCCGATCCGGGAAAGAGCGGGGTGAAGAAAGAGACA 963  
DB 941 ATCCGCTTAAAGACCAATGACCCGATCCGGGAAAGAGCGGGGTGAAGAAAGAGACA 1000  
QY 964 GAATATGATGACAGCGGACGAGAGGAGAGATGACACCTAGAGAGAAAGAGAGCCA 1023  
DB 1001 GAATATGATGACAGCGGACGAGAGGAGAGATGACACCTAGAGAGAAAGAGAGCCA 1060  
QY 1024 AGCTCATCATGAAAGTGTGAGAGTGAATGAGCTTACGCGGGAGTTCCTCGGCTCAG 1083  
DB 1061 AGCTCATCATGAAAGTGTGAGAGTGAATGAGCTTACGCGGGAGTTCCTCGGCTCAG 1120  
QY 1084 CAGGAAATTAAGAGCACTCAGAGGCTTTAAACAGCGACAGCTGACAGAGAGAG 1143  
DB 1121 CAGGAAATTAAGAGCACTCAGAGGCTTTAAACAGCGACAGCTGACAGAGAGAG 1180  
QY 1144 CAGGAGACCCGAGGACACATCAACCTGTGTGACACAGCGGACAGCGGCTATGAG 1203  
DB 1181 CAGGAGACCCGAGGACACATCAACCTGTGTGACACAGCGGACAGCGGCTATGAG 1240  
QY 1204 GAGCAAGAGAGAGCGGCGCGCTGAGAGACAGCGGCGGAGCGGAGCAGCGG 1263  
DB 1241 GAGCAAGAGAGAGCGGCGCGCTGAGAGACAGCGGCGGAGCGGAGCAGCGG 1300  
QY 1264 AAGCTGCAAGAGAGAGAGAGCGGCGCTGAGAGACATGACAGCTCTCGCGGGAG 1323  
DB 1301 AAGCTGCAAGAGAGAGAGAGCGGCGCTGAGAGACATGACAGCTCTCGCGGGAG 1360  
QY 1324 GAGGAGCGGCGGACAGCGGAGGTGAGAGAGATCAAGCGGAGCAGCTGAGAGAG 1383  
DB 1361 GAGGAGCGGCGGACAGCGGAGGTGAGAGAGATCAAGCGGAGCAGCTGAGAGAG 1420  
QY 1384 CGGCACTAGAGACCTTCCAGAGGAGCTGACAGAGAGATGCTTACCTCAAGTCCCTG 1443  
DB 1421 CGGCACTAGAGACCTTCCAGAGGAGCTGACAGAGAGATGCTTACCTCAAGTCCCTG 1480  
QY 1444 CAGCAGCAGCAACAGCAGCAGAGCTTCAAGAAACAGCAGCAGCAGCAGCTCTGCTGG 1503  
DB 1481 CAGCAGCAGCAACAGCAGCAGAGCTTCAAGAAACAGCAGCAGCAGCAGCTCTGCTGG 1540  
QY 1504 GACAGAGAGCCCTGTACATTAATGTCGGGGCATGAATCCCGCTGACAAACCACTGG 1563  
DB 1541 GACAGAGAGCCCTGTACATTAATGTCGGGGCATGAATCCCGCTGACAAACCACTGG 1600

QY 1564 GCCCGAGAGGTAAAGAGAGAAACAAGATGAACAGCAGAGAACTCTCCCTGGCCAG 1623  
 DB 1601 GCCCGAGAGGTAAAGAGAGAAACAAGATGAACAGCAGAGAACTCTCCCTGGCCAG 1660  
 QY 1624 AGCAAGCCAGGACAGACCGGGGCTGAGGCCCTCCATCCCCAGGCTCTCCCAAGGGCCCCA 1683  
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 QY 1684 GGAACCCCTTTTCCAGACTCTCTCTATGCAAGAGCGGTGAGAGCCCAAGAGGAGACCGGAC 1743  
 DB 1721 GGAACCCCTTTTCCAGACTCTCTCTATGCAAGAGCGGTGAGAGCCCAAGAGGAGACCGGAC 1780  
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 QY 1745 -AGTCCCTGACAGACCAAGCCCAACCTGAGCTCTTCCAGCTCTCCATGACCC 1803  
 DB 1841 CAGTCCCTGACAGACCAAGCCCAACCTGAGCTCTTCCAGCTCTCCATGACCC 1900  
 QY 1804 GACCTTCATCCCGACCACTGACGCGCCAGTCCCGAGAGCTGTATCCGCGAG 1863  
 DB 1901 GACCTTCATCCCGACCACTGACGCGCCAGTCCCGAGAGCTGTATCCGCGAG 1960  
 QY 1864 AATTCAAGCCCACTCTGAAGAGACCTGGCCCGAGCCGAAATCCCGAGCTGGGTCCG 1923  
 DB 1961 AATTCAAGCCCACTCTGAAGAGACCTGGCCCGAGCCGAAATCCCGAGCTGGGTCCG 2020  
 QY 1924 CCAATTAACGAGGCCCCCAAGGTCCTGAGAGACCTGATCTATGCGCACTGCCCTT 1983  
 DB 2021 CCAATTAACGAGGCCCCCAAGGTCCTGAGAGACCTGATCTATGCGCACTGCCCTT 2080  
 QY 1984 AACCAAGTGGGGCCGAGGGTCCCGGACAGGCCAGGCACTCCGTGCAAGACTTGCGAGC 2043  
 DB 2081 AACCAAGTGGGGCCGAGGGTCCCGGACAGGCCAGGCACTCCGTGCAAGACTTGCGAGC 2140  
 QY 2044 AACTCCGCTGGCAATCTATCTGCAAGGCGGAGAGCGGGGACCCCAAGCTTCA 2103  
 DB 2141 AACTCCGCTGGCAATCTATCTGCAAGGCGGAGAGCGGGGACCCCAAGCTTCA 2200  
 QY 2104 GGGGCCCCCTGCTCAAGCCCTTGAGCCCGGCCAAGCCTTAAGTAACCCGACCTCAGAGG 2163  
 DB 2201 GGGGCCCCCTGCTCAAGCCCTTGAGCCCGGCCAAGCCTTAAGTAACCCGACCTCAGAGG 2260  
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 QY 2224 CAGGCTGGCTCACTGAGAGCGGAACCGCTGGAGGCTCTTCAAACTGGAACAGCTCCCT 2283  
 DB 2321 CAGGCTGGCTCACTGAGAGCGGAACCGCTGGAGGCTCTTCAAACTGGAACAGCTCCCT 2380  
 QY 2284 GTGCTCTCCCTGGGAATTAAGCCCAAGCCGACGACGCTCAAGGCGAGGCGGCGC 2343  
 DB 2381 GTGCTCTCCCTGGGAATTAAGCCCAAGCCGACGACGCTCAAGGCGAGGCGGCGC 2440  
 QY 2344 GCA----- 2346  
 DB 2441 GCAAGTAGTCACTGTGGAAGGATGAGCTGCTCATCTGTGTTGGGGCTTAAGCTCA 2500  
 QY 2347 ----- 2346  
 DB 2501 GGGTGTGGAGTGTCAAGGGGTGGGTCTCCGCTGATCTACGAGAAAGGCTGTGGGATGG 2560  
 QY 2347 ----- 2346  
 DB 2561 AGGAGCTGTGTCTCTCATGTGTAACTTTCTTAACCTCTCTTAACCTCTCTCTA 2620  
 QY 2347 ----- 2346  
 DB 2621 AACTCTTTTGTGCTCTTTCTTCCCTGCGGCGCTCCCAAGGCTTAAGGAGCAATTG 2680  
 QY 2347 ----- 2346

DB 2681 GTAGGTTAAGTAGATGGGCTCTGTGTGAGAGCCCTCTCTGTGCGCTGTGGGGCTGC 2740  
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 DB 2741 CCGGACCTTTTGTCTACCTCCAGCCAGCCCACTTCTCCCTGACCTGACTCC 2800  
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 DB 2801 TCCCTGACAGACTTGTGTGTGTGAAGAGCGGACTGTGAGCGAGGCCCTCGGCTCC 2860  
 QY 2398 AAGAAGCCATGAGCTACTCGTCTGACGAGGAGGTGGAAGACAGTGAAGAGAGAG 2457  
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 DB 2921 GAGGAAGCGGAAGCGGGCCAGCAGAGGGAGCAGAGATACCTCTGGGGCCCGAGAT 2980  
 QY 2518 GGGGATACAGACAGCTCAGACCATGTGTGTCCAGACGTCGAGAGATACCGGGAGC 2577  
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 QY 2998 TTCAACTCCGAGATCTCTGTGAGCCCTTTGGGGGCTCAACTGTGTGTGGGCAAGGAG 3057  
 DB 3461 TTCAACTCCGAGATCTCTGTGAGCCCTTTGGGGGCTCAACTGTGTGTGGGCAAGGAG 3520  
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 DB 3521 AACGGGCTGATGTGTGTGAGACCGAAGTGGGCAAGGAGTGTGTGATCTCAATTGGGCGG 3580  
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 QY 3178 AAAAGGAACAACTGCGGGGTGTATTACCTGTCTGTGCTCGGAACAAAGATTTGCAAT 3227  
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 DB 3701 GACCCAGAGTGTGAG 3760  
 QY 3298 CACTACGCTGTGTGAATATGAGAGGAGATTAAGTTCCTGTGATGAGCCCTCAAGAGCTCC 3357



Db 3761 CACTACCGTGTGTGAATAACGAGCGATTAAATTCTGTGATCGCCCTCAAGAGCTCC 3820  
Qy 3358 GTGAGAGGTATAGCTGGGGCCCCCAACCTTACCAAAATTTGATGGCCCTTCAAGCTTT 3417  
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Qy 3418 GCCGACCTTCCCCCAACCGCCCTTGTGTGTCGACCTGACAGTAGAGAGGGGCGGCTC 3477  
Db 3881 GCCGACCTTCCCCCAACCGCCCTTGTGTGTCGACCTGACAGTAGAGAGGGGCGGCTC 3940  
Qy 3478 AAGGTATATATAGCTTCAAGTGTGCTTCAATGCTGTGATGTGCACTCGGGAAACAGC 3537  
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Qy 3598 CTCCCAACACCGAGCGGATGAGATGCTGTGTGTCAGAGGAGAGGAGGCTTACGTC 3657  
Db 4061 CTCCCAACACCGAGCGGATGAGATGCTGTGTGTCAGAGGAGAGGAGGCTTACGTC 4120  
Qy 3658 AACAGTACGAGCGGATGATTAAGATGTGTGTGCTGACGTGGGGGAGATGCTTCT 3717  
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Qy 3718 GTGGCTTATATGCTTCCCAACAGATATAGGCTGGGGTGAAGAGCTTGAATCCG 3777  
Db 4181 GTGGCTTATATGCTTCCCAACAGATATAGGCTGGGGTGAAGAGCTTGAATCCG 4240  
Qy 3778 TCTGTGAGACGGGCGACCTGACGGGGCTTTCATGCAAAAGAGCTGAGGCTCAAG 3837  
Db 4241 TCTGTGAGACGGGCGACCTGACGGGGCTTTCATGCAAAAGAGCTGAGGCTCAAG 4300  
Qy 3838 TTCTGTGTGACGGAGATGACAAAGTGTGTTTCTGCTGACGCTCTGGGGGACAGC 3897  
Db 4301 TTCTGTGTGACGGAGATGACAAAGTGTGTTTCTGCTGACGCTCTGGGGGACAGC 4360  
Qy 3898 CAAGTTTACTTATGATCTGTAACCTGATCTGATCATGATCACTGGGAAAGGCG 3951  
Db 4361 CAAGTTTACTTATGATCTGTAACCTGATCTGATCATGATCACTGGGAAAGGCG 4414

RESULT 8

US-09-789-390-12  
; Sequence 12, Application US/09789390  
; Publication No. US20030059768A1  
; GENERAL INFORMATION:  
; APPLICANT: Vernet, Corine  
; APPLICANT: Fernandes, Elma  
; APPLICANT: Macdougall, John  
; APPLICANT: Shinkete, Richard A  
; APPLICANT: Spaderna, Steven K  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 15966-692  
; CURRENT APPLICATION NUMBER: US/09/789,390  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 60/185,548  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: 60/199,957  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 60/184,951  
; PRIOR FILING DATE: 2000-02-25  
; PRIOR APPLICATION NUMBER: 60/185,967  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 60/197,723  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 3735  
; TYPE: DNA  
; ORGANISM: Homo sapiens

; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1) .. (3732)  
US-09-789-390-12

Query Match 85.0%; Score 3158.2; DB 10; Length 3735;  
Best Local Similarity 92.7%; Pred. No. 0;  
Matches 3673; Conservative 0; Mismatches 38; Indels 252; Gaps 4;

Qy 7 ATGGCGACCCAGCGCCCGCCGAGCCTGAGACGATCGACCTGTCCGCCCTGCGGAC 66  
Db 1 ATGGCGACCCAGCGCCCGCCGAGCCTGAGACGATCGACCTGTCCGCCCTGCGGAC 60  
Qy 67 CCTGTGGGATCTTGTGACCTTGTGGAGGTGTGCGCAATGGAACCTTACGACAGGTATAC 126  
Db 61 CCTGTGGGATCTTGTGACCTTGTGGAGGTGTGCGCAATGGAACCTTACGACAGGTATAC 120  
Qy 127 AAGGTCGGCATGTTCAGAACGCGGCGACGCTGCTGCATCAAGTCAATGATGTCAAGAG 186  
Db 121 AAGGTCGGCATGTTCAGAACGCGGCGACGCTGCTGCATCAAGTCAATGATGTCAAGAG 180  
Qy 187 GACGAGGAGAAAGATGAACAGAGATGCAACATGCTGAAGAAAGTACTCTTCAACACGCG 246  
Db 181 GACGAGGAGAAAGATGAACAGAGATGCAACATGCTGAAGAAAGTACTCTTCAACACGCG 240  
Qy 247 AACATCGCACCTTACTACGAGCCTTCAACAAAGAGACCCCGGAGAAAGATGACGAG 306  
Db 241 AACATCGCACCTTACTACGAGCCTTCAACAAAGAGACCCCGGAGAAAGATGACGAG 300  
Qy 307 CTGTGGCTGTGATGAGTCTGTGTGCTGTGCTGTGCTGATGATGATGATGATGATGATGAT 366  
Db 301 CTGTGGCTGTGATGAGTCTGTGTGCTGTGCTGTGCTGTGATGATGATGATGATGATGATGAT 360  
Qy 367 AAAAGCAACGCCCTGAAAGAGACCTGTATCCCTATATCTGAGGAGATCTCAAGGGGT 426  
Db 361 AAAAGCAACGCCCTGAAAGAGACCTGTATCCCTATATCTGAGGAGATCTCAAGGGGT 420  
Qy 427 CTGGCCATCTTCATGACGCCCAAGAGTATGATGATGATGATGATGATGATGATGATGATGAT 486  
Db 421 CTGGCCATCTTCATGACGCCCAAGAGTATGATGATGATGATGATGATGATGATGATGATGAT 480  
Qy 487 CTGACAGAAATGCTGAGGTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 546  
Db 481 CTGACAGAAATGCTGAGGTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
Qy 547 ACCGTGGCAGACCGGAACAATTGATGAGACTCCCTGATGATGATGATGATGATGATGATGAT 606  
Db 541 ACCGTGGCAGACCGGAACAATTGATGAGACTCCCTGATGATGATGATGATGATGATGATGAT 600  
Qy 607 GCCTGTGATGAAACCTGATGACCACTATGATTTACAGAGTATATTTGCTCTTACGGA 666  
Db 601 GCCTGTGATGAAACCTGATGACCACTATGATTTACAGAGTATATTTGCTCTTACGGA 660  
Qy 667 ATCACAGCATGAGATGAGCAGAGGAGCCCGCCCTGTGTGTGATGATGATGATGATGATGAT 726  
Db 661 ATCACAGCATGAGATGAGCAGAGGAGCCCGCCCTGTGTGTGATGATGATGATGATGATGAT 720  
Qy 727 GCCCTTCTTCATTCCTCGAAACCTTCGCCGAGGCTCAAGTCCAAGAGGTCTAAG 786  
Db 721 GCCCTTCTTCATTCCTCGAAACCTTCGCCGAGGCTCAAGTCCAAGAGGTCTAAG 780  
Qy 787 AAGTTCATTGACTTATGATGACATGTCTCATCAAGACTTACCTGAGCGGCCACCCACG 846  
Db 781 AAGTTCATTGACTTATGATGACATGTCTCATCAAGACTTACCTGAGCGGCCACCCACG 840  
Qy 847 GAGCAGCTACTGAAGTTCCTTCAATCCGGAACGACCAAGAGCGGCGAGTCCGATC 906  
Db 841 GAGCAGCTACTGAAGTTCCTTCAATCCGGAACGACCAAGAGCGGCGAGTCCGATC 900  
Qy 907 CAGCTTAAGAGACCAATGATCCGAGAAAGAGCGGGGTGAGAAAGAGAGACAGAA 966  
Db 901 CAGCTTAAGAGACCAATGATCCGAGAAAGAGCGGGGTGAGAAAGAGAGACAGAA 960



OY	967	TATGAGTACACCGGACGGAGGAGGAAATGACAGCCTTGGAGAGGAAGAGACCAAGC	1028
Db	961	TATGAGTACACCGGACGGAGGAGGAAATGACAGCCTTGGAGAGGAAGAGACCAAGC	1020
OY	1027	TCATCATGAAGCTGCTCGAGAGAGTGCATCTCAACCGCGGAGATTCTCCGCTCCAGCAG	1086
Db	1021	TCATCATGAAGCTGCTCGAGAGAGTGCATCTCAACCGCGGAGATTCTCCGCTCCAGCAG	1080
OY	1087	GAATAATGAAGCACTCAGAGCTTTAAACACAGCAGCAGCTGCGACAGCAGCAGCAG	1146
Db	1081	GAATAATGAAGCACTCAGAGCTTTAAACACAGCAGCAGCTGCGACAGCAGCAGCAGCAG	1140
OY	1147	CGAGACCCCGGAGCACAATCAACACTCTGCTGCACAGCGCGCAGCGCGCATAGAGAG	1206
Db	1141	CGAGACCCCGGAGCACAATCAACACTCTGCTGCACAGCGCGCAGCGCGCATAGAGAG	1200
OY	1207	CAGAAAGAGAGCGCGCGCGCGCTGGAGAGCAACAGCGCGGAGACGGAGACAGCGAGAG	1266
Db	1201	CAGAAAGAGAGCGCGCGCGCGCTGGAGAGCAACAGCGCGGAGACGGAGACAGCGAGAG	1260
OY	1267	CTGCAGAGAGAGAGCAGCAGCAGCGCGCGCTGGAGACATGCAAGCTCTTGCGCGGAGAG	1326
Db	1261	CTGCAGAGAGAGAGAGCAGCAGCAGCGCGCTGGAGACATGCAAGCTCTTGCGCGGAGAG	1320
OY	1327	GAGCGGCGGCGCAGCGGAGCGTAGACAGAAATACAGCGAGACAGCTGAGAGACAGCG	1386
Db	1321	GAGCGGCGGCGCAGCGGAGCGTAGACAGAAATATATTCCTCAAGCTTAGAGAGACAGCG	1380
OY	1387	CAGTCAGAACCTCTTCCAGAGCAGCTTGACAGAGAGCAATGCTCAACTCAATCCCTGAG	1446
Db	1381	CAGTCAGAACCTCTTCCAGAGCAGCTTGACAGAGAGCAATGCTCAACTCAATCCCTGAG	1440
OY	1447	CAGCAGCAACAGCAGCAGCAGCTTCAAGAAACAGCAGCAGCAGCAGCTCTCGGAGAC	1506
Db	1441	CAGCAGCAACAGCAGCAGCAGCAGCTTCAAGAAACAGCAGCAGCAGCAGCTCTCGGAGAC	1500
OY	1507	AGGAAGCCCTGTACCAATTATGTCGGGACATGAATCCCGCTGACAAACAGCTGGGCGC	1566
Db	1501	AGGAAGCCCTGTACCAATTATGTCGGGACATGAATCCCGCTGACAAACAGCTGGGCGC	1560
OY	1567	CGAGAGTGTGAAGAGAGAAACAAGATGAACAGCAGCAGAACTCTCCCTTGCCAAAGAC	1626
Db	1561	CGAGAGTGTGAAGAGAGAAACAAGATGAACAGCAGCAGAACTCTCCCTTGCCAAAGAC	1570
OY	1627	AAGCAGAGCAGACAGCGGCGCTGAGCGCCCAATCCCGCAGGCTCCCGAGGCGCCCAAGA	1686
Db	1571	-----TGGCACACCGGGTCCCATGAAGCCATATGACAGACCTGTA	1611
OY	1687	CCCTTTCCAGACCTCTCTATGCAAGGCGGTCGAGGCCCAAGAGGACCGCACAG	1746
Db	1612	CCCGATCC-----AG	1623
OY	1747	TCCCTGCAGACACAGCCCACTCGGAAACTGGCTGCTTCCAGCTCCCATGACCCGAC	1806
Db	1624	TCCCTGCAGACACAGCCCACTCGGAAACTGGCTGCTTCCAGCTCCCATGACCCGAC	1683
OY	1807	CCTGCATATCCCGGACCCGACTGCGACAGCGCCAGTGCACGAGGAGCTGTCAATCCGACAGAT	1866
Db	1684	CCTGCATATCCCGGACCCGACTGCGACAGCGCCAGTGCACGAGGAGCTGTCAATCCGACAGAT	1743
OY	1867	TCAGACCCCACTCTGAAGAGACTTGGCCCCAGCCGGAATCCCGCAGCTTGCGTCCGCCA	1926
Db	1744	TCAGACCCCACTCTGAAGAGACTTGGCCCCAGCCGGAATCCCGCAGCTTGCGGTCCGCCA	1803
OY	1927	GATTAACGAGGCCCCCAAGGTCCTCAAGAGACTTCATCTATGCACTTGCCCTTAAC	1986
Db	1804	GATTAACGAGGCCCCCAAGGTCCTCAAGAGACTTCATCTATGCACTTGCCCTTAAC	1863
OY	1987	ACCAATGGGGCGGAGGGTCCCGGACAGCCAGGAGATCCATGCGAGACCTCGACGAC	2046
Db	1864	ACCAATGGGGCGGAGGGTCCCGGACAGCCAGGAGATCCATGCGAGTCCGAGC-----	1908
OY	2047	TCCGCTGGCAAAATCTATCTGCAAAAGCGGCGCAGACCGGCGACCCCAAGCCTTCAAGG	2106

Db	1909	-----	1908	-----
OY	2107	CCCCCTGTCAGCCCCCTGGCCCGCAACGCTCTAGTAAACCCCGACTTCGAGAGAC	2166	
Db	1909	-----	AGTAAACCCGACCTCAGAGGAGC	1932
OY	2167	GACCTTGCTGGGAACGCTCGGAACAGGCTCTTCCACCTCTCAACGCGCACCTCCCCAG	2226	
Db	1933	GACCTTGCTGGGAACGCTCGGAACAGGCTCTTCCACCTCTCAACGCGCACCTCCCCAG	1992	
OY	2227	GCTGGCTCACTGAGCGGGAACCGGCTGGAGACTCTCCAAACTGGAACAGCTCCCTGTG	2286	
Db	1993	GCTGGCTCACTGAGCGGGAACCGGCTGGAGACTCTCTCCAAACCGGACAGCTCCCTGTG	2052	
OY	2287	CTCTCCCCCTGGGAATTAAGCCAAACCCGACGACACCGCTCAACGCGCAAGCCGACCCGCA	2346	
Db	2053	CTCTCCCCCTGGGAATTAAGCCAAACCCGACGACACCGCTCAACGCGCAAGCCGACCCGCA	2112	
OY	2347	-----GACTTGTGTGTGAATAAGCCGACCTCTGAAGAG	2382	
Db	2113	AGCTATAAGCGAGCAATTGTGAGAGACTTGTGTGCTGAATAAGCCGACTCTGAGAGAG	2172	
OY	2383	GCCCCCTGGGCTCCCAAGAAAGGCATGAGACTACCTGCTGTCACACGAGAGGTGAAGAAGC	2442	
Db	2173	GCCCCCTGGGCTCCCAAGAAAGGCATGAGACTACCTGCTGTCACACGAGAGGTGAAGAAGC	2232	
OY	2443	AGTAGAGACGACGAGAGGAAGAGCGAAAGCGCGGCCAGACAGAGGGAGCAGATATCCCTT	2502	
Db	2233	AGTAGAGACGACGAGAGGAAGAGCGAAAGCGCGGCCAGACAGAGGGAGCAGATATCCCTT	2292	
OY	2503	GGGGGGCGGACGACATGAGGGAATACAGACAGCTACGACAAATGAGTGTCCACAGTGGAG	2522	
Db	2293	GGGGGGCGGACGACATGAGGGAATACAGACAGCTACGACAAATGAGTGTCCACAGTGGAG	2352	
OY	2563	GAGATCAACCGGGAACCCAGCCGCCATTAAGCGGGCGGACCAATGAGTGTCCACAGCCCTT	2622	
Db	2253	GAGATCAACCGGGAACCCAGCCGCCCATTAAGGGGGCGGACCAATGAGTGTCCACAGCCCTT	2412	
OY	2623	GAAAGAGAGCGGAACCTGCTGACTGTCAGACGATGGGTAACAAACCTGCTGAGCTG	2682	
Db	2413	GAAAGAGAGCGGAACCTGCTGACTGTCAGACGATGGGTAACAAACCTGCTGAGCTG	2472	
OY	2683	GTCAGGCCGAGGCCCTACACCCACCGGAACAAGCAAAAGGCCAACCCACCTCGAAGGAT	2742	
Db	2473	GTCAGGCCGAGGCCCTACACCCACCGGAACAAGCAAAAGGCCAACCCACCTCGAAGGAT	2532	
OY	2743	GGGAGGTGTACTACAGTCTCTGCGGCTGTGTAAGGCCCTCTGCAAGAGCTCGTTACG	2802	
Db	2533	GGGAGGTGTACTACAGTCTCTGCGGCTGTGTAAGGCCCTCTGCAAGAGCTCGTTACG	2592	
OY	2803	ATGTTTGTGATCTTAGGGATCTTACACGCTGGAGGCAAGTGGGGAACAGATCCCATCA	2862	
Db	2593	ATGTTTGTGATCTTAGGGATCTTACACGCTGGAGGCAAGTGGGGAACAGATCCCATCA	2652	
OY	2863	GCCCTAGGGGTGGAAGGGGCACTCGGCTGGAACAGCTGCAAGTACGACGTGAGAAAGGT	2922	
Db	2653	GCCCTAGGGGTGGAAGGGGCACTCGGCTGGAACAGCTGCAAGTACGACGTGAGAAAGGT	2712	
OY	2923	TCTGTGTGTCACGTGAATCCCAACCAACCCGCGCCCAAGTGAACCCCTGAGATCCGG	2982	
Db	2713	TCTGTGTGTCACGTGAATCCCAACCAACCCGCGCCCAAGTGAACCCCTGAGATCCGG	2772	
OY	2983	AAAGTAAAGAAAGCAATTCACACTCCGAGATCTCTGTGACAGCCCTTTGGGGGTCAACTG	3042	
Db	2773	AAAGTAAAGAAAGCAATTCACACTCCGAGATCTCTGTGACAGCCCTTTGGGGGTCAACTG	2832	
OY	3043	CTGGTGGGCAACGAGAAACGGGCTAGTGTGCTGGAACGAAAGTGGGACGGGCAAGGTAT	3102	
Db	2833	CTGGTGGGCAACGAGAAACGGGCTAGTGTGCTGGAACGAAAGTGGGACGGGCAAGGTAT	2892	
OY	3103	GGACTCAATTGGGCGGCGACGCTTCCAGACAGTGAATGTCTGAGGGGCTTCAACTGCTC	3162	



QY	727	GCCTCTTCTCATTCTCTGGAACTCTCCGCCAGGCTTCAGAGTGGTCTTAAG	786
Db	721	GCCCTCTTCTCATTCTCTGGAACTCTCCGCCAGGCTTAAGTCCAAAGATGGTCTTAAG	780
QY	787	AAGTTCATTGACCTTATTGACACATGTCATCAGACTTACCTAGCGCGCCACCCAG	846
Db	781	AAGTTCATTGACTTATTGACACATGTCATCAGACTTACCTAGCGCGCCACCCAG	840
QY	847	GAGCAGCTACTGAAATTTCTCCCTTCATCGGGGACCAAGCCACGAGCGCAGGTCCGATC	906
Db	841	GAGCAGCTACTGAAATTTCTCCCTTCATCGGGGACCAAGCCACGAGCGCAGGTCCGATC	900
QY	907	CAGCTTAAAGACCACTTGAACCGATCCCGGAAAGACGGGGGTGAGAAAGAGACACAGA	966
Db	901	CAGCTTAAAGACCACTTGAACCGATCCCGGAAAGACGGGGGTGAGAAAGAGACACAGA	960
QY	967	TATAGATCACCGGAGGAGGAGGAGAAATGACACCCATGAGAGAGAGAGAGCAAG	1026
Db	961	TATAGATCACCGGAGGAGGAGGAGAAATGACACCCATGAGAGAGAGAGAGCAAGC	1020
QY	1027	TCCATCATGAAAGTCCCTGAGAGATCGACTCTACCCGGGAGTTTCTCCGGCTCCAGCAG	1086
Db	1021	TCCATCATGAAAGTCCCTGAGAGATCGACTCTACCCGGGAGTTTCTCCGGCTCCAGCAG	1080
QY	1087	GAAATTAAGACCACTCAGAGGCTTTAAACACGACGACGACGCTGCACGACGACGACG	1146
Db	1081	GAAATTAAGACCACTCAGAGGCTTTAAACACGACGACGACGCTGCACGACGACGACG	1140
QY	1147	CGAAGCCCCGAGGACACATCAAACACTGCTGACACAGCCGACAGCGCCGATAGAGAG	1206
Db	1141	CGAGCCCCGAGGACACATCAAACACTGCTGACACAGCCGACAGCGCCGATAGAGAG	1200
QY	1207	CAGAAAGAGAGCGCGCGCGCTGGAGAGCAACACGCGCGGAGCGGAGACAGCGCAAG	1266
Db	1201	CAGAAAGAGAGCGCGCGCGCTGGAGAGCAACACGCGCGGAGCGGAGACAGCGCAAG	1260
QY	1267	CTGCAGAGGAAGAGACAGCAGCGCGCGCTGAGAGCATGCAAGCTCTCGCGCGGAGAG	1326
Db	1261	CTGCAGAGGAAGAGACAGCAGCGCGCGCTGAGAGCATGCAAGCTCTCGCGCGGAGAG	1320
QY	1327	GAGCGGCGGACGAGCGGAGCTGTAGCA	1352
Db	1321	GAGCGGCGGACGAGCGGAGCTGTAGCA	1380
QY	1353	-----GGAAATAC	1359
Db	1381	CGACAGCTCGAGATCTTTCAGACACAGCTCTCCAGGAACAGGCCCTCTGCTGGAATAC	1440
QY	1360	AAGCGGAAGCAGCTGGAGAGCAGCGCGAGTCAGAACGTCCTTCAGAGGACGCTGCACAG	1419
Db	1441	AAGCGGAAGCAGCTGGAGAGAGAGCGGAGTCAGAACGTCCTTCAGAGGACGCTGCACAG	1500
QY	1420	GAGCATGCTTACCTCAAGTCCCTTCGACGACGACCAACGACGACGACGACTTCAGAAACAG	1479
Db	1501	GAGCATGCTTACCTCAAGTCCCTTCGACGACGACCAACGACGACGACGACTTCAGAAACAG	1560
QY	1480	CAGCAGCAGCAGCTCTGCTGGGAGACAGAAAGCCCTGTACATTAATGATCGGGGACATG	1539
Db	1561	CAGCAGCAGCAGCTCTGCTGGGAGACAGAAAGCCCTGTACATTAATGATGCGGGGACATG	1620
QY	1540	AATCCCGCTGACAAACCAAGCTGGGCGCGAGAGTGAAGAGAGAACAAAGATGACAAAG	1599
Db	1621	AATCCCGCTGACAAACCAAGCTGGGCGCGAGAGTGAAGAGAGAACAAAGATGACAAAG	1657
QY	1600	CAGCAGAACTCTCCCTTGGCCAGAGCAAGCCAGGACAGCGGGGCTGTAGCCCCCATC	1659
Db	1658	-----TGGACACACCGGCTC	1671
QY	1660	CCCCAGGCTCCCAAGGGCCCCAGGAACCCCTTCCAGAGCTCCTCCTATGACAGGCGG	1719
Db	1672	CCACTGAAGCAATATGTCAGACACTTACCCCGATCC-----	1708
QY	1720	GTGAGCCCCAGAGGGAACGCAACAAGTCCCTGTCAGGACAGGCCACCCGAACTCGGCT	1779

Db	1709	-----AGTCCCTGAGAGCCAGGCCACCCGAAACCTGGCT	1743
Qy	1780	GCCTTCCAGGCTCCATGACCCCGACCCCTGCATCCCGGACCCCATCTGCCAGCCCACT	1839
Db	1784	GCCTTCCAGGCTCCATGACCCCGACCCCTGCATCCCGGACCCCATCTGCCAGCCCACT	1803
Qy	1840	GCCCCAGGAGCTGTTCATCCGCAGAAATTGACACCCCACTCTGAAGACCTGGCCCCAGC	1899
Db	1804	GCCCCAGGAGCTGTTCATCCGCAGAAATTGACACCCCACTCTGAAGACCTGGCCCCAGC	1863
Qy	1900	CCGAATCCCCCAGGCTGGGTCCGCCAGATPACAGAGCCCCACCAAGGTGGCTCAGAGG	1959
Db	1864	CCGAATCCCCCAGGCTGGGTCCGCCAGATPACAGAGCCCCACCAAGGTGGCTCAGAGG	1923
Qy	1960	AACCTATCTATCGCACCTGACCCTTAAACACAGTGGGGCCGGAGGGTCCGGCCAGCCAG	2019
Db	1924	AACCTATCTATCGCACCTGACCCTTAAACACAGTGGGGCCGGAGGGTCCGGCCAGCCAG	1983
Qy	2020	GCAGTCCGTGCGCAGACCTTCGAGCACTCGCCTGGCAAAATCTATCTGCAAAAGCGGCA	2079
Db	1984	GCAGTCCGTGCGC-----1995	1995
Qy	2080	GAGCGGGGACCCCAAAAGCTTCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCAAAGCC	2139
Db	1996	-----1995	1995
Qy	2140	TCTAGTAAACCCCGACCTCAGGAGGAGGACCCCTGGCTGGGAAACGCTCGSACAGCTCTT	2199
Db	1996	---AGTAAACCCCGACCTCAGGAGGAGGACCCCTGGCTGGGAAACGCTCGSACAGCTCTT	2052
Qy	2200	CCAGGCTCTCAGGGGACCTTCCCGCAGCTGGCTCACTGAGCCGAAACCGGCTGGAGCC	2259
Db	2053	CCAGGCTCTCAGGGGACCTTCCCGCAGCTGGCTCACTGAGCCGAAACCGGCTGGAGCTC	2112
Qy	2260	TCTCTCAAACCTGACACGCTCCCCCTGTGTCTCTCCCTTGGGAAATAAGCCAAAGCCGAGAC	2319
Db	2113	TCTCTCAAACCTGACACGCTCCCCCTGTGTCTCTCCCTTGGGAAATAAGCCAAAGCCGAGAC	2172
Qy	2230	CACCGCTCAGGGGACGAGGCGGCGCCGCA-----GACTTTGTG	2355
Db	2173	CACCGCTCAGGGGACGAGGCGGCGCCGCAAGCTATAAGGAGCATTTGGTAGAGACTTTGTG	2232
Qy	2236	TTGCTGAAGAAGCGGACTTGTGAGCGAGGCCCCCTCGGCTCTCCCAAGAAAGCCATGACTAC	2415
Db	2233	TTGCTGAAGAAGCGGACTTGTGAGCGAGGCCCCCTCGGCTCTCCCAAGAAAGCCATGACTAC	2292
Qy	2416	TCTGTCTCAGCGAGAGGTGGAAGACGTGAGGACGACGAGAGGAAAGGCGGAGCGGG	2475
Db	2293	TCTGTCTCAGCGAGAGGTGGAAGACGTGAGGACGACGAGAGGAAAGGCGGAGCGGG	2352
Qy	2476	CCACGAGAGGGGAGCAGAGATACCCCTGGGGGGCGGACGATGGGGATACAGACAGGCTC	2535
Db	2353	CCACGAGAGGGGAGCAGAGATACCCCTGGGGGGCGGACGATGGGGATACAGACAGGCTC	2412
Qy	2536	AGCACCATGTGTGTCCACGAGTCCGAGGAGATCACCGGAGCCACGCCCCCATATCGGGGGC	2595
Db	2413	AGCACCATGTGTGTCCACGAGTCCGAGGAGATCACCGGAGCCACGCCCCCATATCGGGGGC	2472
Qy	2596	GGCACCATGTGTGTCCAGCGGACCCCTGGAAGAGGAGCGGAAACCTGTGCACTGTCAGAC	2655
Db	2473	GGCACCATGTGTGTCCAGCGGACCCCTGGAAGAGGAGCGGAAACCTGTGCACTGTCAGAC	2532
Qy	2656	AATGGGATACAAACCTGCGTGAAGTGGTCCAGGCCAGGACCTACACCACGAGAAACAGC	2715
Db	2533	AATGGGATACAAACCTGCGTGAAGTGGTCCAGGCCAGGACCTACACCACGAGAAACAGC	2592
Qy	2716	AAAGGCCAAAGCCACCTCGAAGAGTGGAGTGGTACTTACACAGTCTGTGGCTGGTA	2775
Db	2593	AAAGGCCAAAGCCACCTCGAAGAGTGGAGTGGTACTTACACAGTCTGTGGCTGGTA	2652
Qy	2776	AAAGGCCCTGGCAAGAGCTGGTTACGATGTTTGTGATCTTAAAGGATCTACAGGCTTGA	2835



Qy 490 ACAGAGAAATGCTGAGAGTCAAGTGAATTTGGGGTGAAGTCTCACTGAGCCGACCC 549  
Db 481 ACAGAGAAATGCTGAGAGTCAAGTGAATTTGGGGTGAAGTCTCACTGAGCCGACCC 540  
Qy 550 GTGGGACAGACGGAACATTTTCAATGGGACTCCCTCACTGATGGCTCAAGAGTCAATGCGC 609  
Db 541 GTGGGACAGACGGAACATTTTCAATGGGACTCCCTCACTGATGGCTCAAGAGTCAATGCGC 600  
Qy 610 TGTGATGAGAACCTTGATGCCACTATGATTAACAGAGTGAATTTGGTCTCTAGGAATC 669  
Db 601 TGTGATGAGAACCTTGATGCCACTATGATTAACAGAGTGAATTTGGTCTCTAGGAATC 660  
Qy 670 ACAGACCTGAGATGAG 729  
Db 661 ACAGACCTGAGATGAG 720  
Qy 730 CTCTTCCCTCAATTCCTGAGAACCTTCGCGGCAAGGCTCAAGTCCAGAGAGTGGTCTTAAGAG 789  
Db 721 CTCTTCCCTCAATTCCTGAGAACCTTCGCGGCAAGGCTCAAGTCCAGAGAGTGGTCTTAAGAG 780  
Qy 790 TTCAATGACTTCAATGACACATGCTCTCAACAAGCTTCACTGAGCCGCGCAACCCAGAG 849  
Db 781 TTCAATGACTTCAATGACACATGCTCTCAACAAGCTTCACTGAGCCGCGCAACCCAGAG 840  
Qy 850 CAGCTACTGAAGTTTCCCTTCAATCCGAGACCAAGCCAGAGAGAGAGAGAGAGAGAGAG 909  
Db 841 CAGCTACTGAAGTTTCCCTTCAATCCGAGACCAAGCCAGAGAGAGAGAGAGAGAGAGAG 900  
Qy 910 CTTAAGAGACCAATTTGACCGGATCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGATAT 969  
Db 901 CTTAAGAGACCAATTTGACCGGATCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGATAT 960  
Qy 970 GAGTACAGCGGACAGTCC 1029  
Db 961 GAGTACAGCGGACAGTCC 1020  
Qy 1030 ATCATGAACTGCTGAGAGAGTCACTTCAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAA 1089  
Db 1021 ATCATGAACTGCTGAGAGAGTCACTTCAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAA 1080  
Qy 1090 AATTAAGAGCACTGAGAGAGCTTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1149  
Db 1081 AATTAAGAGCACTGAGAGAGCTTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
Qy 1150 GACCCGAGAGAGACATCAAAACCTGCTGACACAGCGGACAGCGGACGATAGAGAGAGAG 1209  
Db 1141 GACCCGAGAGAGACATCAAAACCTGCTGACACAGCGGACAGCGGACGATAGAGAGAGAG 1208  
Qy 1210 AAGGAGTGT 1269  
Db 1201 AAGGAGTGT 1260  
Qy 1270 CAGGAG 1329  
Db 1261 CAGGAG 1320  
Qy 1330 CGGCGGAG 1389  
Db 1321 CGGCGGAG 1380  
Qy 1390 TCAGAACTGCTCAAG 1449  
Db 1381 TCAGAACTGCTCAAG 1440  
Qy 1450 CAGGAG 1509  
Db 1441 CAGGAG 1500  
Qy 1510 AAGCCCTGATCAATTAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1569  
Db 1501 AAGCCCTGATCAATTAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560

Qy 1570 GAGGTAG 1576  
Db 1561 GAGGTAG 1567

RESULT 11  
US-09-925-297-137  
Sequence 137, Application US/09925297  
Patent No. US2002081659A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: P105  
CURRENT APPLICATION NUMBER: US/09/925,297  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05989  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 928  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 137  
LENGTH: 2345  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (184)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (139)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (1805)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (1887)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (2325)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (2339)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-297-137

Query Match 38.0%; Score 1502.6; DB 9; Length 2345;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 1527; Conservative 3; Mismatches 8; Indels 2; Gaps 2;

Qy 2413 TACTGTGCTCCAGCGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2472  
Db 1 TACTGTGCTCCAGCGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60  
Qy 2473 GGGCCAGACAG 2532  
Db 61 GGGCCAGACAG 120  
Qy 2533 GTGAGACAGATGAGTGTCCAG 2592  
Db 121 GTCA-CACCATGAGTGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 179  
Qy 2593 GGGCGACCATGAGTGTGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2652  
Db 180 GGGCGACCATGAGTGTGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 239  
Qy 2653 AGCAATGGGTACCAAACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2712  
Db 240 AGCAATGGGTACCAAACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 299  
Qy 2713 AGCAAAAGCCAAAGCCCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2771  
Db 300 AGCAAAAGCCAAAGCCCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 359

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QY 2772 GGTAAAGGCCCCCTGGCAAGAGCTCGTTCAGATGTTTGGATCTAGGGATCTACAGCC 2831
DB 360 GGTAAAGGCCCCCTGGCAAGAGCTCGTTCAGATGTTTGGATCTAGGGATCTACAGCC 419
QY 2832 TGGAGGCAAGTGGGGAAGAGATCCCATCAAGCCCTTAGTGGGTGAGAGAGGCACTGGCT 2891
DB 420 TGGAGGCAAGTGGGGAAGAGATCCCATCAAGCCCTTAGTGGGTGAGAGAGGCACTGGCT 479
QY 2892 CGACCAAGCTGCAATACAGATGAGAGAGGTTCTGTGTCAACGTGAATCCCAACCAAC 2951
DB 480 CGACCAAGCTGCAATACAGATGAGAGAGGTTCTGTGTCAACGTGAATCCCAACCAAC 539
QY 2952 CGGGGCCCCAAGTGAAGACCCCTGAGATCCGGAAGTACAAGAGCAATTCACCTCCGAGAT 3011
DB 540 CGGGGCCCCAAGTGAAGACCCCTGAGATCCGGAAGTACAAGAGCAATTCACCTCCGAGAT 599
QY 3012 CCTGTGTGAGCCCTTTTGGGGGGGTCAACCTGTGTGGGCAAGAGAACGGGCTGATGTT 3071
DB 600 CCTGTGTGAGCCCTTTTGGGGGGGTCAACCTGTGTGGGCAAGAGAACGGGCTGATGTT 659
QY 3072 GGTGACCGAAGTGGGCAAGGCAAGTGTATGACATCTTAGGCGGCAAGCTTCCAGCA 3131
DB 660 GGTGACCGAAGTGGGCAAGGCAAGTGTATGACATCTTAGGCGGCAAGCTTCCAGCA 719
QY 3132 GATGATGTGTGAGAGGGGCTCAACCTGTCTACACATCTGAGGGAAGAAAGAACT 3191
DB 720 GATGATGTGTGAGAGGGGCTCAACCTGTCTACACATCTGAGGGAAGAAAGAACT 779
QY 3192 GGGGGTGTATTAATCTGTCTGTGCTCGGAACAAATTCGCAATGACCCAGAAAGTGA 3251
DB 780 GGGGGTGTATTAATCTGTCTGTGCTCGGAACAAATTCGCAATGACCCAGAAAGTGA 839
QY 3252 GAAAGAGCAGGGCTGAGCAACCGTGGGGGACATGAGAGGCTCGGGCACTAACCGTGT 3311
DB 840 GAAAGAGCAGGGCTGAGCAACCGTGGGGGACATGAGAGGCTCGGGCACTAACCGTGT 899
QY 3312 GAAATACGAGCGGATTAAGTTCTGTGTCACTCGCCCTCAAGAGCTCCGTGAGAGTATGC 3371
DB 900 GAAATACGAGCGGATTAAGTTCTGTGTCACTCGCCCTCAAGAGCTCCGTGAGAGTATGC 959
QY 3372 CTGGGCCCCCAACCTTACCAAAATTCATGAGCTTCAAGTCTTTCGCAAGCTCCCA 3431
DB 960 CTGGGCCCCCAACCTTACCAAAATTCATGAGCTTCAAGTCTTTCGCAAGCTCCCA 1019
QY 3432 CGGCCCCCTGTGTGTGACCTTGAAGTAAAGAGGGGCGGGCTCAAGTCTTATG 3491
DB 1020 CGGCCCCCTGTGTGTGACCTTGAAGTAAAGAGGGGCGGGCTCAAGTCTTATG 1079
QY 3492 CTGCAAGTGTGCTTCAATGCTGTGAGTGTGCACTCGGGGAACAGCTATGACATCAAT 3551
DB 1080 CTGCAAGTGTGCTTCAATGCTGTGAGTGTGCACTCGGGGAACAGCTATGACATCAAT 1139
QY 3552 CCCTGTGCAATTCAGAGCCAGATCAAGCCCATGCAATCTTCTCTCCCAACCGCA 3611
DB 1140 CCCTGTGCAATTCAGAGCCAGATCAAGCCCATGCAATCTTCTCTCCCAACCGCA 1199
QY 3612 CGGCAATGAGATGCTGTGTGTGACAGAGAGGCTGTACATCAACAGCTTACGGGG 3671
DB 1200 CGGCAATGAGATGCTGTGTGTGACAGAGAGGCTGTACATCAACAGCTTACGGGG 1259
QY 3672 CATCATTAAGATGTGTGTGCTGCAAGTGGGGGAGATGCTTACTTGTGGCTCAATCTG 3731
DB 1260 CATCATTAAGATGTGTGTGCTGCAAGTGGGGGAGATGCTTACTTGTGGCTCAATCTG 1319
QY 3732 CTGCAACCAAGATTAAGGCTGGGGTGAAGAACCATTTGAATCCGCTCTGTGGAAGCGG 3791
DB 1320 CTGCAACCAAGATTAAGGCTGGGGTGAAGAACCATTTGAATCCGCTCTGTGGAAGCGG 1379
QY 3792 CCACTCTGACGGGGTCTTATGCAAAAGAGCTCAAGAGCTCAAGTTCTGTGTGAGG 3851
DB 1380 CCACTCTGACGGGGTCTTATGCAAAAGAGCTCAAGAGCTCAAGTTCTGTGTGAGG 1439

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QY 3852 GAATGACAGAGTGTGTTTTTGGCTCAGTCCGCTCTGAGGGGCAAGCAAGCTTACTTCAAT 3911
DB 1440 GAATGACAGAGTGTGTTTTTGGCTCAGTCCGCTCTGAGGGGCAAGCAAGCTTACTTCAAT 1499
QY 3912 GACTCTGAACCGTAACTGCAATCAATGAATGAGTGAAGGGC 3951
DB 1500 GACTCTGAACCGTAACTGCAATCAATGAATGAGTGAAGGGC 1539

RESULT 12
US-09-789-390-66
; Sequence 66, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
; APPLICANT: Vermet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: MacDougall, John
; APPLICANT: Shinkels, Richard A
; APPLICANT: Spaderna, Steven K
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-692
; CURRENT APPLICATION NUMBER: US/09/789,390
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185,548
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/199,957
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/184,951
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/185,967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/197,723
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 1787
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-789-390-66

Query Match 37.2%; Score 1468.4; DB 10; Length 1787;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 1566; Conservative 0; Mismatches 1; Indels 87; Gaps 1;

QY 10 GGGGACCGAGGCCCGGCGGAGCTGAGCAAGATGCACTGTCCGCGCTGGGGAGCCCT 69
DB 1 GGGGACCGAGGCCCGGCGGAGCTGAGCAAGATGCACTGTCCGCGCTGGGGAGCCCT 60
QY 70 GCTGGATCTTGTGAGCTTGTGAGGTGTGCGCAATGGAACCTACGGAAGGTGTACAAG 129
DB 61 GCTGGATCTTGTGAGCTTGTGAGGTGTGCGCAATGGAACCTACGGAAGGTGTACAAG 120
QY 130 GGTGGCAATGTCAGAGCGGGGCACTGCTGTCATCAAGTGTATGATGTACAGAGAC 189
DB 121 GGTGGCAATGTCAGAGCGGGGCACTGCTGTCATCAAGTGTATGATGTACAGAGAC 180
QY 190 GAGGAGGAAGATCAAAACAGAGATCAACATGCTGAAGAAAGTACTTCAACACCGCAAC 249
DB 181 GAGGAGGAAGATCAAAACAGAGATCAACATGCTGAAGAAAGTACTTCAACACCGCAAC 240
QY 250 ATGCGCACTTACTAGAGACCTTCAATCAAGAGACCCCGGGAACAGATGACCAAGCTC 309
DB 241 ATGCGCACTTACTAGAGACCTTCAATCAAGAGACCCCGGGAACAGATGACCAAGCTC 300
QY 310 TGGCTGTGATGAGATTTGTGTGTGCTGTGTTCAAGTGAATCTGTGAAGAACCAAAA 369
DB 301 TGGCTGTGATGAGATTTGTGTGTGCTGTGTTCAAGTGAATCTGTGAAGAACCAAAA 360
QY 370 GCGCAAGCCCTGAAGAGAGAGCTGTATGCGCTATATCTGCAAGGAGATCTTCAAGGGGTCTG 429
DB 361 GCGCAAGCCCTGAAGAGAGAGCTGTATGCGCTATATCTGCAAGGAGATCTTCAAGGGGTCTG 420

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Qy	430	ACCCATCTCCCATGCCCAAGGTTTTCATCGAGCATCAAGGGGCAGAAATGTGTGCTG	489
Db	421	GCCCATCTCCCATGCCCAAGGTTGATTCATCGAGCATCAAGGGGCAGAAATGTGTGCTG	480
Qy	490	ACAGAGAAATGCTGAGGTCAAGCTATGGAATTTTGGGGTGAAGTCTCAGCTGGACCGCAC	549
Db	481	ACAGAGAAATGCTGAGGTCAAGCTATGGAATTTTGGGGTGAAGTCTCAGCTGGACCGCAC	540
Qy	550	GTGGGCGACGGAACAATTTCATTGGGACTCCCTACGTGATGCTCCAGAGTCAATGCTCC	609
Db	541	GTGGGCGACGGAACAATTTCATTGGGACTCCCTACGTGATGCTCCAGAGTCAATGCTCC	600
Qy	610	TGTGATGGAACCCCTGATGCCACTATGATTTACAGAGTGAATTTTGGTCTCTAGAAATC	669
Db	601	TGTGATGGAACCCCTGATGCCACTATGATTTACAGAGTGAATTTTGGTCTCTAGAAATC	660
Qy	670	ACAGCCATCGAGATGAGCAGAGGAGACCCCTCTGTGTGACATGCAACCCATGGAAGCC	729
Db	661	ACAGCCATCGAGATGAGCAGAGGAGACCCCTCTGTGTGACATGCAACCCATGGAAGCC	720
Qy	730	CTCTTCTCATTTCTCGGAACCTTCGCGCCAGGCTCAAGTCCAGAAATGCTCTAAGAG	789
Db	721	CTCTTCTCATTTCTCGGAACCTTCGCGCCAGGCTCAAGTCCAGAAATGCTCTAAGAG	780
Qy	790	TTCATTTGACTTTGACACATGTCTCATCAAGACTTACCTGAGCCGCCACCCAGCGAG	849
Db	781	TTCATTTGACTTTGACACATGTCTCATCAAGACTTACCTGAGCCGCCACCCAGCGAG	840
Qy	850	CAGCTACTGAAGTTTCCCTTCACTCGGGACCGGCCAGGGACGGCAGGTCCGATCCAG	909
Db	841	CAGCTACTGAAGTTTCCCTTCACTCGGGACCGGCCAGGGACGGCAGGTCCGATCCAG	900
Qy	910	CTTAAAGACCAATTGACCGATCCCGGAGAAACCGGGTGAAGAAAGAGAGACAGAAATAT	969
Db	901	CTTAAAGACCAATTGACCGATCCCGGAGAAACCGGGTGAAGAAAGAGAGACAGAAATAT	960
Qy	970	GAGTACAGCGCGCAGGAGAGAGAGATGACACCTATGAGAGAAAGAGAGCCAAAGCTCC	1029
Db	961	GAGTACAGCGCGCAGGAGAGAGAGATGACACCTATGAGAGAAAGAGAGCCAAAGCTCC	1020
Qy	1030	ATCATGAAACGTGCCCTGAGAGGTGCACTGAACGCGGAGTTTCTCCGCTCCAGAGGAA	1089
Db	1021	ATCATGAAACGTGCCCTGAGAGGTGCACTGAACGCGGAGTTTCTCCGCTCCAGAGGAA	1080
Qy	1090	AATAAGACCACTCAGAGGCTTTAAACAGCAGCAGCAGCTGACAGCAGCAGCAGCAGCA	1149
Db	1081	AATAAGACCACTCAGAGGCTTTAAACAGCAGCAGCAGCTGACAGCAGCAGCAGCAGCA	1140
Qy	1150	GACCCCGAGGACACATCAAAACACTGCTGCAACAGCGGCAGCGCGCATAGAGGAGCAG	1209
Db	1141	GACCCCGAGGACACATCAAAACACTGCTGCAACAGCGGCAGCGCGCATAGAGGAGCAG	1200
Qy	1210	AAGAGAGAGCGGCGCTCGTGGAGAGACACAGCGGCGGGAGCCGGAGACACCGAAAGCTG	1269
Db	1201	AAGAGAGAGCGGCGCTCGTGGAGAGACACAGCGGCGGGAGCCGGAGAGAAAGCTG	1260
Qy	1270	CAGGAGAAAGAGCAGCAGCGCGGTGAGAGGACATGACAGGCTCTTCGCGCGGGAGGAGAG	1329
Db	1261	CAGGAGAAAGAGCAGCAGCGCGGTGAGAGGACATGACAGGCTCTTCGCGCGGGAGGAGAG	1320
Qy	1330	CGGCGGACGGCGGAGCGTGAACA-----	1353
Db	1321	CGGCGGACGGCGGAGCGGAGCGGAATATATTCGTCAACGGCTGAGAGAGGACGAGCGA	1380
Qy	1353	-----GGAAATCAAG	1367
Db	1381	CAGCTCGAGATCTTTCAGCAACAGTGTCTCCAGAAACAGGCCCTGTGCTGGAATACAG	1440
Qy	1363	CGGAAGCAGCTGAGAGAGCAGCGGCGATCAGAACCTTCCAGAGGCACTGTGACGACGAG	1422
Db	1441	CGGAAGCAGCTGAGAGAGCAGCGGCGATCAGAACCTTCCAGAGGCACTGTGACGACGAG	1500
Qy	1423	CATGCTTACCTCAAGTCCCTGACGAGCAACAGCAGCAGCACTTTCAGAAACAGAG	1482

Query	Local Similarity	Score	Length	DB	Length	Mismatches	Indels	Gaps
1501	CATCCCTACCTCAAGTCCCTCGACACAGCAACAGCAGCCTTCAAAAACAGAC	1566						
1483	CAGCAGACGCTCTGCTGCGGAGCAGAAAGCCCTGTACCTATTATGTCGCGGCATGAT	1542						
1561	CAGCAGACGCTCTGCTGCGGAGCAGAAAGCCCTGTACCTATTATGTCGCGGCATGAT	1620						
1543	CCCCGTGCAAAACCAAGCTTGCGGCCGAGAGTAG	1576						
1621	CCCGCTGCAAAACCAAGCTTGCGGCCGAGAGTAG	1654						

Db 361 GGCACGCGCTGAGAGAGCTGTATCGCTATCTGAGGAGATCCTCAGGGGTCTG 420  
QY 430 GCCCATCTCCATGCCCAACAGGTGATCCATCGACATCAAGGGCAGAAATGTGCTG 489  
Db 421 GCCCATCTCCATGCCCAACAGGTGATCCATCGACATCAAGGGCAGAAATGTGCTG 480  
QY 490 ACAGAAATGTGAGGTCAAGTGTGATTTGGGGGTGAGTGTCACTGAGCCGAC 549  
Db 481 ACAGAAATGTGAGGTCAAGTGTGATTTGGGGGTGAGTGTCACTGAGCCGAC 540  
QY 550 GTGGGACAGCGAACATTTCTATGGGACTCCCTACTGATGCTCCAGAGGTCTCCG 609  
Db 541 GTGGGACAGCGAACATTTCTATGGGACTCCCTACTGATGCTCCAGAGGTCTCCG 600  
QY 610 TGTGATGAAACCTGATGCCCTATGATTTAAGAGATGATTTGGTCTCTAGAAATC 669  
Db 601 TGTGATGAAACCTGATGCCCTATGATTTAAGAGATGATTTGGTCTCTAGAAATC 660  
QY 670 ACAGCATCGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 729  
Db 661 ACAGCATCGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
QY 730 CTCTTCTCTATTTCTCGGAAACCTCCGCGCAGGCTCAAGTCCAGAGAGTGTCTAAG 789  
Db 721 CTCTTCTCTATTTCTCGGAAACCTCCGCGCAGGCTCAAGTCCAGAGAGTGTCTAAG 780  
QY 790 TTGATGATTTATTTGACATGATGCTCATCAAGATTTAAGTCCAGAGAGAGAG 849  
Db 781 TTGATGATTTATTTGACATGATGCTCATCAAGATTTAAGTCCAGAGAGAGAG 840  
QY 850 CAGCTACTGAAATTTCCCTTCATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 909  
Db 841 CAGCTACTGAAATTTCCCTTCATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
QY 910 CTTAAGAGACCATTTGACATTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 969  
Db 901 CTTAAGAGACCATTTGACATTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
QY 970 GAGTACAGGAG 1029  
Db 961 GAGTACAGGAG 1020  
QY 1030 ATCATGAACTGTGCTGAGAGAGTGAAGTCAAGCGCGGAGAGTCTCCGAGTCCAGAGAG 1089  
Db 1021 ATCATGAACTGTGCTGAGAGAGTGAAGTCAAGCGCGGAGAGTCTCCGAGTCCAGAGAG 1080  
QY 1090 AATAAGAGCACTCAAGAGCTTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1149  
Db 1081 AATAAGAGCACTCAAGAGCTTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
QY 1150 GACCCCGAG 1209  
Db 1141 GACCCCGAG 1200  
QY 1210 AAGGAG 1269  
Db 1201 AAGGAG 1260  
QY 1270 CAGGAG 1329  
Db 1261 CAGGAG 1320  
QY 1330 CGGCGGAG 1389  
Db 1321 CGGCGGAG 1380  
QY 1390 TCAGAAAGTCTCAAG 1449  
Db 1381 TCAGAAAGTCTCAAG 1440  
QY 1450 CAGCAACAG 1491

Db 1441 CAGCAACAG 1482  
RESULT 14  
US-09-789-390-62  
Sequence 62, Application US/09789390  
Publication No. US20030059768A1  
GENERAL INFORMATION:  
APPLICANT: Vernet, Corine  
APPLICANT: Fernandes, Elma  
APPLICANT: MacDougall, John  
APPLICANT: Shinkets, Richard A  
APPLICANT: Spaderna, Steven K  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: 15966-692  
CURRENT APPLICATION NUMBER: US/09/789,390  
PRIOR FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 60/185,548  
PRIOR FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: 60/199,957  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: 60/184,951  
PRIOR FILING DATE: 2000-02-25  
PRIOR APPLICATION NUMBER: 60/185,967  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: 60/197,723  
PRIOR FILING DATE: 2000-04-18  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 62  
LENGTH: 1649  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-789-390-62

Query Match 37.0%; Score 1463.4; DB 10; Length 1649;  
Best Local Similarity 94.7%; Pred. No. 0;  
Matches 1561; Conservative 0; Mismatches 1; Indels 87; Gaps 1;

QY 10 GGCACCCAGAGCCCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 69  
Db 1 GGCACCCAGAGCCCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60  
QY 70 GCTGGAGCTTTGAGAGCTTTGAGAGAGTGTGCGCAATGAGACCTACGAGAGGTGAAG 129  
Db 61 GCTGGAGCTTTGAGAGCTTTGAGAGAGTGTGCGCAATGAGACCTACGAGAGGTGAAG 120  
QY 130 GGTGGCATGTCAAG 189  
Db 121 GGTGGCATGTCAAG 180  
QY 190 GAGGAG 249  
Db 181 GAGGAG 240  
QY 250 ATGCGCACTTCAAGAGAGCTTCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 309  
Db 241 ATGCGCACTTCAAGAGAGCTTCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
QY 310 TGGCTGTGATGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 369  
Db 301 TGGCTGTGATGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 360  
QY 370 GGCACCGCCGAG 429  
Db 361 GGCACCGCCGAG 420  
QY 430 GCCCATCTCCATGCCCAACAGGTGATCCATCGACATCAAGGGCAGAAATGTGCTG 489  
Db 421 GCCCATCTCCATGCCCAACAGGTGATCCATCGACATCAAGGGCAGAAATGTGCTG 480  
QY 490 ACAGAAATGTGAGGTCAAGTGTGATTTGGGGGTGAGTGTCACTGAGCCGAC 549

481 ACAGAGATGCTGAGTCAAGTATGTGATTTTGGGGTGAAGTCAAGTCGACGCCGACC 540  
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Db 541 GTGGGCGAGACGAAACATTTTCAATGGGATCTCCCTAATGGATGGCTCCAGAGTCAATGCC 600  
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Db 601 TGTATGAGAACCTTGATGCAACCTTATGATTAAGGATGATTTTGGTCTCTAGGAAATC 660  
QY 670 ACAGCATCGAGATGGCAGAGGAGACCCCTCTGTGTGACATGCAATGCCATGCGAGACC 729  
Db 661 ACAGCATCGAGATGGCAGAGGAGACCCCTCTGTGTGACATGCAATGCCATGCGAGACC 720  
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QY 850 CAGCTACTGAGATTTCCCTTCAATCCGAGACGAGCCAGAGCGGACAGTCCGATCCAG 909  
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QY 910 CTTAAGACCAATTTGACCGATCCCGAAGAAAGCGGGGTGAAGAAAGAGAGACAGAAATAT 969  
Db 901 CTTAAGACCAATTTGACCGATCCCGAAGAAAGCGGGGTGAAGAAAGAGAGACAGAAATAT 960  
QY 970 GAGTACAGCGGCGACGAGAGAGAAATGACAGCATGAGAGAGAGAGAGAGAGAGAGAGAG 1029  
Db 961 GAGTACAGCGGCGACGAGAGAGAAATGACAGCATGAGAGAGAGAGAGAGAGAGAGAGAG 1020  
QY 1030 ATCAATGAACTGTGCTGAGAGATGCACTTAAGCGCGGAGATTTCTCCGACTCAAGAGAGAA 1089  
Db 1021 ATCAATGAACTGTGCTGAGAGATGCACTTAAGCGCGGAGATTTCTCCGACTCAAGAGAGAA 1080  
QY 1090 AATTAAGACCACTGAGAGGCTTTTAAACAGACGACGAGCTGACAGACAGACAGACGAG 1149  
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QY 1150 GACCCCGAGGACATATTAACATCTGCTGACACCGCGGACCGGCGATGAGAGAGAGAG 1209  
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Db 1201 AAGGAGAGCGGCGCGCTGAGAGAGCAAGCGCGGAGAGCGGAGACAGCGAGAGCTG 1260  
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Db 1261 CAGGAGAGGAGCAGCAGCGGCGCTGAGAGCAATGCAAGGCTTTGCGGCGGAGAGAGAG 1320  
QY 1330 CGGCGGCGAGGCGGAGCGTGAACA----- 1352  
Db 1321 CGGCGGCGAGGCGGAGCGGAGCAAGAAATATTTGCTCAAGGCTTAAGAGAGAGAGAGCA 1380  
QY 1353 -----GGAATTAAG 1362  
Db 1381 CAGCTCGAGATCTTTCAAGCAAGCTGCTCAAGAAACGAGCCCTGCTGCTGAATTAACAG 1440  
QY 1363 CGGAGAGAGCTGAGAGAGCAGCGGAGTCAAGAACTCTCAAGAGCAGCTTCAAGAGAGAG 1422  
Db 1441 CGGAGAGAGCTGAGAGAGCAGCGGAGTCAAGAACTCTCAAGAGCAGCTTCAAGAGAGAG 1500  
QY 1423 CATGCTTCACTCAAGTCTCTGCAAGAGAGCAACAGCAGCAGCAGCTTCAAGAAACAGAG 1482  
Db 1501 CATGCTTCACTCAAGTCTCTGCAAGAGAGCAACAGCAGCAGCAGCTTCAAGAAACAGAG 1560  
QY 1483 CAGCAGAGAGCTCTGCTGAGGAGACAGAAAGCCCTGTACCATTTATGCTCGGAGCAGTAA 1542  
Db 1561 CAGCAGAGAGCTCTGCTGAGGAGACAGAAAGCCCTGTACCATTTATGCTCGGAGCAGTAA 1620

QY 1543 CCGGCTGACAAACCAAGCTGGGCGGAG 1571  
Db 1621 CCGGCTGACAAACCAAGCTGGGCGGAG 1649  
RESULT 15  
US-10-355-975-7  
; Sequence 7, Application US/10355975  
; Publication No. US20030162277A1  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Vitco, G. Duke  
; APPLICANT: Martin, Unja  
; APPLICANT: Anderson, Dirk M.  
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES  
; FILE REFERENCE: 2923-A  
; CURRENT APPLICATION NUMBER: US/10/355,975  
; CURRENT FILING DATE: 2003-01-30  
; PRIOR APPLICATION NUMBER: US/09/579,664B  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 4083  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-355-975-7  
Query Match 34.4%; Score 1358.6; DB 14; Length 4083;  
Best Local Similarity 61.7%; Pred. No. 0; Mismatches 1389; Indels 180; Gaps 16;  
Matches 2532; Conservative 0; Mismatch 1389; Indels 180; Gaps 16;  
QY 7 ATGGGCGACCAAGCGCCCGCGCGAGCTGGACGACATGCACTGTCCGCTCGGAGAC 66  
Db 1 ATGGGCGACCAAGCTCCCGGCTCGAGGCTGGATGAATTAATGATCTCTGGGCTCTAGAGAC 60  
QY 67 CTGCTGGGATCTTTGAGCTTTGTGAGGTGTGCGCAATGGAACCTTACGACAGGTATC 126  
Db 61 CTGCAAGGATCTTTGAAATGTGTGAATCTGTTGGAATGGAATGACATACGCGCAAGTTAT 120  
QY 127 AAGGCTGGGATGTCAGAGCGGCGAGCTGCGCATCAAGGTCATGAGATGATGACGAG 186  
Db 121 AAGGCTGTATGTCAAAAGCGGCGACCTTGACCATCAAGGTTATGAGATGTCAAGG 180  
QY 187 GACGAGAGAGAGATCAACAGAGATCAACATGCTGAAAGAAAGTACTTCAACACGCG 246  
Db 181 GATBAAGAGAGAAATCAACAGAAATTAACATGTTGAAGAAATTTCTCATCACCGG 240  
QY 247 AACATGCACTTACGAGAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306  
Db 241 AATATGCTACATCTATGAGGCTTTTATCAAAAGAGAGAGAGAGAGAGAGAGAGAG 300  
QY 307 CTCTGCTGAGAGAGAGATCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366  
Db 301 CTCTGCTGAGAGAGAGATTTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
QY 367 AAAGGCAAGCGCCGAG 426  
Db 361 AAAGGTAACAGCTTGAAG 420  
QY 427 CTGCGCATCTCAATGCGCCCAAGAGTATCATGAGACATCAAGGAGAGAGAGAGAGAG 486  
Db 421 CTGAGTCACTGCAACAGAGATTAAGTATTCATGAGATTTAAAGGAGAGAGAGAGAG 480  
QY 487 CTGCAAG 546  
Db 481 CTGCAAG 540  
QY 547 ACCGTGGGCGAG 606  
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607 GCTGTGATGAGAACTTGATGCACTATGATTAACAGAGATGATATTTGGTCTCTAGGA 666  
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 667 ATCACAGCCATGAGATGGCAGAGGAGCCCCCTCTGTGTGACATGACCCCATGCGA 726  
 661 ATCACCGCATTTGAATGGCAGAGAGTGTCTCCCTCTCTGTGATGATGACCCCATGGA 720  
 727 GCCCTCTTCATTTCTCGGAAACCTCGCCCAAGGCTCAAGTCCAAAGAGTGTCTAG 786  
 721 GCTCTCTCTATCTCCCGAATCAGCGCTCGCTGAGTCTTAAGAGTGTCTAANA 780  
 787 AAGTTCATTTGACTTGAACATATGTCTCATCAAGACTTACCTGAGCCGCCACCAAG 846  
 781 AATTCAGATCATTTATGAGAGCTGTGTGAAGAAATCAACAGCAGAGACCAACAA 840  
 847 GAGCAGCTACTGAACTTCCCTTCATCCGGACCAAGCCACGAGCGGAGTCCGCAATC 906  
 841 GAACATTTGATGAGCATCTTATTAACAGACCAACTAATGAGCGAGGTCGCAAT 900  
 907 CAGCTTAAGGACCAATTTGACGATCCCGAAGAGCGGGGTGAGAAAGAGAGACAGA 966  
 901 CAATCAAGGACCAATTTGATTAAGCAAAAGAGAGCGAGAGAAAGATGAGACAGAG 960  
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 Qy 3685 GTGCTGTGCTGAGTGGGGGAGATGCTTCTGTGGCTTACATGCTGCCAACAGATA 3744

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 Qy 3745 ATGGCTTGGGTGAGAAAGCCATTGAGATCCGCTCTGAGAGACGGGCCACTCGACGGG 3804  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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18781.515 Million cell updates/sec

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Scoring table: IDENTITY NUC  
Gapop 10'-0', Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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15: em\_ectfun:\*  
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23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrt:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1307.2	33.1	7139	11	BC050868 Mus muscu
3	949	24.0	3585	29	AY400358 Mus muscu
4	897	22.7	969	13	B0838349 AGENCOURT

5	893.8	22.6	3585	29	AY400356
6	872.4	22.1	908	13	B0542554
7	848	21.5	951	13	B0706178
8	834.2	21.1	1201	9	AL551911
9	833.4	21.1	3588	29	AY400357
10	814.4	20.6	1026	12	B0541693
11	799.6	20.2	907	13	B0684810
12	799	20.2	866	12	B1756763
13	779.8	19.7	881	13	B0542006
14	772.4	19.5	936	12	B0451246
15	764.4	19.3	881	14	CA454128
16	764.4	19.3	1022	13	B0073811
17	743.8	18.8	1040	13	B0072284
18	736.2	18.6	910	14	CD557921
19	729.2	18.5	1037	12	B0800664
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21	720	18.2	1341	11	AK049630
22	715.8	18.1	903	13	B0527220
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24	704	17.8	999	12	B0477724
25	698.8	17.7	971	13	B0173419
26	690.4	17.5	811	13	B0527825
27	689	17.4	1167	13	BX359762
28	673.6	17.0	744	12	BG755560
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30	655.2	16.6	898	13	BQ885202
31	648.4	16.4	757	14	CB519879
32	646.6	16.1	790	14	CF733432
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34	634.2	16.1	652	12	BG821758
35	632	16.0	720	14	CB249067
36	628.6	15.9	2538	11	AK088459
37	628	15.9	805	10	BE312777
38	623.8	15.8	1320	11	AK041777
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40	618.8	15.7	708	14	CB245214
41	617.6	15.6	1058	12	BM464994
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## ALIGNMENTS

RESULT 1  
LOCUS BC050866  
DEFINITION Mus musculus RIKEN cDNA 1500031A17 gene, mRNA (cDNA clone IMAGE:6333274), containing frame-shift errors.  
ACCESSION BC050866  
VERSION BC050866.1 GI:30047190  
KEYWORDS HTC.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 7139)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionachti; Muridae; Murinae; Mus.  
BC050866 7139 bp mRNA linear HTC 19-NOV-2003  
Mus musculus  
Klusner,R.D., Collins,F.S., Wagner,L.H., Derge,J.G., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diachenko,L., Marsina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scherz,T.E., Brownstein,M.J., Uedlin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Bosak,S.A., McKen,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Huiyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Young,A.C., Shevchenko,Y., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitz, J., Myers, R.M.,  
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalley, D.E.,  
 Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE  
 PUBMED 22388257  
 12477932  
 TITLE 2 (bases 1 to 7139)  
 AUTHORS Strausberg, R.  
 JOURNAL Direct Submission  
 Submitted (09-APR-2003) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
 Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,  
 Ph.D.  
 cDNA Library Preparation: ResGen, Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
 DNA Sequencing by: Genome Sequence Centre,  
 BC Cancer Agency, Vancouver, BC, Canada  
[info@bcgsc.bc.ca](mailto:info@bcgsc.bc.ca)

Steven Jones, Jennifer Asano, Ian Boedeltje, Yaron Butterfield,  
 Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,  
 Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo  
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven  
 Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline  
 Schin, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stott,  
 Michael Thorne, Miranda Tsai, Nastasia van den Bosch, Jill Vardy,  
 George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LIML at: <http://image.llnl.gov>  
 Series: IRAX Plate: 109 Row: C Column: 16  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: Hexamer frequency ORF  
 analysis  
 This clone has the following problem: frame shifted.

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 Location/Qualifiers  
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 Best Local Similarity 61.2%; Pred. No. 1.4e-212;  
 Matches 2336; Conservative 0; Mismatches 1343; Indels 263; Gaps 16;

Db 610 GATGAGAGAGAGAAATCAACAGAAATTAACATGTTGAAGAAATATCTCATCAGG 669  
 QY AACATGCGACCTACTAGAGACCTTCATCAAGAGAGAGAGAGAGAGAGAGAGAG 306  
 Db 247 |||||  
 QY AACATGCTACACTACTACGAGGCTTTTACAAAAGAAACCTCTGGGATGATACAA 729  
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QY	2333	CAGGCGGGCCCGCAGACTTGTGTGTGTGCTGAAGAAGCGGACTCTGGACAGGCGCCCTCGGC	2392
Db	2830	ATCTGACGGCATTAAGCCAAAGATTACAGAACTCCGCA--TTGAGAAACAAACGCC	2888
QY	2393	CTCCCAAGAAAGCCATGGACTACTCGTGTCTCAGCGAGAGAGTGGAAAGAGTGAAGCG	2452
Db	2887	CCCTGAAGAAAGTAGACTGATTACTCTTCCTCAGCGAGAGAGTCCGAGAGCAGTGAAGAG	2946
QY	2453	ACGAGAGGAAGCGGAAAGCGGGCCAGCAGAGGGA-----	2488
Db	2947	AAGAGGAAGATGGAGAGAGTGAACAATACGGAACGGGAGCGTGGCTGTCAATGCCA	3006
QY	2489	-----GCAGAGATACCCCTGGGGGGCCGACGATGGGGATACAGACAGCGTCAAGCA	2539
Db	3007	GACTAATAACCAACCGAGCTTCAGAGAACTAGACAGTACACATGGGGATGGTCCGGA	3066
QY	2540	CCATGTGTGTCCACGACGTCCAGAGATCAACGGGAGCCAGCCGCAACCGGGGGCGCA	2599
Db	3067	CACATGGGCTGGAAACTTGGCATCGGACACTTTTGGCGGACGATTTCAAGAAAGGA	3126
QY	2600	CCATGTGTGTCCAGCGCACTCTGAAGAAGCGGAACTGTCTGATCTCTACAGCAATG	2655
Db	3127	CTTTGATGATCAGAGAGCGGCTTAAGGAAAGGCGATCTGGCCACAGTACAGTAAATG	3186
QY	2660	GGT-----ACACAACCTGTCTGACGATGTCCAGCCGACGCACTCAACCCAGCA	2716
Db	3187	GATTGCGCGGTCACTCAATCATCTCCAGACCTTTGACAGCAGAGCCATTCCGACAGTGGAA	3246
QY	2711	ACAGCAAAAG-----GCCAAAGCCCAACCTTCGAAAGATGGAGTGTGTGACTTACAGTCTC	2764
Db	3247	CTCCCACTGAGAGGGGCTGGGGCGGCGCTCTCACTATTCACAGAAATGAGACTCTGGGGCTG	3306
QY	2765	GTTGGGCTGGTAAAGGCCCTCTGGCAAGAGCTGTTCAAGATTTTGTGATTTAGGAATCT	2822
Db	3307	AATATGTGTAATGAGGAGACGACAAAGCCTTTTCAACCCCTTGTGGACCTCGAGTGT	3366
QY	2825	ACCAAGCTCGAGGAGT-----GGGACAGCATCCCATCAACAGCCCTAG	2865
Db	3367	ACCAAGCATCGCCCATGTAGTAGATGAGATGATGAGTCTTTCAGCTGTGCTGCTGT	3428
QY	2870	TGGGTGAGAGAGGCACTGTGCTCGACAG--CTGCAGTACGAGCTGAGAGAGGTTCTG	2928
Db	3427	TTACTAGGAACTTCTTAGGCAAGAACAGGCCAACTCAATGAAAGCAGAGAAATTTAG	3486
QY	2927	TGGTCAACGTGAATCCCAACCAACCCGGGCCCAAGTAGAGACCTTGAGATCCGGAAT	2986
Db	3487	TGGTAAATGTGAACCAACAAACATTTGGCCCTCATAGTACACACCGGAATTCAGAAAT	3546
QY	2987	ACAAAGAGCGATTCACTCCGAGATCTCTGTGACGCCCTTTGGGGGGTCAACTGTCTGG	3046
Db	3547	ACAAAGAAACGTTCAATTCAAGAAATCTTTGTGAGCTCTAATGGGAGTGAACCTTCTGG	3606
QY	3047	TGGGACGAGAAAGCGGCTGATGTTGTCTGACCCGAGTGGGACAGGCAAGGTGATGAGAC	3106
Db	3607	TGGGACTGAAATAGGCTGATGCTTTTGGACAGAAATGGCCAGAGCGAAATCTACAAAC	3666
QY	3107	TCAATTGGGCGGCGACGCTTCCAGACAGATGATGTGCTGAGAGGGCTCAACTGTCTCA	3166
Db	3667	TAAATCAACCGGAGGCGGTTTCAAGACAGATGATGTGTAGAAAGACTAAATGTTCTTGCA	3726
QY	3167	CCATCTCAGGGAAGAAAGAACAACTGGGGGTGTATTACCTGTCTGTGCTCCGGAACAAG	3226
Db	3727	CGAATATCAGGAAGAAAGAAACAAAGCTCCGTGTGTCTATCTCTCATGTGTTAAGAAACGAA	3786
QY	3227	TTCTGCACAATGAACCAAGAGTGGAGAAAGACAGGCGTGGACCAACGCTGGGGGACATGG	3286
Db	3787	TCTGTCAATATGACCCAGAAATGGAAAGAAAGACAGGCGTGGATCACTGTGCTGATCTTGG	3846
QY	3287	AGGCTGCGGGCACTACCGTGTGTGTGAATACGAGCGGATTAATGTTCTGTGATCTGCC	3346

Db	3847	AAGGCTGATCCATTACAAAGTCGTTAAATATGAAAGATCAAGTTCTTGATTTGCTT	3906
Qy	3347	TCAAGAGCTCCGTGGAGGTGTATGCTTGCGGCCCAACCCGACCAAAATTCATGCGCT	3406
Db	3907	TAAAGATGACGTAGAGATATATATGCTGGGCCCTTAAACCTTATACATAAAGTTACATG	3966
Qy	3407	TCAAGTCTTTTGGCCGACCTCCGCCACCGCCCTCTTGCTGTGTGACCTGACATGAGAGAG	3466
Db	3967	TTAAGTCTTTTGGACATCTTTCAGCATTAAGCCCTGCTGTTGACCTCCACATAGAAAGAG	4026
Qy	3467	GGACGCGGCTCAAGGTCATCTATAGGCTCCAGTGCTGGCTCCATGCTGTGATGCGACT	3526
Db	4027	GTCAAAGGTTTAAAGGTCATATTTGGCTACACACTGGTTTCCATGTAATTAATGTTGATT	4086
Qy	3527	CGGGGAACAGTATATGACATCTTACATCCCTGTGACATCCAGAGCCAGATCAAGCCCCATG	3586
Db	4087	CTGGAAATCTCTAAGATATCTATATATACATCCCATATTCAAGGGAATATCACTCTCATG	4146
Qy	3587	CCATCATTTTCTCTCCCAACACCGACCGCATGAGATGCTGTGCTCTACAGACGAG	3646
Db	4147	CTATGCTATCTTTGCTCTTAAACAGATGGAATGGAGATCTTGCTGCTATAGAGATGAAG	4206
Qy	3647	GATGCTACGTCAACACGATCGGGGCGCATCTTAAGAGATGTGGTGTGTGACAGTGGGGGAGA	3706
Db	4207	GGGTGTAGTGAACACTTACCGCCGAGATCCTAACGATGATGTGTCTCAATGGGGAGAA	4266
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Db	4267	TGCCCACTCTGTGTGGCTCTTACATCTTCCATCAGATATATGGGCTGGGGCGAGAAAGCTA	4326
Qy	3767	TTGAGATCCGCTCTGTGAGAGACGGGCCACTTGCACGGGGTCTTTCATGACAAACGAGCTC	3826
Db	4327	TTGAGATCCGGTCAGTGGAAACAGGACATTTGGATGAGATGTTATGATTAACACGACTC	4386
Qy	3827	AGAGGCTCAAGTTCCTGTGTGACGGGAATGACAGGTGTTTTTGGCTCAGTCCGCTGTG	3886
Db	4387	AAAGGTAAAGTTTCTATGTGTAAGAAATGATTAAGGTATTTTGTGATCCGTCGATCTG	4446
Qy	3887	GGGGGACGAGCCAAAGTTTACTTTCATGACTTGCAGCCCTTAACCTGATCATGAACTGTGAA	3946
Db	4447	GAGGAAGTACCCAGTGTCTTTTCATGACCTCTCCACAGAAATTCATGATGAACTGTAAAC	4506
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SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
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TITLE	Faney, J., Helton, E., Keltman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bonfield, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywninski, M.I., Skalska, U., Smalhus, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
JOURNAL	human and mouse cDNA sequences
REFERENCE	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
AUTHORS	
TITLE	2 (bases 1 to 7139)
JOURNAL	Strauberg, R.
REFERENCE	Submitted (09-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: <a href="http://mgc.ncl.nih.gov">http://mgc.ncl.nih.gov</a>
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> Tissue Procurement: Mark Macconochie, Ph.D. and Nancy L. Freeman, Ph.D. cDNA Library Preparation: Reegen, Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada <a href="mailto:info@cgsc.bc.ca">info@cgsc.bc.ca</a> Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywnski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Nees, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Seedi, Jacqueline Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Series: IRAX Plate: 109 Row: d Column: 16 This clone has the following problem: frame shifted. location/Qualifiers 1..7139 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="IMAGE:6334359" /tissue.type="Embryo, day 9 mouse (C57BL/6 background) otocysts" /clone_id="NIH_MGC_130" /lab_host="DH10B" /note="Vector: pCMV-SPORT6.1"
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Query Match	33.1%, Score 1307.2, DB 11, Length 7139;
Best Local Similarity	61.2%; Pred. No. 1.4e-212;
Matches 2536; Conservative	0; Mismatches 1343; Indels 263; Gaps 16
7	ATGGGCGACCGAGCCCGCCCGGAGCTGGACGACGATCGCTGCGCCCTGCGGGAC 66
430	ATGGGAGCGACCTCCCGAGCTGGAGCTGGATGAATCGATCTTCGGCCTTAGGGAGC 489
67	CCTGCTGGATCTTTGAGCTTGTGAGAGGTGTCGGCAATGGAACCTACGAGAGGTGAC 126
490	CCTGAGGAGATCTTGAGTTGTGTGGAATCTTGTCCGAATGGAAGATATGTCGAAGTTAT 549
127	AAGGTCGCGCATGTTCAGACGCGGCGAGCTGCTGTCATCAAGGTCATGATGTCACGGAG 186
550	AAGGTCGTCAATGTCAAAACGGGCGACGCTTCTGTCATTAAGGTTATGATGTCACAGGG 609
187	GACGAGAGGAAGATCAACACAGGAGATCAACATGCGAAAAGTACTCTACACACGGC 246
610	GATGAAGGAGAAATCAACAGAAATTTAACTGTTGAAGAAATATTTCTATCATCACGG 669

OY	247	AAACATCGCACTTACTAGGAAECCTTCACTAAAGAAAGCCCCCGGGAACGATGACGAG	306
Db	670	AAACATGGCTAACATCTACGGTGCCTTTATCAAAAAAGAACCCCTCTGGGACATGGATACCAA	729
OY	307	CTCTGCGTGTGATGAGATTCTGTGGTGTGGTTCTAGTACGTGACTGGTAAAGAACACA	366
Db	730	CTCTGTGTGTTATGAGATTCTGTGTGTGTGGCTCTGTCACTGACTGATCAAGAACACG	789
OY	367	AAAGGCAACGCCCTGAAGAGGAGCTGTATCGCTATATCTTCGAGGAGATCCTCAGGGGT	426
Db	790	AAAGGCAACACATTTAGAAAGAGAGTGGATTGCATCATCTCGCAGGAGAGATCTTACGGGGC	849
OY	427	CTGGGCCCATCTCCCAATGCCCAAGAGTATCCATCGAGACATCAAGGGGCGAAGATGTGCTG	486
Db	850	CTGAGTCACTCTGCACCAAGCAAAAGTATTCATCGAGATATCAAAAGGGCGAAGACGTTTG	909
OY	487	CTGACAGAGATAGCTGAGGTCAAGCTAGTGTATTTTGGGGGTGAGTCTCAGCTGACCGC	546
Db	910	TTGATCTGAAAAATGCAAGGTTTAAAGTATGATGATTTTGGAGTGAAGTGGCCAGCTTACCGA	969
OY	547	ACCGTGGGCAACGGGAACCTTTCATTGGGACCTCCCTACTGATGGCTTCAGAGGTCACT	606
Db	970	ACTGTGGGCGAGGAGGAACAGCTTTCATCGGAGCTCCCTACTGATGGCAACAGAGTCAATT	1026
OY	607	GCCTGTGATGAGAACCTTGATGCGCATATGATTAAGG-----	645
Db	1030	GCCTGTGATGAGAACCCGGATGCCACATATGATTTCAAGGAGATGGGCGTTTATGATAGCT	1086
OY	646	-----	645
Db	1090	GCAGGCACGGACGCCAGTGTGAGAAAGATGAAATTTCCACCAACGACGATGAGTAG	1149
OY	646	-----AGTGAATTTGGTCTCTAGAAATCAAGCCATCGGA	682
Db	1150	CCGCAACCATGGCCAGAGAGAAACAGTATCTTGATCTTTGGGAATCAACCGCATTTGAGA	1209
OY	683	TGGCAGAGGGAGCCCCCTCTGTGTGACATGCAACCCCATGCGAGCCCTCTTCCATCTC	742
Db	1210	TGGCAGAAAGGTGCCCCCCCCCTCTGTGACATGCAATCCCATGAGAGCCCTCTTCCATCTC	1266
OY	743	CTCGGAACCCCTCCGCCCAAGCTCAAGATGAGTGTCTTAAAGATTCAATTGACTTCA	802
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OY	803	TTGACACATGTCTCATCAAGCTTACTGAGCGGCCCAACCCAGGAGCAGTACTGAAGT	862
Db	1330	TCGAGAGCTGCTTGGTAAAGATCACAGCCAGCGGCCCAACCCAGGAGCAGTGAATGAAC	1386
OY	863	TYTCCCTTATCCGGGACCAAGCCCAAGAGCCGAGGTCCGATCCAGCTTAAAGACCA	922
Db	1390	AACCATTTCAATCGAAGCAACCTAATGAGAGGCAAGTCCGCACTCAGCTGAAGGACACCA	1449
OY	923	TTGACCCGATCCCCGAAGAAAGCGGGGTGAAAGAGAGACAGATATGATGATACAGGCA	982
Db	1450	TTGATCTGAACAAAGAAAGAGCCAGAGAAAGAAAGATGAGCTGAGTATGAAATCACGGAA	1509
OY	983	GCGAGAGAAAGATATACAGCCTAGAGAGAGAGAGAGCCCAAGTCTCAATGAAAGCTGC	1042
Db	1510	GTCAGGAAGAGAGAGAGAGAT---GACTCTGGGGGAACCCAGCTCCATTTGAAACCTAC	1566
OY	1043	CTGAGAGTCCGACTTACGCGCGGAGTTTCTCCGCTCCAGCAGAAATTAAGCAACT	1107
Db	1567	CAGGGAGATCAACATCTGCGAAGGAGCTTCTGAAGCTGACGTGCGCAACAGAGAGCGCT	1626
OY	1103	CAGAGGCTTTAAACAGCAGCAGCAGCTGCAACACACAGCAGCAGGAGAGCCCGAGGAC	1167
Db	1627	CAGAGG-----CTGCGGCGCCCAACAGCTGAGACGAGCAGCGGAGATGAAGAAC	1686
OY	1163	ACATCAAAACCTGTGCAACAGCGGCAAGCGCGCATAGAGGACAAAGAGAGCGCG	1222
Db	1681	ACAAACGCGAGCTTACGTGGCTGAGCGCCAGAAACCGATCGAAGAGAGAGAGGCAAGGC	1740

QY	1223	GCCGCTGTGAGAGCAACAAGCGGCGGAGCGGGAGCGACCGGAACTCTGACGAGAAAGAGCG	1282
Db	1741	GAGGCTGTGAGAGCAACAAGGCGGAGAAAAAGAGCTTCTGGAAAACAGACGAGAGCGGAGAC	1800
QY	1283	AGCAGCGGCGGCTGAGAGCACTGCAAGGCTCTGCGCGGGAGAGAGAGCGCGGCGAGCGG	13442
Db	1801	AGCGCGGCACTTACGAGAGACAG-----ATGCGTCTGGAGAGAGAGAGAGGCGCTGCCG	1854
QY	1343	AGCGTGAACAGAAATACAGCGGAGAGCAAGCTGAGAGAGCAGCGGCACTCAGAAAGTCTCC	1402
Db	1855	AAACATGAGCAGAAATATATAGCGCAAAACAATTGGAAGAACAGAGACAAGAGAAAGACTGC	1914
QY	1403	AGAGGCACTGACAGAGAGATGCTTACTTCAAGTCCCTGACAGACAGACAGACAGACAGC	1462
Db	1915	AGAGGCAAGCTTAAACCAAGAGCGGAGACTATCGTGTTCCTTCACAGATCAGCGGACGAGGC	1974
QY	1463	AGCAGCTTCAAAAACAGACAGAGAGCGTCTGCGCTGGGAGAGAGAGCCCTGTACC	1522
Db	1975	AG-----AGCCCCCTGGAAGAGAGGCACTGTACC	2004
QY	1523	ATTATGTGCGGAGATGATTCGCCGTGACAAACCAAGCCTGGGCCCGAGAGGTAGAGAGA	1582
Db	2005	ATTACAGAGAGGCGATAGTCTGTAGTAGAGCCGCGCTGGCGCAAGAGGTATAGAGAAC	2064
QY	1583	GAACAGAGTAAACAAGCAGACAACTCTCCCTTGGCCAGAGACAGACGACGACGACG	1642
Db	2065	GCTCAAGACTCAACCGACAGAGTTCACTCGCCATGCGCTCAAGAGTTGCCAACAGAGACT	2124
QY	1643	GG-----CTGAGACCGCCCAATCCGCCAGGCTCCCGAGGCGCCCAAGAACCCCTTCC	1696
Db	2125	CGGACCCCAACTGCGCCCAAGATGAGTCTTCAGACTTATGTGGGTTTACGCTTGCA	2184
QY	1697	AGACTCTCTATGTCAGAGGCGGCTGAGGCCCGCAGAGAGAGCCGACACAGTCCCTGCAG	1756
Db	2185	GGAACACCCCAATGCTCAGACCTGTGACCCCGCAGATCCGCACTGGTATCTGTCAAT	2244
QY	1757	ACCAAGCCCAACCTGGCTGCTCCAGCCTCCATGACCC-----CGACC	1807
Db	2245	CCCAAGGACCTGCTTGAAGCGCTCCCAAGTACATGAGCAACCAAAAGGCGCTGT	2304
QY	1808	CTTGCCATCCCCGACCCACTGCGCACGCGCCAGTGGCCAGAGAGATGTCATCCGCGAGAA	1867
Db	2305	CTGGGTTTCAAGAGGCTCTGATGTGACTCTCAACCGGCTGAGATGCAAGCCAGAACT	2364
QY	1868	CAGACCCCACTCTGAAGAGCTGAGCCCAAGCCGCA-----ATCCCCAG	1912
Db	2365	CGGATCCCACTCAGAAAAACCTCTCTCTCCCAAGAGAAATTGAGAAAGTTTGAAGAACT	2424
QY	1913	CCTGGGTCGCGCCAGATTAACGAGGCCCAACCAAGTGCCTCAGAGGACTCTATCTATCG	1972
Db	2425	CTTGGTTTACAGAGAGAAAGACATTCACCAAAAGTGCCTCAAAAGAACATTTCTATAT	2484
QY	1973	CCAAGTCCCTTAAACACAGTGGGGCGGAGGGTCCCGCCAGGCCAGGCAATCCGTGCCA	2032
Db	2485	CCCCAGCACTAGCCAGAAAGAAATTCCTCCCTGCAATGCGAGTCTCTGGGCCCAAGACTTG	2544
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QY	2153	ACCTCAGAGAGAGCAACCTGCGTGGGAAACGCTCGACAGCGTCTCTTCAGCCTCTCAGC	2212
Db	2650	CTCCACAGCTCCAGCGCCAGCTCCCAAGAGGCTCTCAACTGAGTCTCCCAACAGAGATCTA	2709
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 VERSION  
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 SOURCE  
 ORGANISM  
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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 gene trios  
 Science 302 (5652), 1960-1963 (2003)  
 JOURNAL  
 PUBMED  
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 2 (bases 1 to 3585)  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,  
 Adams, M.D. and Cargill, M.



TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
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Matches 1996; Conservative 0; Mismatches 1584; Indels 237; Gaps 12;  
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KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 969)				
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/				
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 1 (bases 1 to 908)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: DCTD/DTF  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
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 http://image.llnl.gov  
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 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 22.1%; Score 872.4; DB 13; Length 908;  
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## RESULT 7

BO706178

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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 BO706178.1 GI:21845077  
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 1 (bases 1 to 951)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgsab@biml.nih.gov  
 Tissue Procurement: Dr. Mark Watson  
 cDNA Library Preparation: Rubin Laboratory  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILNI at:  
 http://image.llnl.gov  
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 EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
 into EcoRI/XhoI sites using the following 5' adaptor:  
 GGCACGAG(G). Library constructed by Ling Hong in the  
 laboratory of Gerald M. Rubin (University of California,  
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
 Superscript II RT (Life Technologies). Note: this is a  
 NIH\_MGC Library."

## FEATURES

source

## ORIGIN

Query Match 21.5%; Score 848; DB 13; Length 951;  
 Best Local Similarity 97.2%; Pred. No. 1.7e-134;  
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 Db 624 GCTGAGAGGAGCTCAACCTGCTCATCAACATCTCAGGAAAGAAACAACTGCGGCTGA 683  
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 Db 684 TTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 743  
 Qy 3261 GGGCTGACACACCGTGGGGGACATGAGAGGCTGCGGGACCTACGTTGTGAAATAGA 3320  
 Db 744 GGGCTGACACACCGTGGGGGACATGAGAGGCTGCGGGACCTACGTTGTGAAATAGA 803  
 Qy 3321 GCGGATTAAATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3379  
 Db 804 GCGGATTAAATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 863  
 Qy 3380 CCAAACTTACCAAAATTT-CATGCTTTCAGAGTCC-TTGGCCGACCTCCCGACCGCC 3436  
 Db 864 CCAAACTTACCAAAATTT-CATGCTTTCAGAGTCC-TTGGCCGACCTCCCGACCGCC 923  
 Qy 3437 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3456  
 Db 924 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 943

RESULT 8  
 AL551911 1201 bp mRNA linear EST 31-MAY-2003  
 LOCUS DEFINITION AL551911 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
 AL551911  
 ACCESSION AL551911  
 VERSION  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 1201)  
 L.I.W.B., Gruber, C., Jessup, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 unpublished (2001)  
 On Feb 15, 2001 this sequence version replaced gi:12890305.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 8486.f. For more information about this cluster, see  
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0D1060CD120P1&cluster=8486.f>. Contact :  
 Feng Liang Email : fliang@life.techn.com URL :  
<http://fulllength.invitrogen.com/InvitrogenCorporation1600>  
 Faraday Avenue Genoscope sequence ID : CS0D1060CD120P1.

FEATURES  
 SOURCE  
 1..1201  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0D1060YH23"  
 /issue\_type="PLACENTA COT 25-NORMALIZED"  
 /clone\_id="Homo sapiens PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
 Query Match 21.1%; Score 834.2; DB 9; Length 1201;  
 Best Local Similarity 91.7%; Pred. No. 4,3e-132;  
 Matches 857; Conservative 20; Mismatches 58; Indels 0; Gaps 0;

7 ATGGGCGACCGACGCCCGCCGCGAGCTGACGACATCGACTGTCCGCTGCGGAC 66  
 Db 258 ATGGGCGACCGACGCCCGCCGCGAGCTGACGACATCGACTGTCCGCTGCGGAC 317  
 Qy 67 CCGTGGGATCTTGAAGCTTGTGAGGTGTGGCAATGGAACCTACGACAGGTATAC 126  
 Db 318 CCGTGGGATCTTGAAGCTTGTGAGGTGTGGCAATGGAACCTACGACAGGTATAC 377  
 Qy 127 AAGGTCGCAATGTCAGAACCGGCGAGCTGCTCCATCAAGTCTATGATGTCACGAG 186  
 Db 378 AAGGTCGCAATGTCAGAACCGGCGAGCTGCTCCATCAAGTCTATGATGTCACGAG 437  
 Qy 187 GACGAGAGAGAGATCAACAGAGATCAACATGCTGAAAGAAAGTCTCTACACCGC 246  
 Db 438 GACGAGAGAGAGATCAACAGAGATCAACATGCTGAAAGAAAGTCTCTACACCGC 497  
 Qy 247 AACATCGCACCTACTACGAGGCTTCTCATCAAGAAAGAGCCCGGGGAAAGATGACGAG 306  
 Db 498 AACATCGCACCTACTACGAGGCTTCTCATCAAGAAAGAGCCCGGGGAAAGATGACGAG 557  
 Qy 307 CTCTGCTGCTGATGAGATTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366  
 Db 558 CTCTGCTGCTGATGAGATTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 617  
 Qy 367 AAAGGCAACCGCTGAAAGAGAGCTGATGCGCTATATCTGACAGGAGATCTTCAAGGGGT 426  
 Db 618 AAAGGCAACCGCTGAAAGAGAGCTGATGCGCTATATCTGACAGGAGATCTTCAAGGGGT 677  
 Qy 427 CTGGCCCATCTCCATGCGCCCAAGAGTATCATGAGACATCAAGGGGCAAGATGTGCTG 486  
 Db 678 CTGGCCCATCTCCATGCGCCCAAGAGTATCATGAGACATCAAGGGGCAAGATGTGCTG 737  
 Qy 487 CTGACAGAGATGCTGAGGCTCAAGCTAGTGAATTTGGGAGTGAAGTCTGACAGCCG 546  
 Db 738 CTGACAGAGATGCTGAGGCTCAAGCTAGTGAATTTGGGAGTGAAGTCTGACAGCCG 797  
 Qy 547 ACCGTGGGACGAGCAACCTTCTATGGAAGTCTCCCTACTGAGTGGCTCCAGAGTATC 606  
 Db 798 ACCGTGGGACGAGCAACCTTCTATGGAAGTCTCCCTACTGAGTGGCTCCAGAGTATC 857  
 Qy 607 GCGTGTATAGAAACCTGATGCACTATGATTAAGAGATGATTTGGTCTCTAGGA 666  
 Db 858 GCGTGTATAGAAACCTGATGCACTATGATTAAGAGATGATTTGGTCTCTAGGA 917  
 Qy 667 ATCACACCATCGATGAG 726  
 Db 918 ATCACACCATCGATGAG 977

[illegible]

OY	310	TGCTGTGGATAGGAATTCTGTGTGGTCTGTGTCAAGTACAGACTGTGTAAAGAACAAAA	366
Dd	181	NNNCTTTTAAATAGAGTTCTGTGTGGGCTGGTCCATTAACAAGCTTTGTGAAGAACCAAA	240
OY	370	GGAACGCCCTGGAAGAGAGACTGTATCGCCTATATCTCAGGGAGATCCTCAGGGTCTG	429
Dd	241	GGGAACACACTCAAAGAAAGACTGGATCGCTTACATCTCCAGAGAAATCTTGAGGGGACTG	300
OY	430	GCCCCATCTCATGCCCCACAGGTGATTCATGAGACATCAAGGGGCAGATGTGCTGCTG	489
Dd	301	GCACATCTTCAATCATTCATGATGATTCACGGGGATATCAAGGGCCAGAAATGTGTTGCTG	360
OY	490	ACAGAGAAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTAGTGCTCTCAGCTGGAACCGCAC	549
Dd	361	ACTGGAATGACAGAGGTAACTTGTTAATCTTGTGTGAGTGCTCAGCTGGAACAGAACT	420
OY	550	GTTGGGCAACAGGAACACTTTCATTTGGGACTCCCTCTAGTGGATGGCTCCAGAGGTCACTCGCC	609
Dd	421	GTTGGGCGGAATAATACCTTCATAGGACCTCCCTACTGATGGCTCTGAGGTCACTCGCC	480
OY	610	TGTGATGAAACCCCTGATGCCACTATGATTAACAGAGTGAATATTGGTCTTAGAGATC	669
Dd	481	TGTATGAGAACCCGATGCCCACCTATGATTAACAANNNNNNNNNNNNNNNNNNNNNNNN	540
OY	670	AACAGCATGAGATGGCAGAGGAGACCCCCCTCTGTGTGACATGACCCCATGCGAGCC	729
Dd	541	NNNT	600
OY	730	CTCTTCCTCATTCCTCGGAAACCTCGCGCCAGGCTCAAGTCCAAAGAGTGTCTAAGAAG	789
Dd	601	CTGTTCTCATATCCAGAAACCTCTCTCCCGGCTGAAGTCAAAAATAATGTGTGAAGAA	660
OY	790	TTCAATGACTTCATTGACACATGTCTCAAGACTTACCTGAGCCGCCACCCAGCGAG	849
Dd	661	TTTTTTAATTTTATAGAAAGGGTGCCTGTGTGAAGAAATTAATGCAAGCGCCCTTACAGAG	720
OY	850	CAGCTACTGAAGTTTCCCTTCAATCCGGGACAGAGCCACGAGCGGCAAGTCCGATCCAG	909
Dd	721	CAGCTTTTGAACAACCTCTTTTATTAAGGATCAGCCMAATGAAAGGCAAGTTAGAAATCCAG	780
OY	910	CTTAAGGACCAATTGACCGAATCCCGGAAGAACGGGGGTGAAAGAGAGAGACAGAAATAT	969
Dd	781	CTTAAGGATCATATGATGATCGACCAAGGAANNNGAAGCGAGAAAGNNNNNNNNNNNN	840
OY	970	GAGTACAGCGCAGCAGAGAGGAAGATGACAGCCATGAGAGGAAGAGAGGCCAAGC---	1022
Dd	841	NNNT	900
OY	1027	TTCATCATGAAGCGTGCCTGAGAGTCGACTTAAGCGCGGAGTTTCTCGGCTCCAGCAG	108
Dd	901	TCCATTTGGAAGGTGCTGTTGATGCTACTCTTCTGTGAGATTTCTTGAGACTGCGACAG	960
OY	1087	GAATAATAGACAATCAGAGGCTTTAAAAACAGCAGCAGCAGCTGCAAGCAGACAGCAG	1144
Dd	961	GAGAACAAAGAACGTTTCGAGGCTTTTCGAGACAAACGTTTACTACAGAGAACACAGCTC	1022
OY	1147	CGAGACCCCGAGGCAACATCAAAACACTGCTGCAACAGCGGCACAGCGGCTATAGAGAG	1200
Dd	1021	CGGAGCAGAGAAATATTAAGGCACTGCTGCGAGAGACACAGACGGAATTTAGACGAG	108
OY	1207	CAGAGAGAGAGCGCGCGCTGTGAGAGCAACAGCGCGGGAGCGGGAGCAGCGGAAG	1266
Dd	1081	CAGAAAGAACAGAGCGACGCTTAAGAGCAACAAAGAGAGAGCGTGAAGCTGAAGAG	1144
OY	1267	CTGCAAGGAAGAGACAGAGCGCGCTGGAAGCATGCAAGGCTTCTGCGCGGAGAGAG	1332
Dd	1141	CAGCAGGAACGTGAACAGCGAAGGAGAAACAAGAGAAAAGAGCGCTTAGAGAGTTG	1200
OY	1327	GAGCGCGGCAAGCGGACGCTGAGAGAAATACAGCGGAAGCAGCTGGAGAGAGCAGCGG	138
Dd	1201	GAGAG-----AAAGCGCAAGAGAAAGAGAGAGACA	123

OY	1387	CAGTCAGAACCTCTCACAAGCGACTGACAGAGCATGCCTTCACTCAATGCCCTGTGAC	1446
Db	1234	CGGGCAGAAAGAAAAGAGAGATTGAAGAAGAACAGAGTATATCAGG----	GSA CAG 1290
OY	1447	CAGCAGCAAACGACAGCACAGCTTGAAAAACAGACGACGACAGCTTCGTCCGTGGAC	1506
Db	1291	CTAAGAAGAGAGCAGACGGCCTTTGGAAATCTTTCAGCAGCAGCTGTCTCAAGAGAGCC	1350
OY	1507	AGGAAGCCCCCTGTATCATTTATGTGTGGGGCATGAATCCCCTGTACAACCAAGCTGGACC	1566
Db	1351	ATGTTATCTGTACATGACATATGAGAGCCGACACCCGACGACCTGTGACAGACCCTGCACACCG	1410
OY	1567	CGAAGGTAGAAGAGAGAAACAAGATGAACAAGCAGACAGAACTCTCCCTTGCCAAAGAC	1626
Db	1411	CAGCAGAAAGAGCAAGCAAGCTTCATGCTC-----	1444
OY	1627	AAGCCAGGACAGACGGGGCTTAGGCCCTCCATCCCCAGGCTCTCCAGGGCCCCCAGGA	1686
Db	1445	-----CCGAGCCCCAAGGCCCATTAAGAGCTGTGTGACGAGCCCGAAGGTA	1491
OY	1687	CCCCCTTCCCAAGCTCTCTTATGAGAGGGCGGAGAGCCCAAGAGGACCCGACAAG	1746
Db	1492	CAGTGGTCCCACTGGSCATCTCTCAAG-----ACAA T 1524	
OY	1747	TCCCTGCAGACCAAGCCCACTGGCTGTCTTCCAGACTCCCATGACCCCGAC	1806
Db	1545	GTTTTCCCTGTCTGGCATTCCTTCTTCAGTGACCTTTCCTCCCAATTTGACAC	1584
OY	1807	CCTGCCATTCCTCCGACCCACTGCACGCCCATGTGCCGAGAGCTGTATCCGCAGAAT	1866
Db	1585	CACCATCTTCTGTTCAGAGCCCATGTCACTTCCCGCATGTAGTGTCAATGCTCAAGC	1644
OY	1867	TCAGACCCCACTCTGAAGAGACTGTGGCCCCAGCCCCGAATCCCAGCTGGGATCCGCCCA	1926
Db	1645	CTGTG---TAAGTCAGAGGCGCTGACCTTACCAAAAGA CTGGTTTATATCAGACAT	1701
OY	1927	GATAACGAGGCCCACTCCAGAGTGCTCTCAGAGACCTCATCTATGSCCACTGACCTTTAAC	1986
Db	1702	GGCAGAGTGCTTCCAAAGAGGGTTCTGTGAAGAACATCTCGCTCCCTGTGTGCC	1761
OY	1987	ACCA GTGGGGCCGAGGGTCCCGGCAGGCCCAAGS CATGCCGTGCACACTTCGACGAC	2046
Db	1762	CGTGA GATTTCCCACTCAGGGCAGTGGGACGAGAA TACAGGCGACGACAGAGAA C	1821
OY	2047	TCCGCTTGGCAATCTATCTGTGA AAGGGGAGAGCGGGGACCCCAAACTCCAGG	2106
Db	1822	TTCCACAANNN	1881
OY	2107	CCCCCTGT CAGCCCCCTGTGCCCCCAAGCTTCTAGTAACCCGACTCAGAGGAGC	2166
Db	1882	NN	1941
OY	2167	GACCTGTGCTGGGAACGCTCGGACAGCGTCTTTCAGCTTTCACGGGCACTTCCCCAG	2226
Db	1942	NN	1982
OY	2227	GCTGCTCACTGAGCGGGAACCGCGGTGGGAACCTCTCAAACTGGA CAGCTCCCTGTG	2286
Db	1983	-----ATCATCCAAAGTCTGMAAGCTCTCATCTTCAGCGCTGGA AAATGCA GTG	2031
OY	2287	CTCTCCCTGGGAATPAAAGCCCAAGCCCAAGCAACAACGCTCA CGGCGCAGGCCGCA	2346
Db	2032	AAAAAACCTTGAAGATPAAAGGAATTTTCAAA CCCCCTCAAGCTGTGTAAAGATTGAT	2091
OY	2347	GACTTTGTGTGCTGA AAGCGGA CTTCGACGAGGCCCTTGGCTCTCCAGAAAGCC	2406
Db	2092	CTGACCGCACTGGCCAAAGAGCTTTCGACAGTGAAGATGTACGGCCACTTCACAAAGTA	2151
OY	2407	ATGGA CTACTGCTGCTCCAGCGAGGAGGTGAAAAGCACTGAGAGCAAGAGAAAGAAAGCC	2466
Db	2152	ACGGA CTACTCTCTATCCA GTGAGGAGTCCGGGAGAGAGATGAGAGAGAGAGATGTG	2211
OY	2467	GAAAGCGGGCAGACGAGGGGACAGAAATACCTCTGGGGGCCGAGAGTGGGAAATCA	2526

Db	2212	GAGCAGGAAGGGGCTGAGAGTCCACTCAGAGACCAAGGACACCAAG-----	2260
Qy	2527	GACACGCTCAGACACCACTGGTGGTCCACGACGTCCAGAGATCACCGGACCACGCCCA	2586
Db	2261	--CAGCGTCATCTCTGAAATTGGACGAAATGGTGAACGGAAATCTGTGAAA-----	2307
Qy	2587	TACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGAGCGGAACCTGCTGCAT	2646
Db	2308	-----ACCATGATGTGCTCATGTAGATGATAGAAAAGTGAAGCGGCGCAT-----	2348
Qy	2647	GCTGACAGCAATGGGTACACAACTGCTGTGACGTGGTCCAGGCCACCTACCCACC	2706
Db	2349	-----GACCCCATCCAGAGAGGCGCACTCTAATCGTCGCGCCAGACTCAGATCC	2394
Qy	2707	GAGAAACAGCAAAAGGCCAAAGCCCAACCCCTGAAGAGTGGAGTGGACTACAGTCTCGT	2766
Db	2395	GCTTATACCACTCTCAGAAACACAAATCTTCTCTCTTAAACCTTTTATAGACCC	2454
Qy	2767	GGGCTGTAAAGGCCCTGGCGAAGCTCGTTCAAGATGTTTGTGGATCTAGGATCTAC	2826
Db	2455	AGATTACTACAGATTCTTCATCTAGGGGGAACAAGTACCTTGTGGTGGATTCTTC	2514
Qy	2827	CAGCTGGAAGCATGGTGGGACAGCATCCCACTCACAGCCCTTAGTGGTGGAGAGGCACT	2886
Db	2515	TGTGATGGGATGAGACCAAGACCAT-----	2541
Qy	2887	CGGCTCGACAGCTGCAAGTACGAGTGAAGGAGGTTCTGTGTCAACTGAATCCCAAC	2946
Db	2542	-----AGCAAGATCTTACCAGGAGGCTCAGTGGTCAATGTGAATCTTACC	2589
Qy	2947	AACACCCGGGCGCCACAGTGAAGCCCTTGAGATCCGGAAGTACAAAGACGATTCACCTCC	3006
Db	2590	AAACATAGGCAACAGATGACACCCCGGAGATTGTAAATACAAAGAGGTTTAACTCT	2649
Qy	3007	GAGATCTCTGTGCAAGCCCTTTGGGGGTCAACTGCTGGTGGGACGAGAAACGGCTG	3066
Db	2650	GAGATCTGTGTGCTGCTTATGGGGAGTGAATTTGCTAGTGGGTACAGAGATGGCTGTG	2709
Qy	3067	ATGTTGCTGGAACCAAGTGGGCGGAGGGAAGGTGATGGAATCATTTGGGCGGCGAGCTTC	3126
Db	2710	ATGCTGCTGGAACAGAGTGGCCAGAGGAGGCTTATCTCTGATCAACCGAAGACGATTT	2769
Qy	3127	CAGCAGATGATGTGTCTGAGAGGGGCTCAACTGCTGATCAACATCTCAGGAAAGGAAAC	3186
Db	2770	CAACAAATGGAAGTACTTGAAGGCTGAAATGTCTTGGTGAACAATCTGGCAAAAGGAT	2829
Qy	3187	AAACTGCGGGGTGTATTACCTGTCTGTGCTCCGGAACAAGATTCTGCACATGACCCAGAA	3246
Db	2830	AAAGTTACGTGTCTACTATTGTCTCGGTTAAGAAATAAATACTTCAAAATGATCCAGAA	2889
Qy	3247	GTGGAAGAAAGCAGGGCTGGAACAACGTGGGGGACATGAGGGCTCGGGCACTACCGT	3306
Db	2890	GTTGGAAGAAAGCAGGAGTGAACAACGTAGGGGATTTGGAAGGATGTGACATTATPAA	2949
Qy	3307	GTTTGAATAACGAGCGGATTAAGTTCTGTGTCATCGCCCTCAAGAGCTCGTGAAGTG	3366
Db	2950	GTTGNN	3009
Qy	3367	TATGCTGGGCCCCCAACCTTACACAATTCATGACCTTCAAGTCTTTGGCCGACCTC	3426
Db	3010	NN	3069
Qy	3427	CCCCACGGCCCTCTGCTGTGTCGACCTGACAGTAAAGAGGGGCGCGCTCAAGCTATC	3486
Db	3070	GTAACAAGCATTAACGTGTGGTAATCTCACTGTTAGGAAGGCCAGAGGTTGAAGTATTC	3129
Qy	3487	TATGGCTCAGATGCTGCTTCCATGCTGTGGATGTCACTCGGGAACAGCTATGACATC	3546
Db	3130	TATGATCTCTGTGCTGAATTCATGCTGTGTTATGTGAATTCAGATCTATGACATT	3189
Qy	3547	TACATCCCTGTGACATTCAGAGCCAGATCGGCCCCAATGCAATCTTCTCCCAAC	3606

Db 3190 TATCTACCAACATATCCAGTGTAGCATCAAAACCCATGCAATCATCTCCCCAT 3249  
QY 3607 ACCGACGGCATGAGATGCTGTGTGTCTACGAGACGAGGGGTCTAGTCAACAGTAC 3666  
Db 3250 ACAGATGGAATGAGCTTCTGTGTGTCTATGAAATGAGGGGCTTTATGTAACATAT 3309  
QY 3667 GGGCCATCATTAAGATGTGTGTGTGTGAGTGGGGGAGATGCTTCTGTGTGTGTG 3726  
Db 3310 GGAAGATGACCAAGATGTATGTTCTACAGTGGGAGAGATGCTTACGTCAATACATAT 3369  
QY 3727 ATCTCTCCACCAATATATGGGCTGGGGGTGAGAAAGCCATGAGATCCGCTCTGTGAG 3786  
Db 3370 ATTCATCCAAATCAACATATGGGCTGGGAGAGAGCCATGAGATCCGATCTGTGAA 3429  
QY 3787 ACGGCGACCTGAGAGGGGTCTTCATGCAAAACAGCTCAGAGGTCAAGTCCGTGTGT 3846  
Db 3430 ACTGTCTCTGAGATGTGTGTCTTCATGCAAAAGGGCTCAAAAGCTTAATTTCTGTGT 3489  
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Db 3430 GAACCAATGACAAAGGTGTTTTTTCCTTCAGTCCGCTGTGGGGGAGAGCCAAAGTTAC 3549  
QY 3907 TTCTGACTCTGACCCGTACTGCAATCATGAAGTGT 3943  
Db 3550 TTCTGACTCTGACCCGTACTGCAATCATGAAGTGT 3586

RESULT 10  
BM541693 1026 bp mRNA linear EST 20-FEB-2002  
LOCUS AGENCOURT 6448280 NIH\_MGC\_71 Homo sapiens cDNA clone IMAGE:5531587  
DEFINITION 5', mRNA sequence.  
ACCESSION BM541693  
VERSION BM541693.1 GI:18770559  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 1026)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LHAM12213 row: h column: 20  
High quality sequence stop: 681.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:5531587"  
/issue\_type="leiomycarcoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1ib="NIH\_MGC\_71"  
/note="Organ: uterus; Vector: pCMV-Sport6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 2.1 kb."

ORIGIN  
Query Match 20%; Score 814.4; DB 12; Length 1026;  
Best Local Similarity 95.5%; Pred.No.9.7e-129;  
Matches 871; Conservative 0; Mismatches 36; Indels 5; Gaps 3;  
QY 2360 TGAAGAGCGGACTGTGACGAGGCCCTCGGCTCCCAAGAGCCATGACTACTCGT 2419

Db 1 TGACAGCGCTGGCTCTGACAGAGGCCCTCCGCTCCCAAGGCCATGACTACTCGT 60  
QY 2420 CGTCCAGGAGAGGTGGAAGAGTGTGAGACGACGAGAGAAAGGCGAGCGGCGAG 2479  
Db 61 GGTCCAGGAGAGGTGGAAGAGTGTGAGACGACGAGAGAAAGGCGAGCGGCGAG 120  
QY 2480 CAGAGGAGAGAGATACCCCTGGGGGCGCAGCGATGGGATACAGACGCTCAGCA 2539  
Db 121 CAGAGGAGAGAGATACCCCTGGGGGCGCAGCGATGGGATACAGACGCTCAGCA 180  
QY 2540 CCAATGTGTGTCCAGACGTCCAGAGATCACCGGAGCCCAAGCCCAATACCGGGGGCGCA 2599  
Db 181 CCATGTGTGTCCAGACGTCCAGAGATCACCGGAGCCCAAGCCCAATACCGGGGGCGCA 240  
QY 2600 CCATGTGTGTCCAGAGCCCTCGTGAAGAGAGCGGAACTGTGATCTGATCAGCAATG 2659  
Db 241 CCATGTGTGTCCAGAGCCCTCGTGAAGAGAGCGGAACTGTGATCTGATCAGCAATG 300  
QY 2660 GGTACACAAACCTGTGACGTGTCCAGCCAGCCACTCAACCAACGAGAAACAGCAAG 2719  
Db 301 GGTACACAAACCTGTGACGTGTCCAGCCAGCCACTCAACCAACGAGAAACAGCAAG 360  
QY 2720 GCCAAAGCCACCTCCAGAGATGGAGTGTGACTACATCTCTGTGGCTGTGAAGG 2779  
Db 361 GCCAAAGCCACCTCCAGAGATGGAGTGTGACTACATCTCTGTGGCTGTGAAGG 420  
QY 2780 CCCCTGGAGAGGCTCGTTCAGATGTTTGTGATCTAGGGATCAACGAGCTGAGGCA 2839  
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QY 2840 GTGGGACAGATCCCATCAACAGCCCTTATGTGTGAGAGAGGCACTGGGCTGACAGC 2899  
Db 481 GTGGGACAGATCCCATCAACAGCCCTTATGTGTGAGAGAGGCACTGGGCTGACAGC 540  
QY 2900 TGCACTACAGATGTGAGAAAGGTTTGTGTCTCAACGTGAATCCCAACCAACCCGGGGCC 2959  
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QY 2960 ACAGTGAACCCCTGAGATCCGGAAGTACAGAAAGCCATTCACCTCCGAGATCCTCTGTG 3019  
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QY 3020 CAGCCCTTGTGGGGGTCAACCTGTCTGTGTGGGCAAGAGAGGAGTGTGTGTGAGCC 3079  
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QY 3080 GAATGTGGCAGGAGCAAGGTGTATGTGACTATTTGGGCGGAGCTTCCAGCAGATGATG 3139  
Db 721 GAATGTGGCAGGAGCAAGGTGTATGTGACTATTTGGGCGGAGCTTCC-GCAGATGATG 779  
QY 3140 TGCTGAGAGGGGTCAACCTGTGATCACCATC-TCAGGGAAAAGGAACTGCGGGTG 3198  
Db 780 TGCTGAGAGGGGTCAACCTGTGATCACCATC-TCAGGGAAAAGGAACTGCGGGTG 839  
QY 3199 TATTACTGTCTGTG---CTCCGGAACAAGATTCTGCACAATGACCGAAGTGTGAGAG 3255  
Db 840 TATTACTGTCTGTG---CTCCGGAACAAGATTCTGCACAATGACCGAAGTGTGAGAG 899  
QY 3256 AAGCAGGCGTGG 3267  
Db 900 AAGCAGCCTGGG 911

RESULT 11  
BO684810 907 bp mRNA linear EST 15-JUL-2002  
LOCUS AGENCOURT 8346064 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6250774  
DEFINITION 5', mRNA sequence.  
ACCESSION BO684810  
VERSION BO684810.1 GI:21810126  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM	Human sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS	1 (bases 1 to 907)
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strusberg, Ph.D. Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: L16CM2394 row: F column: 23 High quality sequence stop: 665. Location/Qualifiers
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ORIGIN	
Query Match	20.2%; Score 799.6; DB 13; Length 907;
Best Local Similarity	98.9%; Pred. No. 3,1e-126;
Matches	805; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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Ds	1 ATGTGCTGAGAGGGGCTCAACTGCTCATCACCCTCAGAGAAAGAAACAACTGCGG 60
Ds	3197 TGTATTACTCTGTCTGCTCCGGAACAGATTCTGCACATACCCAGATGTGGAAGA 3255
Ds	61 TGTATTACTCTGTCTGCTCCGGAACAGATTCTGCACATACCCAGATGTGGAAGA 120
Ds	3257 AGCAGGGCTGGACACCGTGGGGGACATGAGAGGGCTGCGGGACCTACCGTGTGGAAT 3315
Ds	121 AGCAGGGCTGGACACCGTGGGGGACATGAGAGGGCTGCGGGACCTACCGTGTGGAAT 180
Ds	3317 ACAGCGGATTAAAGTTCTGTGTCATCGCCTTCAAGAGCTCCGTGAGGTGTATGCGT 3376
Ds	181 ACAGCGGATTAAAGTTCTGTGTCATCGCCTTCAAGAGCTCCGTGAGGTGTATGCGT 240
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Ds	241 CCCCCAAACCTTACACAAATTATGCGCTTCAAGTCTTTTCCGACCTCCCCACCGC 300
Ds	3437 CTCTGCTGAGTGAAGCTGACAGTAGAGAGAGGGGACAGGCTCAAGGTCAATGTGAGTCA 3499
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Ds	3497 GTGCTGAGTTCATGCTGTGATGTGCACTCGGGGAAACAGCTATGACATTAATCCCTG 3556
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Ds	3557 TGCATCTCAAGAGCCAGATCAAGCCCATATGCAATCTTCTCCCAACACCAAGGCA 3618
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QY	3737	ACCAAGATTAATGGGCTGTGGGTGTGAGAAAGCCATTGATTCGGCTCTGTGTGAGACGGGGCCACC	3796
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QY	3797	TCGACGGGGCTTTTATATGACAAAGACCTCAGAGCTCAAGTTCCTGTGTGAGGGGGAATG	3856
Db	661	TCGACGGGGCTTTTATATGACAAAGACCTCAGAGCTCAAGTTCCTGTGTGAGGGGAATG	720
QY	3857	ACAAGGTGTTTTTTGGCTCAGTTCGGCTCTGTGGGGGACAGACGCAAGTATTCTTACATGATCTC	3916
Db	721	ACAAGGTGTTTTTTGGCTCAGTTCGGCTCTGTGGGGGACAGACGCAAGTATTCTTACATGATCTC	780
QY	3917	TGAACCGTAACTGCATCATGAACTGTGGAAAGG	3950
Db	781	TGAACCGGTACTGCATCATGAACTGTGGAAAGG	814

	RESULT 12	
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LOCUS	866 bp	mRNA linear EST-25-SEP-2001
DEFINITION	603024432P1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5194998 5' , mRNA sequence.	
ACCESSION	B1756763	
VERSION	B1756763.1	GI:15748341
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
TITLE	NIH-MGC http://mgc.nci.nih.gov/.	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT	Unpublished (1999)	
	Contact: Robert Strausberg, Ph.D.	
	Email: csapbs@remail.nih.gov	
	Tissue Procurement: Life Technologies, Inc.	
	cDNA Library Preparation: Life Technologies, Inc.	
	GNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
	DNA Sequencing by: Incyte Genomics, Inc.	
	Clone distribution: MGC clone distribution information can be	
	found through the I.M.A.G.E. Consortium/LLNL at:	
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	/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;	
	Site_2: EcoRV (destroyed); RNA source anonymous pool of 6	
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	primed and directionally cloned (EcoRV site is destroyed	
	upon cloning). Average insert size 1.5 kb, insert size	
	range 1-3 kb. Library is normalized and enriched for	
	full-length clones and was constructed by C. Gruber	
	(Invitrogen). Research Genetics Genetics screening code 019. Note:	
	this is a NIH_MGC Library."	
ORIGIN		
Query Match	20.2%	Score 799; DB 12; Length 866;
Best Local Similarity	98.8%	Pred. No. 3.8e-126;



Matches	857; Conservative	0; Mismatches	5; Indels	5; Gaps	5;
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QY	3039	CCTGCTGGTGGGCAAGAGAGCGGGCTGATGTTGTGTGAGCCGAGTGGGCAAGGT	3098		
DB	61	CCTGCTGGTGGGCAAGAGAGCGGGCTGATGTTGTGTGAGCCGAGTGGGCAAGGT	120		
QY	3099	GTATGACTCATTTGGGGCGGCGACGCTTCCAGAGATGATGTGTGAGGGGCTCAACT	3158		
DB	121	GTATGACTCATTTGGGGCGGCGACGCTTCCAGAGATGATGTGTGAGGGGCTCAACT	180		
QY	3159	GCTCATCAACATCTCAAGGAAAGAAACAACGCGGGGTATTAACCTGCTCTGGCTCG	3218		
DB	181	GCTCATCAACATCTCAAGGAAAGAAACAACGCGGGGTATTAACCTGCTCTGGCTCG	240		
QY	3219	GAACAAGATTCGACCAATGACCCAGAAAGTGAAGAAAGCAGGGCTGAGCAACCGTGG	3278		
DB	241	GAACAAGATTCGACCAATGACCCAGAAAGTGAAGAAAGCAGGGCTGAGCAACCGTGG	300		
QY	3279	GGACATGAGAGGCTGCGGCACTACCGTGTGTGAATAACGACGAGTTAAGTCTCTGT	3338		
DB	301	GGACATGAGAGGCTGCGGCACTACCGTGTGTGAATAACGACGAGTTAAGTCTCTGT	360		
QY	3339	CATGCCCTTCAGAGAGCTCCGTGAGAGTGTATCCTGGGGCCCCCAACCTTACCAAAAT	3398		
DB	361	CATGCCCTTCAGAGAGCTCCGTGAGAGTGTATCCTGGGGCCCCCAACCTTACCAAAAT	420		
QY	3399	CATGCCCTTCAGAGAGCTCCGTGAGAGTGTATCCTGGGGCCCCCAACCTTACCAAAAT	3458		
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QY	3579	GGCCCATGTCATCTCTCCGCCAACACGACGCGCATGAGATCTCTGTGCTACGA	3638		
DB	600	GGCCCATGTCATCTCTCCGCCAACACGACGCGCATGAGATCTCTGTGCTACGA	659		
QY	3639	GGACGAGGAGTGTCTACGTCACACGTAACGAGGCGCATCTTAAAGATGTGTGTGCAAT	3697		
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## RESULT 13

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 ACCESSION BUS42006  
 VERSION BUS42006.1 GI:22852489  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	NIH-MGC	http://mgi.nci.nih.gov/	Unpublished (1999)	Contact: Robert Strausberg, Ph.D. Email: cga@bbs-remail.nih.gov Tissue Procurement: DCTD/DRP
				CDNA Library Preparation: Rubin Laboratory
				cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
				DNA Sequencing by: Agencourt Bioscience Corporation
				Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
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				/clone_1ib="NIH MGC 40"
				/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN				
Query Match	19.7%; Score 779.8; DB 13; Length 881;			
Best Local Similarity	98.9%; Pred. No. 7.4e-123;			
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DB	1	CGTGTCCAGCCCGACCTCAACCCAGAGAACGCAAGGCCAAAGCCCTCCGA	60	
QY	2739	GGATGGAGTGGTGACTCAAGTCTGCGGGGTGTAAGGCCCTGGCAAGCTCGT	2798	
DB	61	GGATGGAGTGGTGACTCAAGTCTGCGGGGTGTAAGGCCCTGGCAAGCTCGT	120	
QY	2799	CACGATGTTTGTGATCTAGGATCTTACCAAGCTGAGGCAAGTGGGACAGCATCCCAT	2858	
DB	121	CACGATGTTTGTGATCTAGGATCTTACCAAGCTGAGGCAAGTGGGACAGCATCCCAT	180	
QY	2859	CACAGCCCTAGTGGGTGAGAGGGCACTCGGTGACACAGCTGCAATGAGTAAAGAA	2918	
DB	181	CACAGCCCTAGTGGGTGAGAGGGCACTCGGTGACACAGCTGCAATGAGTAAAGAA	240	
QY	2919	GGGTTCTGGGTCAACGTGAATCCACCAACACCGGGGCCCAAGTGAAGCCCTGAGAT	2978	
DB	241	GGGTTCTGGGTCAACGTGAATCCACCAACACCGGGGCCCAAGTGAAGCCCTGAGAT	300	
QY	2979	CCGGAAGTACAAAGAGCATTCGAGATCTCTGTGTGAGCCCTTTGGGGGTCAA	3038	
DB	301	CCGGAAGTACAAAGAGCATTCGAGATCTCTGTGTGAGCCCTTTGGGGGTCAA	360	
QY	3039	CCTGCTGGTGGGCAAGAGAGCGGCTGATGTTGTGTGAGCCGAGTGGGCAAGGT	3098	
DB	361	CCTGCTGGTGGGCAAGAGAGCGGCTGATGTTGTGTGAGCCGAGTGGGCAAGGT	420	
QY	3099	GTATGACTCATTTGGGGCGGCGACGCTTCCAGAGATGATGTGTGAGGGGCTCAACT	3158	
DB	421	GTATGACTCATTTGGGGCGGCGACGCTTCCAGAGATGATGTGTGAGGGGCTCAACT	480	
QY	3159	GCTCATCAACATCTCAGGAGAAAGAAACAACGCGGGGTATTAACCTGTCTGTGCTCG	3218	



Db 481 GCTCATCCATCTCAGGAAAGAAACAACTGCGGTGTTTACTCTGTCTGCTCCG 540  
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 1 (bases 1 to 936)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgsab@remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov  
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 High quality sequence stop: 686.  
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ORIGIN  
 Query Match 19.5%; Score 772.4; DB 12; Length 936;  
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 VERSION CA454128.1 GI:24903563  
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 1 (bases 1 to 881)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@rs-remail.nih.gov  
Tissue Procurement: Kristi A. Eglund, Ira Pastan  
cDNA Library Preparation: Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Place: LNL14275 row: k column: 13  
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Location/Qualifiers

FEATURES  
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/note="Vector: PCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
Subcloned with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Eglund, James J. Vincent, Robert Strausberg,
Bungkok Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
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## ORIGIN

Query Match 19.3%; Score 764.4; DB 14; Length 881;

Best Local Similarity 97.5%; Pred. No. 3.2e-120; Matches 821; Conservative 0; Mismatches 11; Indels 10; Gaps 4;

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QY 2518 GGGGATACAGACGCTCAGCAACATGTGTGTCACGACGTGAGAGATACCGGGGACC 2577
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DB 538 GGGGATACAGACGCTCAGCAACATGTGTGTCACGACGTGAGAGATACCGGGGACC 597
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Job time : 6322 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 14:44:02 ; Search time 9933 Seconds  
(without alignments)  
17240.343 Million cell updates/sec

Title: US-10-029-115-1

Perfect score: 3951  
Sequence: 1 gccctctatggcgaccaccagc.....tcacgaactggtgaaggagc 3951

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 2167151695 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_ay:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vi:\*  
30: em\_hcg\_hum:\*  
31: em\_hcg\_in:\*  
32: em\_hcg\_other:\*  
33: em\_hcg\_mus:\*  
34: em\_hcg\_pln:\*  
35: em\_hcg\_rtd:\*  
36: em\_hcg\_mam:\*  
37: em\_hcg\_vrt:\*  
38: em\_ay:\*  
39: em\_hcg\_hum:\*  
40: em\_hcg\_mus:\*  
41: em\_hcg\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2201	55.7	5014	9	BC034673 Homo sapi
2	1787	45.2	4133	6	BD243845 STE20-rel
3	1787	45.2	4133	6	AR435598 Sequence
4	1701	43.1	3888	9	AB035698 Homo sapi
5	1689	42.7	4863	9	AB041926 Homo sapi
6	1599	40.5	3735	6	AX235365 Sequence
7	1599	40.5	3822	6	AX235363 Sequence
8	1599	40.5	3912	6	AX235361 Sequence
9	1599	40.5	3999	6	AX235359 Sequence
10	1599	40.5	4590	9	HSM802420 Homo sapi
11	1337	33.8	1482	6	AX235417 Sequence
12	1337	33.8	1649	6	AX235415 Sequence
13	1337	33.8	1717	6	AX235422 Sequence
14	1337	33.8	1787	6	AX235419 Sequence
15	1078	27.3	3824	6	BD183377 Novel gen
16	970	24.6	1964	9	AF218033 Homo sapi
17	575	14.6	1539	6	AX011641 Sequence
18	575	14.6	1539	6	BD262522 Pancreat
19	555	14.0	3152	6	AX834264 Sequence
20	555	14.0	3152	6	AK096610 Homo sapi
21	225	5.7	129169	2	AC032038 Homo sapi
22	225	5.7	129169	2	AC005973 Homo sapi
23	225	5.7	181825	2	AC109333 Homo sapi
24	225	5.7	184595	2	AC015913 Homo sapi
25	205	5.2	58311	2	AC110596 Homo sapi
26	177	4.5	129169	2	AC032038 Homo sapi
27	172	4.4	184595	2	AC015913 Homo sapi
28	128	3.2	151999	2	AC005973 Homo sapi
29	92	2.3	57205	2	AC107995 Homo sapi
30	86	2.2	62919	2	AC107963 Homo sapi
31	77	1.9	146	6	AX139136 Sequence
32	77	1.9	146	6	BD014753 Gene and
33	69	1.7	283	6	AX917332 Sequence
34	69	1.7	283	6	BD052865 Sequence
35	69	1.7	285	6	BD076893 5' EST of
36	62	1.6	295	11	CG9516 human STS C
37	62	1.6	1665	9	AB070507 Homo sapi
38	54	1.4	1628	9	AB070512 Callitric
39	54	1.4	1632	9	AB070513 Lemur cat
40	54	1.4	1655	9	AB070509 Pongo pyg
41	54	1.4	1664	9	AB070508 Pan panis
42	54	1.4	1669	9	AB070510 Hylobates
43	53	1.3	4381	10	BC011346 Mus muscu
44	53	1.3	4842	10	BC052474 Mus muscu
45	53	1.3	4848	10	AB035697 Mus muscu
46	53	1.3	4873	10	AB041925 Mus muscu
47	53	1.3	123943	10	AL592547 Mouse DNA
48	53	1.3	171697	2	AC119116 Rattus no
49	53	1.3	194609	2	AC013775 Mus muscu
50	53	1.3	228232	2	AC090293 Mus muscu
51	53	1.3	263882	2	AC107344 Rattus no
52	51	1.3	1666	6	AB070511 Macaca ar
53	47	1.2	194609	2	AC013775 Mus muscu
54	47	1.2	194609	2	BC056650 Mus muscu
55	44	1.1	1488	6	AX235384 Sequence
56	44	1.1	1657	6	AX235382 Sequence
57	44	1.1	1725	6	AX235389 Sequence
58	44	1.1	1788	6	AX235386 Sequence
59	44	1.1	3915	10	MM088984 U88984 Mus muscu
60	44	1.1	4301	10	AK129191 AK129191 Mus muscu
61	44	1.1	110000	2	AC101727-1 Continuation (2 of
62	44	1.1	110000	2	AC132909 Mus muscu
63	44	1.1	11363	2	AC015383 Drosophi
64	42	1.1	11363	2	AC015383 Drosophi
65	42	1.1	192681	3	AC011905 Drosophi

Pred. No. is the number of results predicted by chance to have a



C 212	27	0.7	199071	10	AL66938	285	26	0.7	463	6	AX210423	AX210423 Sequence
C 213	27	0.7	200202	10	AC112154	286	26	0.7	471	9	HSACG40	X65325 H. sapiens m
C 214	27	0.7	204954	10	AC128028	287	26	0.7	476	6	BD129613	BD129613 Polynucle
C 215	27	0.7	211343	10	AC122630	288	26	0.7	476	9	HSCBPA152	AF001444 Homo sapi
C 216	27	0.7	229684	3	AE003815	289	26	0.7	478	11	AF021127	AF021127 Homo sapi
C 217	27	0.7	236096	3	AE003775	290	26	0.7	496	11	GF0491	G09491 human STS C
C 218	27	0.7	238466	2	AC097567	291	26	0.7	508	10	MUSIERFES	M35872 Mouse MHC C
C 219	27	0.7	239986	2	AC107150	292	26	0.7	520	9	HSAT29554	AZ79564 Homo sapi
C 220	27	0.7	243210	2	AC136831	293	26	0.7	532	8	AY158017	AY158017 Fucoseae
C 221	27	0.7	243530	2	AC130913	294	26	0.7	533	9	HSU80756	U80756 Homo sapien
C 222	27	0.7	267603	3	AE003676	295	26	0.7	536	11	G64267	G64267 10 Human Ho
C 223	27	0.7	290773	2	AC129162	296	26	0.7	567	8	AF442381	AF442381 Pinus tae
C 224	27	0.7	295883	2	AC138459	297	26	0.7	575	9	HSADAN15	Y08266 H. sapiens m
C 225	27	0.7	309958	3	AE003479	298	26	0.7	575	11	BV037017	BV037017 S212P6034
C 226	27	0.7	314957	3	AE003581	299	26	0.7	585	10	MMITGA	X05428 Mouse j1 ge
C 227	27	0.7	320010	2	AC122275	300	26	0.7	588	11	G97681	G97681 S20BP631RG
C 228	27	0.7	338399	2	AC131975	301	26	0.7	594	10	MUSOPA	M16362 Mouse opa r
C 229	26	0.7	36	6	AE2704	302	26	0.7	606	11	G16005	G16005 Mouse opa r
C 230	26	0.7	57	6	AE2703	303	26	0.7	623	6	AR159546	AR159546 Sequence
C 231	26	0.7	57	6	AE2703	304	26	0.7	700	8	AF483857	AF483857 Phaeocitu
C 232	26	0.7	66	6	AE2702	305	26	0.7	716	9	HSAD10	Y08267 H. sapiens m
C 233	26	0.7	69	6	AR159553	306	26	0.7	766	9	AF467252	AF467252 Homo sapi
C 234	26	0.7	75	6	AR159550	307	26	0.7	780	9	HSAC124720	AJ324720 Homo sapi
C 235	26	0.7	78	6	AR159551	308	26	0.7	788	10	AF083656	AF083656 Mus muscu
C 236	26	0.7	78	6	AR159552	309	26	0.7	792	6	BD124983	BD124983 Primer fo
C 237	26	0.7	87	6	AX384806	310	26	0.7	793	6	BD126651	BD126651 Primer fo
C 238	26	0.7	107	6	BD274846	311	26	0.7	800	6	BD079422	BD079422 Cancer-48
C 239	26	0.7	107	6	AR205312	312	26	0.7	800	6	A92446	A92446 Sequence 7
C 240	26	0.7	112	11	G64274	313	26	0.7	800	6	AR018062	AR018062 Sequence
C 241	26	0.7	119	11	G64277	314	26	0.7	800	6	AR020961	AR020961 Sequence
C 242	26	0.7	156	11	G10850	315	26	0.7	800	6	AR022342	AR022342 Sequence
C 243	26	0.7	163	4	BOVMBR	316	26	0.7	800	6	EACDSB	A22653 E. acervulin
C 244	26	0.7	169	6	BD274843	317	26	0.7	800	6	I66468	I66468 Sequence 7
C 245	26	0.7	169	6	AR205309	318	26	0.7	800	6	BD131291	BD131291 Coccidioid
C 246	26	0.7	175	3	AF418589	319	26	0.7	818	11	BV036574	BV036574 S212P6452
C 247	26	0.7	183	6	AR401376	320	26	0.7	837	10	MMUS3564	U53564 Mus musculu
C 248	26	0.7	184	4	PICTRBP	321	26	0.7	849	9	HUMMNAD	L10375 Human (clon
C 249	26	0.7	190	4	HSTBPR	322	26	0.7	850	9	HSU80758	U80758 Homo sapien
C 250	26	0.7	190	6	BD274848	323	26	0.7	877	9	PEY133272	AJ133272 Pongo pyg
C 251	26	0.7	190	6	AR205314	324	26	0.7	900	3	AY339956	AY339956 Drosophi
C 252	26	0.7	218	11	G64270	325	26	0.7	912	3	HSU80741	U80741 Homo sapien
C 253	26	0.7	234	9	AY368204	326	26	0.7	925	3	AY339971	AY339971 Drosophi
C 254	26	0.7	237	3	AY333193	327	26	0.7	926	3	AY339948	AY339948 Drosophi
C 255	26	0.7	238	3	AY333194	328	26	0.7	936	3	AY339958	AY339958 Drosophi
C 256	26	0.7	239	9	HSAT279566	329	26	0.7	942	6	AX794681	AX794681 Sequence
C 257	26	0.7	240	3	AY333191	330	26	0.7	945	6	AX794594	AX794594 Sequence
C 258	26	0.7	240	3	AY333195	331	26	0.7	967	8	AK058253	AK058253 Oryza sat
C 259	26	0.7	243	3	AY333196	332	26	0.7	1049	9	HSU92983	U92983 Homo sapien
C 260	26	0.7	250	3	AY029717	333	26	0.7	1065	6	EO9296	EO9296 cDNA encodi
C 261	26	0.7	252	10	MMIR	334	26	0.7	1065	10	HAMTRP	D30051 Mesocricetu
C 262	26	0.7	256	11	G64278	335	26	0.7	1114	9	AF322859	AF322859 Macaca mu
C 263	26	0.7	264	9	AF330032	336	26	0.7	1124	9	AF284423	AF284423 Homo sapi
C 264	26	0.7	270	3	AY333192	337	26	0.7	1156	10	MMU80889	U80889 Mus musculu
C 265	26	0.7	271	11	G16013	338	26	0.7	1181	3	AY089280	AY089280 Drosophi
C 266	26	0.7	281	3	AY333200	339	26	0.7	1257	9	AF467253	AF467253 Homo sapi
C 267	26	0.7	282	3	AY333198	340	26	0.7	1293	9	AF467258	AF467258 Homo sapi
C 268	26	0.7	285	5	GGRE16E1	341	26	0.7	1350	3	D83241	DB3241 Antherea p
C 269	26	0.7	292	11	G16008	342	26	0.7	1368	9	AF467259	AF467259 Homo sapi
C 270	26	0.7	303	9	AF330031	343	26	0.7	1374	10	S74520	S74520 Cdx-2=clisu
C 271	26	0.7	305	6	BD129589	344	26	0.7	1375	10	BC003476	BC003476 Mus muscu
C 272	26	0.7	306	6	BD129589	345	26	0.7	1389	9	AF322864	AF322864 Homo sapi
C 273	26	0.7	339	3	AY333202	346	26	0.7	1403	4	AB070516	AB070516 Canis fam
C 274	26	0.7	354	11	G09937	347	26	0.7	1411	9	HUMCBFA	LA0992 Homo sapien
C 275	26	0.7	390	9	AF330028	348	26	0.7	1412	9	HSMPQROT	Z50192 H. sapiens m
C 276	26	0.7	393	3	AY333203	349	26	0.7	1413	3	AF364332	AF364332 Antherea
C 277	26	0.7	397	3	HSJ002193	350	26	0.7	1492	6	BD190352	BD190352 Propytlac
C 278	26	0.7	398	3	SGANDBG	351	26	0.7	1509	3	AF454830	AF454830 Homo sapi
C 279	26	0.7	398	6	BD129604	352	26	0.7	1524	3	AY119111	AY119111 Drosophi
C 280	26	0.7	409	6	AF330029	353	26	0.7	1533	6	AX260069	AX260069 Sequence
C 281	26	0.7	423	3	AY333206	354	26	0.7	1547	6	AX401992	AX401992 Sequence
C 282	26	0.7	441	3	HAR504785	355	26	0.7	1547	10	RNU94710	U94710 Rattus norv
C 283	26	0.7	458	3	AF229981	356	26	0.7	1562	3	DMU33015	U33015 Drosophila
C 284	26	0.7	459	6	AR401373	357	26	0.7	1628	5	AB012300	AB012300 Lampetra

358	26	0.7	1630	3	AY118785	Drosophill	431	26	0.7	2774	3	AF053079	AF053079 Drosophill
359	26	0.7	1631	6	BD190351	Prophyliac	432	26	0.7	27891	3	S79891	S79891 str-stripe {
360	26	0.7	1641	10	BC009120	Mus muscu	433	26	0.7	2811	3	AB087582	AB087582 Aplysia k
361	26	0.7	1659	9	BC018929	Homo sapi	434	26	0.7	2813	10	BC011132	BC011132 Mus muscu
362	26	0.7	1680	6	E09295	cdna encodi	435	26	0.7	2814	3	DNAK4	DNAK4
363	26	0.7	1694	6	BD190350	Prophyliac	436	26	0.7	2824	3	AY061493	AY061493 Drosophill
364	26	0.7	1709	5	AB001868	Anolis ca	437	26	0.7	2830	3	AF009676	AF009676 Drosophill
365	26	0.7	1710	3	AF027123	Drosophill	438	26	0.7	2833	8	AK110285	AK110285 Oryza sat
366	26	0.7	1719	3	HSU80746	Homo sapien	439	26	0.7	2834	3	DROPOHC	DROPOHC
367	26	0.7	1722	4	AB048335	Equis cab	440	26	0.7	2868	3	AF084525	AF084525 Drosophill
368	26	0.7	1725	9	HUMRNAH	Human (clon	441	26	0.7	2896	10	AY125963	AY125963
369	26	0.7	1726	9	HSU80759	Homo sapien	442	26	0.7	2901	3	DME252124	DME252124
370	26	0.7	1725	9	HSU80759	Homo sapien	443	26	0.7	2922	10	MMU05252	MMU05252
371	26	0.7	1791	10	AF010284	Mus muscu	444	26	0.7	2943	10	BC052726	BC052726
372	26	0.7	1802	6	AX440493	Sequence	445	26	0.7	2954	5	AB001869	AB001869
373	26	0.7	1852	9	HSADN26	Y08265 H. sapiens m	446	26	0.7	2957	3	BT004853	BT004853
374	26	0.7	1862	9	BC012182	Homo sapi	447	26	0.7	2960	3	DMTRACDEF	DMTRACDEF
375	26	0.7	1889	8	AK101253	Oryza sat	448	26	0.7	2969	8	AF321465	AF321465
376	26	0.7	1922	9	MMU242441	Macaca mu	449	26	0.7	2993	10	BC050858	BC050858
377	26	0.7	1922	9	MMU291498	Macaca mu	450	26	0.7	2994	3	AF461101	AF461101
378	26	0.7	1922	9	MMU291499	Macaca mu	451	26	0.7	3009	3	AY070882	AY070882
379	26	0.7	1926	10	AF339104	Mus muscu	452	26	0.7	3054	10	RNIP2	RNIP2
380	26	0.7	1956	9	HSAD14	Y08263 H. sapiens m	453	26	0.7	3095	6	AX800484	AX800484
381	26	0.7	2021	3	AY119100	Drosophill	454	26	0.7	3095	9	HSAD251016	HSAD251016
382	26	0.7	2024	6	AX701640	Sequence	455	26	0.7	3207	3	BT001514	BT001514
383	26	0.7	2024	10	AF349723	Rattus no	456	26	0.7	3215	3	AGRNAG1	AGRNAG1
384	26	0.7	2066	6	MMU65159	Mus muscu	457	26	0.7	3237	9	AY165003	AY165003
385	26	0.7	2092	3	AY060224	Drosophill	458	26	0.7	3251	10	AF532598	AF532598
386	26	0.7	2118	10	AF339103	Mus muscu	459	26	0.7	3254	6	AF039842	AF039842
387	26	0.7	2145	10	AF339106	Mus muscu	460	26	0.7	3263	10	MMJ225123	MMJ225123
388	26	0.7	2151	9	AF512947	Pan trogl	461	26	0.7	3280	10	RNO242781	RNO242781
389	26	0.7	2151	9	AY143178	Pan trogl	462	26	0.7	3302	9	AY186997	AY186997
390	26	0.7	2151	9	AY143179	Pan panis	463	26	0.7	3305	10	AF028737	AF028737
391	26	0.7	2156	6	AR280336	Sequence	464	26	0.7	3314	3	AY122076	AY122076
392	26	0.7	2156	6	BD128682	BD128682 OSF2/CBFA	465	26	0.7	3315	3	DME1BGENE	DME1BGENE
393	26	0.7	2176	10	MUSPEBP2A2	DI4637 Mouse mRNA	466	26	0.7	3321	10	BC057085	BC057085
394	26	0.7	2187	9	AF467257	Homo sapi	467	26	0.7	3321	6	BD183248	BD183248
395	26	0.7	2201	6	AR141679	Sequence	468	26	0.7	3327	6	BD183248	BD183248
396	26	0.7	2201	6	AX058278	Sequence	469	26	0.7	3334	6	BD128616	BD128616
397	26	0.7	2215	3	DMCF1AMRN	X58435 D.melanogas	470	26	0.7	3335	9	HSU80743	HSU80743
398	26	0.7	2294	6	AR280334	Sequence	471	26	0.7	3336	6	AX784160	AX784160
399	26	0.7	2294	6	BD128680	OSF2/CBFA	472	26	0.7	3336	6	AX058280	AX058280
400	26	0.7	2315	10	AF005936	Mus muscu	473	26	0.7	3336	6	BD183250	BD183250
401	26	0.7	2361	9	BC041088	Homo sapi	474	26	0.7	3339	6	BD183250	BD183250
402	26	0.7	2393	9	AY049734	Homo sapi	475	26	0.7	3433	3	AY060442	AY060442
403	26	0.7	2415	6	AS9887	Sequence 5	476	26	0.7	3439	6	BD183247	BD183247
404	26	0.7	2424	6	AX686703	Sequence	477	26	0.7	3459	3	AK123604	AK123604
405	26	0.7	2427	2	AC019751	Drosophill	478	26	0.7	3520	6	AX780441	AX780441
406	26	0.7	2427	3	DMRNAMSH	X85331 D.melanogas	479	26	0.7	3560	3	AF421370	AF421370
407	26	0.7	2439	8	AY237405	Phytophth	480	26	0.7	3597	6	BD127355	BD127355
408	26	0.7	2444	3	AF395904	Sequence 6	481	26	0.7	3597	9	AK074900	AK074900
409	26	0.7	2453	6	AS9888	Sequence 6	482	26	0.7	3604	3	BT010072	BT010072
410	26	0.7	2453	10	MMNT1IGN	X95518 M.musculini	483	26	0.7	3641	6	BD183416	BD183416
411	26	0.7	2472	9	AF337817	Homo sapi	484	26	0.7	3641	9	AB058768	AB058768
412	26	0.7	2499	10	AB019259	Rattus no	485	26	0.7	3655	10	BC020488	BC020488
413	26	0.7	2521	6	AR122323	Sequence	486	26	0.7	3658	3	AF395905	AF395905
414	26	0.7	2521	6	AR431867	Sequence	487	26	0.7	3708	3	DVA1GB5	DVA1GB5
415	26	0.7	2521	9	AF031815	Homo sapi	488	26	0.7	3722	10	BC032191	BC032191
416	26	0.7	2526	6	AR122326	Sequence	489	26	0.7	3732	8	AX505243	AX505243
417	26	0.7	2526	6	AR431870	Sequence	490	26	0.7	3738	6	AK110335	AK110335
418	26	0.7	2543	3	AY095077	Drosophill	491	26	0.7	3763	8	AY040324	AY040324
419	26	0.7	2546	4	AY038044	Sus scrofa	492	26	0.7	3765	6	BD251818	BD251818
420	26	0.7	2585	10	AF337877	Mus muscu	493	26	0.7	3792	9	AY121247	AY121247
421	26	0.7	2589	10	AB019258	Rattus no	494	26	0.7	3798	6	BD243843	BD243843
422	26	0.7	2594	3	AY144615	Homo sapi	495	26	0.7	3798	6	AR435596	AR435596
423	26	0.7	2598	3	AY061260	Drosophill	496	26	0.7	3810	6	BT003479	BT003479
424	26	0.7	2600	10	BC052705	Mus muscu	497	26	0.7	3819	6	I13749	I13749
425	26	0.7	2607	10	AY079903	Mus muscu	498	26	0.7	3864	9	AF096300	AF096300
426	26	0.7	2647	3	AY070708	Drosophill	499	26	0.7	3882	10	AF104261	AF104261
427	26	0.7	2649	6	AX763684	Sequence	500	26	0.7	3925	6	AX179648	AX179648
428	26	0.7	2669	3	AY058313	Drosophill	501	26	0.7	3930	9	HSU94836	HSU94836
429	26	0.7	2733	6	AR307660	Sequence	502	26	0.7	4061	9	AF536542	AF536542
430	26	0.7	2733	6	BD139754	Ion chan	503	26	0.7				



504	26	0.7	4077	10	BC040256	BC040256 Mus muscu	577	26	0.7	7326	10	S66385	S66385 CREB-binding
505	26	0.7	4105	9	BC021294	BC021294 Homo sapi	578	26	0.7	7568	9	HSNM1	X82209 H. sapiens M
506	26	0.7	4163	9	HSNANCA2	Y08262 H. sapiens m	579	26	0.7	7568	11	G28534	G28534 human SRS S
507	26	0.7	4197	6	AX828638	AX828638 Sequence 7	580	26	0.7	7757	11	G28534	AX521671 Homo sapi
508	26	0.7	4200	6	A62706	A62706 Sequence 7	581	26	0.7	7757	6	AX780089	AX780089 Sequence
509	26	0.7	4262	6	AF239986	AF239986 Homo sapi	582	26	0.7	8207	6	AX780089	AX780089 Sequence
510	26	0.7	4266	6	AR193118	AR193118 Sequence	583	26	0.7	8680	2	AC020188	AC020188 Drosophill
511	26	0.7	4266	6	AX828638	AX828638 Sequence	584	26	0.7	8772	6	AX224128	AX224128 Sequence
512	26	0.7	4266	6	AB014587	AB014587 Homo sapi	585	26	0.7	8871	6	AX224126	AX224126 Sequence
513	26	0.7	4368	3	DR0DPP	M81795 Drosophilla	586	26	0.7	9282	3	AF083334	AF083334 Antieraea
514	26	0.7	4393	3	BT003517	BT003517 Drosophilla	587	26	0.7	9321	6	AX367102	AX367102 Sequence
515	26	0.7	4458	3	DMU42402	U42402 Drosophilla	588	26	0.7	9658	10	MM1G	X13414 Murine I ge
516	26	0.7	4481	6	AR153580	AR153580 Sequence	589	26	0.7	10017	9	AY044869	AY044869 Homo sapi
517	26	0.7	4481	6	AR401379	AR401379 Sequence	590	26	0.7	10515	10	AB092695	AB092695 Mus muscu
518	26	0.7	4481	6	AX392465	AX392465 Sequence	591	26	0.7	10531	6	AX549238	AX549238 Sequence
519	26	0.7	4481	6	HSU70323	U70323 Human ataxi	592	26	0.7	10531	6	AF234887	AF234887 Homo sapi
520	26	0.7	4495	9	AF010227	AF010227 Homo sapi	593	26	0.7	10623	10	AB092694	AB092694 Mus muscu
521	26	0.7	4568	10	BC062926	BC062926 Mus muscu	594	26	0.7	10810	2	AC015172	AC015172 Drosophill
522	26	0.7	4578	10	AF104410	AF104410 Mus muscu	595	26	0.7	11296	3	AF175223	AF175223 Drosophill
523	26	0.7	4599	9	HSU46023	U46023 Human Xq28	596	26	0.7	11948	2	AC020253	AC020253 Drosophill
524	26	0.7	4622	10	AY185125	AY185125 Mus muscu	597	26	0.7	12091	2	AC015048	AC015048 Drosophill
525	26	0.7	4627	10	AF162853	AF162853 Mus muscu	598	26	0.7	12749	4	AB016793	AB016793 Sub pectol
526	26	0.7	4653	10	AF200687	AF200687 Mus muscu	599	26	0.7	12749	6	E26529	E26529 Malievine h
527	26	0.7	4668	9	AF016031	AF016031 Homo sapi	600	26	0.7	13040	10	AF453571	AF453571 Mus muscu
528	26	0.7	4734	10	AF369980	AF369980 Mus muscu	601	26	0.7	14009	9	AF515051	AF515051 Pan trogl
529	26	0.7	4959	6	AX686679	AX686679 Sequence	602	26	0.7	14009	9	AF515052	AF515052 Pan trogl
530	26	0.7	4959	6	HS277365	AX277365 Homo sapi	603	26	0.7	14063	9	AF515031	AF515031 Homo sapi
531	26	0.7	4960	6	AX686708	AX686708 Sequence	604	26	0.7	14063	9	AF515032	AF515032 Homo sapi
532	26	0.7	4960	10	AF384055	AF384055 Mus muscu	605	26	0.7	14063	9	AF515033	AF515033 Homo sapi
533	26	0.7	5012	10	BC022153	BC022153 Mus muscu	606	26	0.7	14063	9	AF515034	AF515034 Homo sapi
534	26	0.7	5082	3	DMU67935	U67935 Drosophilla	607	26	0.7	14063	9	AF515035	AF515035 Homo sapi
535	26	0.7	5129	10	AY303755	AY303755 Mus muscu	608	26	0.7	14063	9	AF515036	AF515036 Homo sapi
536	26	0.7	5164	9	AB058719	AB058719 Homo sapi	609	26	0.7	14063	9	AF515037	AF515037 Homo sapi
537	26	0.7	5419	9	AB058722	AB058722 Homo sapi	610	26	0.7	14063	9	AF515038	AF515038 Homo sapi
538	26	0.7	5419	9	AY040322	AY040322 Homo sapi	611	26	0.7	14063	9	AF515039	AF515039 Homo sapi
539	26	0.7	5481	10	AK123281	AK123281 Mus muscu	612	26	0.7	14063	9	AF515040	AF515040 Homo sapi
540	26	0.7	5529	3	DR0MASTM	M92914 Drosophilla	613	26	0.7	14063	9	AF515041	AF515041 Homo sapi
541	26	0.7	5729	3	AY069076	AY069076 Drosophill	614	26	0.7	14063	9	AF515042	AF515042 Homo sapi
542	26	0.7	5734	3	DR0SHSA	L42512 Drosophilla	615	26	0.7	14063	9	AF515043	AF515043 Homo sapi
543	26	0.7	5754	3	DMU42403	U42403 Drosophilla	616	26	0.7	14063	9	AF515044	AF515044 Homo sapi
544	26	0.7	5811	10	BC043125	BC043125 Mus muscu	617	26	0.7	14063	9	AF515045	AF515045 Homo sapi
545	26	0.7	5895	6	AX686475	AX686475 Sequence	618	26	0.7	14063	9	AF515046	AF515046 Homo sapi
546	26	0.7	5970	6	E22895	E22895 Carcinogene	619	26	0.7	14063	9	AF515047	AF515047 Homo sapi
547	26	0.7	5972	9	AB003039	AB003039 Homo sapi	620	26	0.7	14063	9	AF515048	AF515048 Homo sapi
548	26	0.7	5992	10	AY050663	AY050663 Mus muscu	621	26	0.7	14063	9	AF515049	AF515049 Homo sapi
549	26	0.7	6087	9	AB102670	AB102670 Pongo pyg	622	26	0.7	14063	9	AF515050	AF515050 Homo sapi
550	26	0.7	6147	6	AX704766	AX704766 Sequence	623	26	0.7	14440	3	AB047034	AB047034 Ap18 me11
551	26	0.7	6170	9	HSCGGE7	AJ001216 Homo sapi	624	26	0.7	14859	6	AX823282	AX823282 Sequence
552	26	0.7	6200	10	AK129272	AK129272 Mus muscu	625	26	0.7	14874	9	AF010404	AF010404 Homo sapi
553	26	0.7	6212	10	AY007594	AY007594 Mus muscu	626	26	0.7	14912	10	AF512563	AF512563 Mus muscu
554	26	0.7	6267	9	AB058721	AB058721 Homo sapi	627	26	0.7	15029	2	AC015150	AC015150 Drosophill
555	26	0.7	6282	3	DME75B	X51549 Drosophilla	628	26	0.7	15362	2	AC019547	AC019547 Drosophill
556	26	0.7	6380	10	AK122517	AK122517 Mus muscu	629	26	0.7	15578	2	AC015029	AC015029 Drosophill
557	26	0.7	6463	6	BD211793	BD211793 Mus muscu	630	26	0.7	15645	6	AX921118	AX921118 Sequence
558	26	0.7	6478	10	AF071310	AF071310 Mus muscu	631	26	0.7	15750	6	AX821965	AX821965 Sequence
559	26	0.7	6518	10	MUSEBEP2A1	DI4636 Mouse mRNA	632	26	0.7	15789	9	AF010403	AF010403 Homo sapi
560	26	0.7	6558	6	AR322158	AR322158 Sequence	633	26	0.7	19631	2	AC017798	AC017798 Drosophill
561	26	0.7	6642	10	BC057119	BC057119 Mus muscu	634	26	0.7	20113	2	AC015413	AC015413 Drosophill
562	26	0.7	6733	3	MSQRT2RET	M93691 Anopheles g	635	26	0.7	22307	2	AC015297	AC015297 Drosophill
563	26	0.7	6832	6	AX384818	AX384818 Sequence	636	26	0.7	22307	2	AC015297	AC015297 Drosophill
564	26	0.7	6835	6	AR316837	AR316837 Sequence	637	26	0.7	24194	2	AC018183	AC018183 Drosophill
565	26	0.7	6835	6	BD192354	BD192354 AIB1, a g	638	26	0.7	24370	6	AX646739	AX646739 Sequence
566	26	0.7	6883	9	AF012108	AF012108 Homo sapi	639	26	0.7	24370	9	AB065955	AB065955 Homo sapi
567	26	0.7	6888	9	AF286598	AF286598 Homo sapi	640	26	0.7	24487	2	AC019452	AC019452 Drosophill
568	26	0.7	7072	3	AB090813	AB090813 Anopheles	641	26	0.7	25598	2	AC015404	AC015404 Drosophill
569	26	0.7	7164	4	AF225897	AF225897 Bos tauru	642	26	0.7	29358	3	DMBH6115	DMBH6115 Drosophill
570	26	0.7	7200	10	U00454	U00454 Mus muscu	643	26	0.7	31202	2	AC013022	AC013022 Drosophill
571	26	0.7	7288	10	AY079443	AY079443 Mus muscu	644	26	0.7	31311	2	AC017192	AC017192 Drosophill
572	26	0.7	7288	10	AY079444	AY079444 Mus muscu	645	26	0.7	35722	2	AC015427	AC015427 Drosophill
573	26	0.7	7326	6	AR006845	AR006845 Sequence	646	26	0.7	37388	2	AC017823	AC017823 Drosophill
574	26	0.7	7326	6	E36595	E36595 Anticience n	647	26	0.7	37388	2	AC087161	AC087161 Leishmani
575	26	0.7	7326	6	AR203333	AR203333 Sequence	648	26	0.7	37569	2	AC019771	AC019771 Drosophill
576	26	0.7	7326	6	AR430182	AR430182 Sequence	649	26	0.7	37888	2	AC017571	AC017571 Drosophill

c 650	26	0.7	38230	8	AC067939	Neurospor	723	26	0.7	110000	2	AC114446_4	Continuation (5 of
c 651	26	0.7	39619	2	AC017644	AC017644 Drosophila	c 724	26	0.7	110000	2	AC020884_2	Continuation (3 of
c 652	26	0.7	40621	3	AC087836	AC087836 Leishmani	c 725	26	0.7	110000	2	AC128384_0	AC128384 Rattus no
c 653	26	0.7	40933	3	DMC140G11	DMC140G11	c 726	26	0.7	110000	2	AL672265_2	Continuation (3 of
c 654	26	0.7	41818	2	AC018239	AC018239 Drosophila	c 727	26	0.7	110073	10	AL928567	AL928567 Mouse DNA
c 655	26	0.7	42248	2	AC020375	AC020375 Drosophila	c 728	26	0.7	111893	2	AC120419	AC120419 Mus muscu
c 656	26	0.7	44671	2	AC019872	AC019872 Drosophila	c 729	26	0.7	11810	2	AC010302	AC010302 Homo sapi
c 657	26	0.7	45046	2	AC013093	AC013093 Drosophila	c 730	26	0.7	113816	2	AC004358	AC004358 Drosophila
c 658	26	0.7	45449	2	AC012817	AC012817 Drosophila	c 731	26	0.7	114181	2	AC110875	AC110875 Gallus ga
c 659	26	0.7	45912	2	AC091265	AC091265 Mus muscu	c 732	26	0.7	114532	9	AL389883	AL389883 Human DNA
c 660	26	0.7	46427	3	AY190956	AY190956 Drosophila	c 733	26	0.7	116603	2	AL157901	AL157901 Homo sapi
c 661	26	0.7	47636	2	AC014385	AC014385 Drosophila	c 734	26	0.7	117037	2	AC023269	AC023269 Homo sapi
c 662	26	0.7	47872	2	AC106844	AC106844 Mus muscu	c 735	26	0.7	117812	2	AC020493	AC020493 Drosophila
c 663	26	0.7	49399	6	AX015907	AX015907 Sequence	c 736	26	0.7	118036	2	AC008198	AC008198 Drosophila
c 664	26	0.7	50185	2	AC020507	AC020507 Drosophila	c 737	26	0.7	118044	2	AC010044	AC010044 Mus muscu
c 665	26	0.7	50714	3	AC005471	AC005471 Drosophila	c 738	26	0.7	120637	10	CNS07YPL	CNS07YPL
c 666	26	0.7	53124	2	AC012698	AC012698 Drosophila	c 739	26	0.7	120864	2	AC079884	AC079884 Mus muscu
c 667	26	0.7	54667	2	AC139419	AC139419 Homo sapi	c 740	26	0.7	121310	2	AC141831	AC141831
c 668	26	0.7	54943	2	AC14816	AC14816 Drosophila	c 741	26	0.7	121474	2	AC007150	AC007150
c 669	26	0.7	54987	2	AC131499	AC131499 Lytechinu	c 742	26	0.7	122163	8	AC125783	AC125783
c 670	26	0.7	56088	2	AC146714	AC146714 Mus muscu	c 743	26	0.7	122871	2	AC144617	AC144617
c 671	26	0.7	57336	3	AC005416	AC005416 Drosophila	c 744	26	0.7	123290	2	AC016020	AC016020 Drosophila
c 672	26	0.7	59498	3	AC004252	AC004252 Drosophila	c 745	26	0.7	125479	9	HS2244E24	HS2244E24
c 673	26	0.7	6107	2	AC017941	AC017941 Drosophila	c 746	26	0.7	128729	9	AC137590	AC137590
c 674	26	0.7	63024	2	AC129476	AC129476 Mus muscu	c 747	26	0.7	128747	10	AL669846	AL669846
c 675	26	0.7	64294	2	AC018047	AC018047 Drosophila	c 748	26	0.7	129690	9	AC004827	AC004827 Homo sapi
c 676	26	0.7	64294	2	AC016133	AC016133 Drosophila	c 749	26	0.7	131135	2	AC147551	AC147551 Mus muscu
c 677	26	0.7	65031	2	AC114338	AC114338 Mus muscu	c 750	26	0.7	131344	9	AC019226	AC019226 Homo sapi
c 678	26	0.7	65531	10	AY129964	AY129964 Mus muscu	c 751	26	0.7	133918	8	AL512290	AL512290 Human DNA
c 679	26	0.7	65725	8	NCB2J23	NCB2J23	c 752	26	0.7	134804	9	AP004888	AP004888 Oryza sat
c 680	26	0.7	67436	2	AC014142	AC014142 Neurospor	c 753	26	0.7	134809	10	AL683892	AL683892 Mouse DNA
c 681	26	0.7	68457	2	AC010702	AC010702	c 754	26	0.7	137334	10	AC121952	AC121952 Mus muscu
c 682	26	0.7	68897	2	DMB6E64	DMB6E64	c 755	26	0.7	137960	2	AC103889	AC103889
c 683	26	0.7	69692	2	AC114446_5	AC114446_5	c 756	26	0.7	138091	2	AC133583	AC133583
c 684	26	0.7	72187	2	AC013433	AC013433 Drosophila	c 757	26	0.7	139074	2	AC131191	AC131191 Mus muscu
c 685	26	0.7	73638	2	AC015613	AC015613 Homo sapi	c 758	26	0.7	139258	2	AC073673	AC073673
c 686	26	0.7	73889	2	AC009983	AC009983 Drosophila	c 759	26	0.7	139258	2	AC012837	AC012837
c 687	26	0.7	74759	2	AC100661	AC100661 Mus muscu	c 760	26	0.7	139480	2	AP000865	AP000865 Homo sapi
c 688	26	0.7	77409	3	AC004248	AC004248 Drosophila	c 761	26	0.7	139685	2	AC122437	AC122437 Mus muscu
c 689	26	0.7	77656	2	AC015522	AC015522 Drosophila	c 762	26	0.7	140244	2	AC119962	AC119962 Mus muscu
c 690	26	0.7	78874	2	AL355521	AL355521 Homo sapi	c 763	26	0.7	142037	10	AL844516	AL844516
c 691	26	0.7	81210	2	AC019242	AC019242 Homo sapi	c 764	26	0.7	146349	2	AP005010	AP005010 Oryza sat
c 692	26	0.7	83607	2	AC019889	AC019889 Drosophila	c 765	26	0.7	146349	2	AC021970	AC021970 Homo sapi
c 693	26	0.7	83824	2	AC014992	AC014992 Homo sapi	c 766	26	0.7	150122	10	EX088567	EX088567 Mouse DNA
c 694	26	0.7	85740	2	AC014992	AC014992 Homo sapi	c 767	26	0.7	150122	2	AC009462	AC009462 Drosophila
c 695	26	0.7	86453	9	HS1049616	HS1049616 Human DNA	c 768	26	0.7	151610	9	AC020606	AC020606 Homo sapi
c 696	26	0.7	89376	2	DMB41A22	DMB41A22	c 769	26	0.7	151822	2	AC010923	AC010923
c 697	26	0.7	89376	2	AC139073	AC139073 Homo sapi	c 770	26	0.7	151822	2	AC011199	AC011199 Homo sapi
c 698	26	0.7	89566	9	AL390204	AL390204 Human DNA	c 771	26	0.7	152021	9	AC011680	AC011680 Apts mell
c 699	26	0.7	90223	9	AC0010105	AC0010105 Homo sapi	c 772	26	0.7	152224	2	AC141680	AC141680
c 700	26	0.7	90596	2	AC017624	AC017624 Drosophila	c 773	26	0.7	152564	10	AC127549	AC127549 Mus muscu
c 701	26	0.7	91170	2	AC014779	AC014779 Drosophila	c 774	26	0.7	153291	2	AC117653	AC117653 Mus muscu
c 702	26	0.7	91240	9	AC130566	AC130566 Homo sapi	c 775	26	0.7	154771	3	AC009214	AC009214 Drosophila
c 703	26	0.7	91318	2	AC015391	AC015391 Drosophila	c 776	26	0.7	154771	3	AC020329	AC020329 Drosophila
c 704	26	0.7	91809	2	AC012832	AC012832 Drosophila	c 777	26	0.7	154695	2	AC091228	AC091228 Drosophila
c 705	26	0.7	92586	2	AC005978	AC005978 Drosophila	c 778	26	0.7	156142	3	AC008219	AC008219 Drosophila
c 706	26	0.7	92785	10	CNS07YOV	CNS07YOV	c 779	26	0.7	156705	3	AL929037	AL929037 Mouse DNA
c 707	26	0.7	92958	2	DMB11J17	DMB11J17	c 780	26	0.7	157057	2	AC127160	AC127160 Rattus no
c 708	26	0.7	94045	2	AC010039	AC010039 Drosophila	c 781	26	0.7	157833	9	AC132186	AC132186 Homo sapi
c 709	26	0.7	95856	2	AC020304	AC020304 Drosophila	c 782	26	0.7	158169	2	AC141751	AC141751 Apts mell
c 710	26	0.7	96426	2	AC014908	AC014908 Drosophila	c 783	26	0.7	160445	3	AC023741	AC023741 Drosophila
c 711	26	0.7	97033	2	AC015146	AC015146 Drosophila	c 784	26	0.7	160504	3	AC091207	AC091207 Drosophila
c 712	26	0.7	99745	2	AC017305	AC017305 Drosophila	c 785	26	0.7	160827	5	AR374388	AR374388 Sequence
c 713	26	0.7	100984	10	AL929138	AL929138 Mouse DNA	c 786	26	0.7	161552	6	AC004774	AC004774 Homo sapi
c 714	26	0.7	103196	2	AC026404	AC026404 Homo sapi	c 787	26	0.7	161552	2	AC119935	AC119935 Mus muscu
c 715	26	0.7	107514	2	AF125313	AF125313 Mus muscu	c 788	26	0.7	161773	2		
c 716	26	0.7	107642	10	AF125313	AF125313 Mus muscu	c 789	26	0.7	161773	2		
c 717	26	0.7	107717	9	AC137055	AC137055 Homo sapi	c 790	26	0.7	161773	2		
c 718	26	0.7	108139	2	AC004085_3	AC004085_3	c 791	26	0.7	161773	2		
c 719	26	0.7	110000	2	AC106698_5	AC106698_5	c 792	26	0.7	161773	2		
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C 811	26	0.7 165014	3	AC104609	C 884	26	0.7 180961	10	AC121838	AC121838 Mus muscu
C 812	26	0.7 165928	3	AC023725	C 885	26	0.7 181037	2	AC116729	AC116729 Mus muscu
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C 827	26	0.7 169680	3	AC008337	C 900	26	0.7 183252	2	AC113907	AC113907 Rattus no
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C 829	26	0.7 170053	3	AC133069	C 902	26	0.7 183729	2	AC136383	AC136383 Rattus no
C 830	26	0.7 170301	2	AC023694	C 903	26	0.7 184091	2	EX294393	EX294393 Mus muscu
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C 837	26	0.7 171115	9	AC068385	C 910	26	0.7 186008	2	AC129123	AC129123 Rattus no
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C 859	26	0.7 175781	3	AC008091	C 932	26	0.7 190379	2	AC134136	AC134136 Rattus no
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C 861	26	0.7 176394	3	AC007928	C 934	26	0.7 190944	2	AC147417	AC147417 Papio ham
C 862	26	0.7 176952	2	AC113805	C 935	26	0.7 191300	2	AC109020	AC109020 Rattus no
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## ALIGNMENTS

RESULT 1  
BC034673  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE

BC034673 5014 bp mRNA  
Homo sapiens misshapen/NTK-related kinase, transcript variant 3,  
complete cds.  
BC034673  
BC034673.1 GI:21961594  
MGC.  
Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
1 (bases 1 to 5014)

1 (bases 1 to 5014)  
Straussberg, R.L., Feringold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, J., Shemen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Diatchenko, L., Marzina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Scheet, T.E., Brownstein, M.J., Ueda, T.B., Tohyuki, S.,  
Carninci, P., Prange, C., Rana, S.S., Loquiano, N.A., Peters, G.J.,  
Abrahamson, R.D., Mullany, S.J., Bosak, S.A., McSwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huijck, S.W.,  
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,  
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Boutard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smal, D.E.,  
Scherer, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
2 (bases 1 to 5014)  
Straussberg, R.  
Direct Submission  
Submitted (24-JUL-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

REMARK  
COMMENT  
Email: cga@bcm.tmc.edu  
Tissue Procurement: Lou Staudt  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC  
Web site: http://www.hgsc.bcm.tmc.edu/cdna/  
Contact: amg@bcm.tmc.edu  
Gunnar, P.H., Garcia, A.M., Lu, X., Huijck, S.W., Louesged, H.,  
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov  
Series: IRAX Plate: 26 Row: n Column: 8  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 27436515.

## FEATURES

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gene

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RESULT 3  
AR435598  
LOCUS AR435598  
DEFINITION Sequence 11 from patent US 6656716.  
ACCESSION AR435598  
VERSION AR435598.1 GI:40198579  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 4133)  
AUTHORS Plowman,G., Martinez,R. and Whyte,D.  
TITLE Polypeptide fragments of human PAK5 protein kinase  
JOURNAL Patent: US 6656716-A 11 02-DEC-2003;  
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 REFERENCE  
 AUTHORS Dan, I., Watanabe, N.M., Kobayashi, T., Yamashita-Suzuki, K.,  
 Fukagawa, Y., Kajikawa, E., Kimura, W.K., Nakashima, T.M.,  
 Matsumoto, K., Nimomiyu-Tsui, J., and Kusumi, A.  
 TITLE Molecular cloning of MINK, a novel member of mammalian GSK family  
 kinases, which is up-regulated during postnatal mouse cerebral  
 development  
 JOURNAL FEBS Lett. 469 (1), 19-23 (2000)  
 MEDLINE 20175403  
 PUBMED 10708748  
 REFERENCE 2 (bases 1 to 3888)  
 AUTHORS Dan, I., Watanabe, N.M., and Kusumi, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-DEC-1999) Ippelita Dan, ERATO, Kusumi Membrane

Organizer Project: 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi  
460-0012, Japan (E-mail: dango@bio.nagoya-u.ac.jp,  
Tel: 81-52-789-2497, Fax: 81-52-789-2368)

## FEATURES

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Location/Qualifiers

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VERSION AX235365.1 GI:15593897
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REFERENCE 1
AUTHORS Vernhet,C.A., Fernandez,E., Shimketa,R.A., Macdougall,J. and
Spaderna,S.K.
TITLE Polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0162928-A 12 30-AUG-2001,
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Query Match 40.5%; Score 1599; DB 6; Length 3735;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 10 from Patent WO0162928.  
ACCESSION AX235363  
VERSION AX235363.1 GI:15593895  
KEYWORDS  
SOURCE  
ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
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1 Verret, C.A., Fernandes, E., Shinkets, R.A., MacDougall, J. and Spaderna, S.K.  
TITLE Polypeptides and nucleic acids encoding same  
JOURNAL Patent: WO 0162928-A 10 30-AUG-2001;  
Curagen Corporation (US)  
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## ORIGIN

40.5%; Score 1599; DB 6; Length 3822;

Query Match

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8  
AX235361 3912 bp DNA linear PAT 11-SEP-2001  
LOCUS AX235361  
DEFINITION Sequence 8 from Patent WO0162928.  
ACCESSION AX235361  
VERSION AX235361.1 GI:15593893  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 Vernet,C.A., Fernandez,E., Shinkets,R.A., Macdougall,J. and Spaderna,S.K.  
TITLE Polypeptides and nucleic acids encoding same  
JOURNAL Patent: WO 0162928-A 8 30-AUG-2001;  
Curagen Corporation (US)  
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DEFINITION	AX235359				
ACCESSION	AX235359				
VERSION	AX235359.1	GI:15593891			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	1	Vernec, C.A., Fernandes, E., Shinkens, R.A., Macdougall, J., and Spaderna, S.K.			
AUTHORS	Humo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
TITLE	Polypeptides and nucleic acids encoding same				
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Db	3661	ACCGACGGCAATGAGATGTCTGTGTGACGAGAGACGAGGGTGTCTAGTCAACAGCGTAC	37220
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Db	3397	TACATCCCTGTGCATCATCCAGACCCAGATCAAGCCCATGCTCATCTTCTCCCAAC	3456
Qy	3697	ACCGACGGCATGAGATGCTGCTGTGTCATCGAGAGACGAGGGGTCTACTGCAACACGAC	3666
Db	3457	ACCGACGGCATGAGAGATGCTGCTGTGTCATCGAGAGACGAGGGGTCTACTGCAACACGAC	3518
Qy	3667	GGGGGCATCATTTAAGAGATGTGGTGTCTGAGTGGGGGGAGATGCTCACTTCTGTGGCTTAC	3728
Db	3517	GGGGGCATCATTTAAGAGATGTGGTGTCTGAGTGGGGGGAGATGCTCACTTCTGTGGCTTAC	3578
Qy	3727	ATCTGCTTCAACACAGATTAATGGGCTGGGGGTGAGAAAGCATTTGAGATCCGCTCTGTGGAG	3788
Db	3577	ATCTGCTTCAACACAGATTAATGGGCTGGGGGTGAGAAAGCATTTGAGATCCGCTCTGTGGAG	3638
Qy	3787	ACGGGGCAACCTCGACGGGGTCTTCAATGCACAACACGAGCTCAGAGGCTCAAGTTCTGTGT	3848
Db	3637	ACGGGGCAACCTCGACGGGGTCTTCAATGCACAACACGAGCTCAGAGGCTCAAGTTCTGTGT	3698
Qy	3847	GAGCGGAATGACAAAGGTGTTTTTGTGCTCAGTCCGCTCTGCGGGGACGACGCCAAGTTTAC	3908
Db	3697	GAGCGGAATGACAAAGGTGTTTTTGTGCTCAGTCCGCTCTGCGGGGACGACGCCAAGTTTAC	3758
Qy	3907	TTCAATGACTTGAAACCGTTAATCGCATCATGAACTGTGTGA	3945
Db	3757	TTCAATGACTTGAAACCGTTAATCGCATCATGAACTGTGTGA	3795

RESULT 11					
AX235417					
LOCUS	AX235417	1482 bp	DNA	linear	PAT 11-SEP-2001
DEFINITION	Sequence 64 from Patent WO0162928.				
ACCESSION	AX235417				
VERSION	AX235417.1	GI:15593928			

SOURCE ORGANISM	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	AUTHORS
1	Vernet, C.A., Fernandes, E., Shimkets, R.A., Macdougall, J. and Spaderna, S. K.

**TITLE** Polypeptides and nucleic acids encoding same  
**JOURNAL** Patent: WO 0162928-A 64 30-AUG-2001;

**Curagen Corporation (US)**  
**Location/Qualifiers**

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Best Local Similarity	100.0%	Pred. No. 0		
Matches 1337; Conservative	0	Mismatches	0	Indels 0
				Gaps 0

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QY	70	GCTGGGATCTTGAAGCTGTGAGAGGTGTGGGCAATGGAACTTACCGACAGGTGTAAACA	129
Db	61	GCTGGGATCTTGAAGCTGTGAGAGGTGTGGGCAATGGAACTTACCGACAGGTGTAAACA	120
QY	130	GGTGGGATCTTGAAGCTGTGAGAGGTGTGGGCAATGGAACTTACCGACAGGTGTAAACA	189
Db	121	GGTGGGATCTTGAAGCTGTGAGAGGTGTGGGCAATGGAACTTACCGACAGGTGTAAACA	180
QY	190	GAGGAGGAAGAGATCAACAGAGATCAACATGCTGAAAAAAGTACTTTCACCAACCGAAC	249
Db	181	GAGGAGGAAGAGATCAACAGAGATCAACATGCTGAAAAAAGTACTTTCACCAACCGAAC	240
QY	250	ATGCGCACCTTCTAAGGAGCCTTCTCAAGAGAGAGAGCCCCCGGGGAAACGATGACCAAGCTC	309

Db	241	ATCCCAACCTTACCTACGGAGCCTTATATCAAGAAAGCCCCCGGGAAACGATGACCACTC	300
OY	310	TGGCTGGTGAATGAGAGTTCTGTGTGTGCTGTGTTCACTGACTGA.CTGTGTAAAGAACAAAA	369
Db	301	TGGCTGGTGAATGAGAGTTCTGTGTGTGCTGTGTTCACTGACTGA.CTGTGTAAAGAACAAAA	360
OY	370	GGCAACGCCCTGAAAGAGAGACTGTATGCGCTTATATCTGCAGAGAGATCTTCAGGGGCTCTG	429
Db	361	GGCAACGCCCTGAAAGAGAGACTGTATGCGCTTATATCTGCAGAGAGATCTTCAGGGGCTCTG	420
OY	430	GCCCATCTCCATGCCCAAGGTATTCATTCGAGACATCAAGGGGCGAAATGTCTCTGCTG	489
Db	421	GCCCATCTCCATGCCCAAGGTATTCATTCGAGACATCAAGGGGCGAAATGTCTCTGCTG	480
OY	490	ACAGAGATGTGTAGGTCAAGCTGTAGGATTTTGTGGGTGTAGTGTCTCAGCTGGAACGGACCC	549
Db	481	ACAGAGATGTGTAGGTCAAGCTGTAGGATTTTGTGGGTGTAGTGTCTCAGCTGGAACGGACCC	540
OY	550	GTGGGCGAGACGGAA.CACTTTCATTGGGACCTCCCTACTGTATGTGCTCCAGAGSTCATGCC	609
Db	541	GTGGGCGAGACGGAA.CACTTTCATTGGGACCTCCCTACTGTATGTGCTCCAGAGSTCATGCC	600
OY	610	TGTATGATGAACCTCTGATGCCACTTATGATTTACAGAGTATATTGGTCTCTAGAAATC	669
Db	601	TGTATGATGAACCTCTGATGCCACTTATGATTTACAGAGTATATTGGTCTCTAGAAATC	660
OY	670	ACAGCCATTCGAGTGGAGAGAGGGAGCCCCCTGTGTGTACATGCAACCCCATGCGAGCC	729
Db	661	ACAGCCATTCGAGTGGAGAGAGGGAGCCCCCTGTGTGTACATGCAACCCCATGCGAGCC	720
OY	730	CTCTTCTCTCATCTCTCGGAA.CCTCTCCGCCAGGCTCAAGTCTCAAGAGTGTCTTAAAGAG	789
Db	721	CTCTTCTCTCATCTCTCGGAA.CCTCTCCGCCAGGCTCAAGTCTCAAGAGTGTGTAAAGAG	780
OY	790	TTCAATTGACTTCATTGACACATGTCTCATCAAGACTTACTGTAGCCGCGCCACCCACGGAG	849
Db	781	TTCAATTGACTTCATTGACACATGTCTCATCAAGACTTACTGTAGCCGCGCCACCCACGGAG	840
OY	850	CAGCTACTGMAAGTTTCCCTTCATCCCGGAGCAAGCCCAAGAGCGGCAAGTCCGATCCAG	909
Db	841	CAGCTACTGMAAGTTTCCCTTCATCCCGGAGCAAGCCCAAGAGCGGCAAGTCCGATCCAG	900
OY	910	CTTAAAGACCA.CATTGACCGATCCCGGAGAGCGGGGTGAGAAAGAGAGACAAATAT	969
Db	901	CTTAAAGACCA.CATTGACCGATCCCGGAGAGCGGGGTGAGAAAGAGAGACAAATAT	960
OY	970	GAGTACAGCGGCAAGCAAGAGAGAGATGACAGCCATGAGAGAGAAAGAGACCAAGCTCC	1029
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OY	1030	ATCATGAA.CGTGCTGTGAGAGTGCATCTTACGCCGGGAGTTTCTCCGCTTCACAGAGAA	1089
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OY	1090	AATAAGAGCA.CTCAAGGCTTTTAAACACACAGAGCAGCTGCAGACAGACAGCAGCAGAA	1149
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OY	1150	GACCCCGAGGCA.CACTCAACACTTGTCTGACCA.CCAGCGGAGCGGCGCATAGAGAGCAG	1209
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OY	1210	AAGAGAGACGGCGCCCGCTGTGAGAGAGCA.CAGCGGTGGAGCGGAGACAGCGGAAGCTG	1269
Db	1201	AAGAGAGACGGCGCCCGCTGTGAGAGAGCA.CAGCGGTGGAGCGGAGACAGCGGAAGCTG	1260
OY	1270	CAGGAGAAAGAGACAGCAGCGCGGCTGGAAGACATGCAAGCTCTGCGCGGAGAGAGAGAG	1329
Db	1261	CAGGAGAAAGAGACAGCAGCGCGGCTGGAAGACATGCAAGCTCTGCGCGGAGAGAGAGAG	1320
OY	1330	CGGCGGACGCGGAGCG 1346	







## ORIGIN

Query Match 33.8%; Score 1337; DB 6; Length 1717;  
 Best Local Similarity 100.0%; Pred. No. 0;  
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 1 GGGGACCCAGGCCCCCGGAGCCTTGAGCAATCGACTGTCCGCCCTGGGGACCT 60  
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 61 GCTGGATCTTTGAGCTTGTGAGGTGTGCGCAATGAACTTACGACAGGTGTACAG 120  
 130 GGTGGCATTTCAAGACGGGGCAGTGGCTGCATCAAGGTCTATGATGTCAAGAGAC 189  
 121 GGTGGCATTTCAAGACGGGGCAGTGGCTGCATCAAGGTCTATGATGTCAAGAGAC 180  
 190 GAGGAGAAAGATCAAAACAGAGATCAACATGCTGAAAAAGTACTCTACACCGAAC 249  
 181 GAGGAGAAAGATCAAAACAGAGATCAACATGCTGAAAAAGTACTCTACACCGAAC 240  
 250 ATGCGCACTTACTACGAGCCTTCAACAGAAAGCCCCCGGAAACGATGACAGCTC 309  
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 361 GGGAAAGCCGCTGAGGAGGAGGAGTATGCTATATATCTGCAAGGAGATCTGAGGGGTCTG 420  
 430 GCCCATCTCATGCGCCCAACAGGTATCCATCGAGACATCAAGGGGAGAGTGTGCTG 489  
 421 GCCCATCTCATGCGCCCAACAGGTATCCATCGAGACATCAAGGGGAGAGTGTGCTG 480  
 490 ACAGAGAAATGCTGAGGTCAAGCTAGTGAATTTTGGGGTGAAGTGTCTGACCGCAC 549  
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 730 CTCTTCCATCTCTCCGAAACCTCCCGCCAGGCTCAAGTCAAGAAAGTGTCTTAAAGAG 789  
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Query Match 33.8%; Score 1337; DB 6; Length 1787;  
 Best Local Similarity 100.0%; Pred. No. 0;  
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 1330 CGCGCGAGCGCGAGCG 1346  
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RESULT 14  
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 DEFINITION Sequence 66 from Patent WO162928.  
 ACCESSION AX235419  
 VERSION AX235419.1 GI:15593929  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 Vernet,C.A., Fernandes,E., Shimkets,R.A., Macdougall,J. and Spaderne,S.K.  
 TITLE Polypeptides and nucleic acids encoding same  
 JOURNAL Patent: WO 0162928-A 66 30-AUG-2001;  
 Curregen Corporation (US)  
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 181 GAGGAGAAAGATCAAAACAGAGATCAACATGCTGAAAAAGTACTCTACACCGAAC 240  
 250 ATGCGCACTTACTACGAGCCTTCAACAGAAAGCCCCCGGAAACGATGACAGCTC 309  
 241 ATGCGCACTTACTACGAGCCTTCAACAGAAAGCCCCCGGAAACGATGACAGCTC 300

OY	310	TGGCTGTGTATGGAGTTCTGTGTGTGTGTGTCACTGACCTGTGTAAGAACA	365
DB	301	TGGCTGTGTGTATGGAGTTCTGTGTGTGTGTGTCACTGACCTGTGTAAGAACA	360
OY	370	GGCAACGCCCTTAAGAGAGACTGTATCGCTTATCTGACGGGAGATCTCAAGGGTCTG	425
DB	361	GGCAACGCCCTTAAGAGAGACTGTATCGCTTATCTGACGGGAGATCTCAAGGGTCTG	420
OY	430	GCCCATCTTCATGATGCCCAAGGTGATCCATCGAACAATCAAGGGCGAGAATGCTGCTG	485
DB	421	GCCCATCTTCATGATGCCCAAGGTGATCCATCGAACAATCAAGGGCGAGAATGCTGCTG	480
OY	490	ACAGAGATNGCTGAAGTCAAGCTAAGATGATTTTGGGGTGTAGTGCTCAGCTGGACCGCAC	545
DB	481	ACAGAGATNGCTGAAGTCAAGCTAAGATGATTTTGGGGTGTAGTGCTCAGCTGGACCGCAC	540
OY	550	GTGGGCAGACGGAAACATTTCATTGCGAATCCCTCACTGATGGCTTCAGAGGTCAATCGCC	605
DB	541	GTGGGCAGACGGAAACATTTCATTGCGAATCCCTCACTGATGGCTTCAGAGGTCAATCGCC	600
OY	610	TGTGATGAGAACCCCTGATGCCACTATGATTTACAGAGTGAATTTTGGTCTTAAGGAATC	665
DB	601	TGTGATGAGAACCCCTGATGCCACTATGATTTACAGAGTGAATTTTGGTCTTAAGGAATC	660
OY	670	ACAGGCATGAGATGGCAGAGGAGGCCCCCTCTGTGTGACATGCAACCCATCGAGCC	725
DB	661	ACAGGCATGAGATGGCAGAGGAGGCCCCCTCTGTGTGACATGCAACCCATCGAGCC	720
OY	730	CTCTTCTCTGATTTCTTGGAACCTCTCCGCCAGGGTCAAGTCCAAAGATGTCTTAAGAG	785
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OY	790	TTTCATTGATTTGATTTGACACATGTCTCATCAAGACTTACTGAGCGGCCCAACCAGAG	845
DB	781	TTTCATTGATTTGATTTGACACATGTCTCATCAAGACTTACTGAGCGGCCCAACCAGAG	840
OY	850	CAGCTTACTGAAGTTTCCCTTTCATCCGGGAGCAAGCCACAGAGGCGAGGTCCGCATCCAG	905
DB	841	CAGCTTACTGAAGTTTCCCTTTCATCCGGGAGCAAGCCACAGAGGCGAGGTCCGCATCCAG	900
OY	910	CTTTAAGAGCAACATTTGACCGATTCGCCGAAGAGCGGGGTGAGAAACAGAGACAGAAAT	965
DB	901	CTTTAAGAGCAACATTTGACCGATTCGCCGAAGAGCGGGGTGAGAAACAGAGACAGAAAT	960
OY	970	GAGTACAGCGGCGACGAGAGAGAAATGACACGCTATGAGAGAGAAAGAGCCAACTCC	1025
DB	961	GAGTACAGCGGCGACGAGAGAGAAATGACACGCTATGAGAGAGAAAGAGCCAACTCC	1020
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ACCESSION	BD183377				
VERSION	BD183377.1	GI:1875577			
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ORGANISM	Homo sapiens				
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	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 3824)				
AUTHORS	Ohara,O., Nagase,T. and Nakajima,D.				
TITLE	Novel genes and proteins encoded by the genes				
JOURNAL	Patent: JP 2002345492-A 90 03-DEC-2002;				
	KAZUO DNA RESEARCH INSTITUTE				
COMMENT	OS Homo sapiens (human)				
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	PF 26-FEB-2002 JP 2002049009				
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PC	A61P25/14,				
PC	A61P15/18,A61P35/00,C12N15/00,A61K37/02				
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## ORIGIN

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Best Local Similarity	100.0%;	Pred. No. 0;		
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QY	2928	GGTCAACGTGATCCCAACCAACCCCGGGCCACAGTATGAGACCCCTGAGATCCGGAAGTA	2987
Db	2037	GGTCAACGTGATCCCAACCAACCCCGGGCCACAGTATGAGACCCCTGAGATCCGGAAGTA	2096
QY	2988	CAAGAAAGGATTCAACTCCGAGATCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGT	3047
Db	2097	CAAGAAAGGATTCAACTCCGAGATCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGT	2156
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Db	2157	GGGCAACGGAGAACGGGCTGATGTTGCTGTGACCGAAGTGGGGACGGGCAGAGTGTATGAACT	2211
QY	3108	CATTAGGCGGCGACGCTTCACAGAGATGATGTGCTGAGGGGGCTCAACTGCTCATCAC	3167
Db	2217	CATTAGGCGGCGACGCTTCACAGAGATGATGTGCTGAGGGGGCTCAACTGCTCATCAC	2276
QY	3168	CATCTCAGGGAAAGAGAACAACTGCGGGGTGTATTACTGTGCTCTGCGCTCCGGAACAGAT	3227
Db	2277	CATCTCAGGGAAAGAGAACAACTGCGGGGTGTATTACTGTGCTCTGCGCTCCGGAACAGAT	2336
QY	3228	TTCGACATATGACCCAGAAAGTGGAGAAAGACGAGGCTGGACACACCGTGGGGGACATATGA	3287
Db	2337	TTCGACATATGACCCAGAAAGTGGAGAAAGACGAGGCTGGACACACCGTGGGGGACATATGA	2396
QY	3288	GGGCTGCGGGGACCTACCGTGTGTGAATAAGAGCGGATTAAGTTCCTGGTCATCGCCCT	3347
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## OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 14:48:42 ; Search time 974 Seconds

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Title: US-10-029-115-1

Perfect score: 3951  
Sequence: 1 gccctatggcgaccaccagc.....tcatactggtgaagagc 3951Scoring table: OLIGO-MNC  
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 212409041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

1: N\_Geneseq\_29Jan04:\*  
2: geneeqn1980s:\*  
3: geneeqn2000s:\*  
4: geneeqn2001as:\*  
5: geneeqn2001bs:\*  
6: geneeqn2002s:\*  
7: geneeqn2003as:\*  
8: geneeqn2003bs:\*  
9: geneeqn2003cs:\*  
10: geneeqn2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3951	100.0	3951	9 ADE34151	AdE34151 Human DNA
2	1907	48.3	4033	9 ADE34155	AdE34155 Human DNA
3	1701	43.1	3888	6 AAL48627	AaL48627 Human ins
4	1694	42.9	4133	2 AAZ40485	AaZ40485 Human ins
5	1689	42.7	4863	4 AAK52286	AaK52286 Human pol
6	1689	42.7	4863	4 AAL48626	AaL48626 Human ins
7	1683	42.6	4414	9 ADE34153	AdE34153 Human DNA
8	1599	40.5	3912	5 AAD17762	AaD17762 Human nov
9	1599	40.5	3912	5 AAD17761	AaD17761 Human nov
10	1599	40.5	3912	5 AAD17760	AaD17760 Human nov
11	1599	40.5	3912	5 AAD17759	AaD17759 Human nov
12	1599	40.5	3912	5 AAD17758	AaD17758 Human nov
13	1340	33.9	7132	5 AAS88207	AaS88207 DNA encod
14	1340	33.9	7132	5 AAS88207	AaS88207 DNA encod
15	1340	33.9	7132	5 AAS88207	AaS88207 DNA encod
16	970	22.0	1131	4 ABA08794	AbA08794 Human can
17	869	22.0	1131	4 ABA08793	AbA08793 Human can
18	869	22.0	1131	4 ABA08792	AbA08792 Human can
19	869	22.0	1131	4 ABA08791	AbA08791 Human can
20	869	22.0	1131	4 ABA08790	AbA08790 Human can
21	869	22.0	1131	4 ABA08789	AbA08789 Human can
22	869	22.0	1131	4 ABA08788	AbA08788 Human can
23	869	22.0	1131	4 ABA08787	AbA08787 Human can

C 24	224	5.7	467	4 AAI31367	AaI31367 Probe #53
C 25	224	5.7	467	4 ABA21580	AbA21580 Probe #46
C 26	224	5.7	467	4 AAK25497	AaK25497 Human bon
C 27	224	5.7	467	4 AAK00060	AaK00060 Human bra
C 28	224	5.7	467	4 ABA25065	AbA25065 Human bra
C 29	224	5.7	467	5 AAI00062	AaI00062 Probe #53
C 30	224	5.7	467	6 ABA00063	AbA00063 Human gen
C 31	224	5.7	257	4 AAI19418	AaI19418 Probe #93
C 32	222	5.6	257	4 ABA64431	AbA64431 Human foe
C 33	222	5.6	257	4 AAI44606	AaI44606 Probe #13
C 34	222	5.6	257	4 ABA46568	AbA46568 Human bre
C 35	222	5.6	257	4 ABA31568	AbA31568 Probe #10
C 36	222	5.6	257	4 AAK38617	AaK38617 Human bon
C 37	222	5.6	257	4 AAK12889	AaK12889 Human bra
C 38	222	5.6	257	4 ABA38182	AbA38182 Human bra
C 39	222	5.6	257	5 AAI05143	AaI05143 Probe #51
C 40	222	5.6	257	6 ABA12684	AbA12684 Human gen
C 41	207	5.2	428	5 AAS88201	AaS88201 DNA encod
C 42	205	5.2	500	8 ACH45103	AaC45103 Human foe
C 43	194	4.9	403	3 AAA44094	AaA44094 Human sec
C 44	174	4.4	289	7 ACD96631	AaC96631 Human col
C 45	172	4.4	12400	6 ABL88357	AbL88357 Human CHR
C 46	172	4.4	12400	6 ABL88357	AbL88357 Human CHR
C 47	171	4.3	481	4 AAI10122	AaI10122 Probe #55
C 48	171	4.3	481	4 ABA51752	AbA51752 Human foe
C 49	171	4.3	481	4 AAI31368	AaI31368 Probe #54
C 50	171	4.3	481	4 ABA21581	AbA21581 Probe #47
C 51	171	4.3	481	4 AAK25498	AaK25498 Human bon
C 52	171	4.3	481	4 AAK00061	AaK00061 Human bra
C 53	171	4.3	481	4 ABA25066	AbA25066 Human liv
C 54	171	4.3	481	5 AAI00063	AaI00063 Probe #54
C 55	171	4.3	481	6 ABA00064	AbA00064 Human gen
C 56	168	4.3	1784	9 ADC24925	AaC24925 Human bre
C 57	142	3.6	179	4 AAI19419	AaI19419 Probe #93
C 58	142	3.6	179	4 ABA64432	AbA64432 Human foe
C 59	142	3.6	179	4 AAI44607	AaI44607 Probe #13
C 60	142	3.6	179	4 ABA46569	AbA46569 Human bre
C 61	142	3.6	179	4 ABA31569	AbA31569 Probe #10
C 62	142	3.6	179	4 AAK38618	AaK38618 Human bon
C 63	142	3.6	179	4 AAK12890	AaK12890 Human bra
C 64	142	3.6	179	4 ABA38183	AbA38183 Human liv
C 65	142	3.6	179	5 AAI05144	AaI05144 Probe #51
C 66	142	3.6	179	6 ABA12685	AbA12685 Human gen
C 67	130	3.3	387	5 AAS41305	AaS41305 DNA encod
C 68	130	3.3	387	5 AAS88203	AaS88203 DNA encod
C 69	128	3.2	140	4 AAI19417	AaI19417 Probe #93
C 70	128	3.2	140	4 ABA64430	AbA64430 Human foe
C 71	128	3.2	140	4 AAI44605	AaI44605 Probe #13
C 72	128	3.2	140	4 ABA46567	AbA46567 Human bre
C 73	128	3.2	140	4 ABA31567	AbA31567 Probe #10
C 74	128	3.2	140	4 AAK38616	AaK38616 Human bon
C 75	128	3.2	140	4 AAK12888	AaK12888 Human bra
C 76	128	3.2	140	4 ABA38181	AbA38181 Human liv
C 77	128	3.2	140	5 AAI05142	AaI05142 Probe #51
C 78	128	3.2	140	6 ABA12683	AbA12683 Human gen
C 79	128	3.2	140	6 AAI10120	AaI10120 Probe #53
C 80	128	3.2	140	4 ABA51750	AbA51750 Human foe
C 81	128	3.2	140	4 AAI31366	AaI31366 Probe #52
C 82	128	3.2	140	4 ABA21579	AbA21579 Probe #45
C 83	128	3.2	140	4 AAK25496	AaK25496 Human bra
C 84	128	3.2	140	4 AAK00059	AaK00059 Human bra
C 85	128	3.2	140	4 ABA25064	AbA25064 Human liv
C 86	128	3.2	140	5 AAI00061	AaI00061 Probe #52
C 87	128	3.2	140	6 ABA00062	AbA00062 Human gen
C 88	125	3.2	334	3 AAC76758	AaC76758 Human ORF
C 89	109	2.8	570	5 AAS94350	AaS94350 DNA encod
C 90	109	2.8	570	5 AAS88205	AaS88205 DNA encod
C 91	109	2.8	1954	4 AAS91549	AaS91549 DNA encod
C 92	99	2.5	2023	4 AAS42114	AaS42114 Genomic s
C 93	94	2.4	466	8 ACH27850	AaC27850 Human adu
C 94	91	2.3	386	3 AAC77225	AaC77225 Human ORF
C 95	82	2.1	274	6 ABL71349	AbL71349 Corrn ta88
C 96	80	2.0	330	7 ACD93686	AaC93686 Human col

97	77	1.9	146	4	AAE30493	AAE30493	Human	Y5K
98	69	1.7	283	2	AAC29120	AAC29120	Human	sec
99	69	1.7	285	3	AAx40546	AAx40546	Human	sec
100	68	1.7	387	5	AAE80795	AAE80795	DNA	encod
101	68	1.7	387	5	ADBE09489	ADBE09489	Novel	DNA
102	68	1.7	756	9	ADBE07226	ADBE07226	Novel	cod
103	58	1.5	449	4	ABA55381	ABA55381	Human	foe
104	58	1.5	449	4	AAI35029	AAI35029	Probe	#37
105	58	1.5	449	4	ABA44911	ABA44911	Human	brc
106	58	1.5	449	4	AAK29083	AAK29083	Human	bon
107	58	1.5	449	4	AAK03622	AAK03622	Human	brc
108	58	1.5	449	4	ABE28700	ABE28700	Human	liv
109	58	1.5	449	6	ABE30630	ABE30630	Human	gen
110	57	1.4	95	4	ABAE7982	ABAE7982	Human	foe
111	57	1.4	95	4	AAI48190	AAI48190	Probe	#16
112	57	1.4	95	4	ABA50050	ABA50050	Human	brc
113	57	1.4	95	4	AAK42126	AAK42126	Human	brc
114	57	1.4	95	4	AAK16375	AAK16375	Human	brc
115	57	1.4	95	4	ABE41733	ABE41733	Human	liv
116	57	1.4	95	6	ABE16170	ABE16170	Human	gen
117	57	1.4	303	5	AAE66097	AAE66097	DNA	encod
118	54	1.4	96	7	ACD97410	ACD97410	Human	col
119	47	1.2	337	5	AAE88204	AAE88204	DNA	encod
120	47	1.2	896	4	AAE90430	AAE90430	Murine	De
121	42	1.1	4635	4	ABE18571	ABE18571	Drosophi	l
122	31	0.8	74	7	ABE281743	ABE281743	HuntIngro	
123	31	0.8	74	7	ABE281744	ABE281744	HuntIngro	
124	31	0.8	2480	8	AAE161078	AAE161078	Human	MAP
125	31	0.8	2871	8	AAE161076	AAE161076	Human	MAP
126	31	0.8	2906	8	AAE161075	AAE161075	Human	MAP
127	31	0.8	2906	8	AAE31756	AAE31756	Human	209
128	31	0.8	2964	8	AAE161077	AAE161077	Human	MAP
129	29	0.7	241	7	ABE47469	ABE47469	Bovine	ES
130	29	0.7	417	7	ABE47892	ABE47892	Bovine	ES
131	29	0.7	421	7	ABE43482	ABE43482	Bovine	ES
132	29	0.7	424	7	ABE41718	ABE41718	Bovine	ES
133	29	0.7	443	7	ABE48099	ABE48099	Bovine	ES
134	29	0.7	2214	2	AAV22682	AAV22682	New DNA	s
135	29	0.7	3331	2	AAV22683	AAV22683	New DNA	s
136	29	0.7	3331	2	AAE22021	AAE22021	Human	MET
137	29	0.7	3331	5	AAE30078	AAE30078	DB6074	CD
138	28	0.7	416	7	ABE53657	ABE53657	Bovine	ES
139	28	0.7	3894	4	ABE30127	ABE30127	Drosophi	l
140	28	0.7	5604	4	ABE12147	ABE12147	Drosophi	l
141	28	0.7	5824	4	ABE15249	ABE15249	Drosophi	l
142	28	0.7	6705	4	AAE32778	AAE32778	Human	sec
143	28	0.7	8055	4	ABE30126	ABE30126	Drosophi	l
144	28	0.7	10286	4	ABE19684	ABE19684	Drosophi	l
145	28	0.7	11743	4	ABE15248	ABE15248	Drosophi	l
146	28	0.7	138	4	ABE23985	ABE23985	Cenotrib	hab
147	27	0.7	570	7	AAE50974	AAE50974	Probe	#13
148	27	0.7	1218	4	AAE123344	AAE123344	Human	foe
149	27	0.7	1218	4	ABE68451	ABE68451	Human	foe
150	27	0.7	1218	4	AAI48666	AAI48666	Probe	#17
151	27	0.7	1218	4	ABA50502	ABA50502	Human	brc
152	27	0.7	1218	4	ABA35441	ABA35441	Probe	#13
153	27	0.7	1218	4	AAK42584	AAK42584	Human	bon
154	27	0.7	1218	4	AAK16823	AAK16823	Human	brc
155	27	0.7	1218	4	ABE42209	ABE42209	Human	liv
156	27	0.7	1218	5	AAI08981	AAI08981	Probe	#89
157	27	0.7	1218	6	ABE16646	ABE16646	Human	gen
158	27	0.7	1218	6	AAI4134	AAI4134	Probe	#40
159	27	0.7	1218	6	ABE55860	ABE55860	Human	foe
160	27	0.7	1218	6	AAI35517	AAI35517	Probe	#42
161	27	0.7	1218	6	ABE45372	ABE45372	Human	brc
162	27	0.7	1218	6	ABE25535	ABE25535	Probe	#40
163	27	0.7	1218	6	AAE29561	AAE29561	Human	bon
164	27	0.7	1218	6	AAE29561	AAE29561	Human	brc
165	27	0.7	1218	6	AAE29561	AAE29561	Human	brc
166	27	0.7	1218	6	AAE29561	AAE29561	Human	brc
167	27	0.7	1218	6	AAE29561	AAE29561	Human	brc
168	27	0.7	1218	6	AAE29561	AAE29561	Human	brc
169	27	0.7	1218	6	AAE29561	AAE29561	Human	brc



C 243	26	0.7	448	5	AAS91969	DNA encod
244	26	0.7	459	4	AA112263	Probe #21
245	26	0.7	459	4	ABAS3968	Human foe
246	26	0.7	459	4	AA133617	Probe #23
247	26	0.7	459	4	ABRA3516	Human bre
248	26	0.7	459	4	ABRA23716	Probe #21
249	26	0.7	459	4	AAK27681	Human bra
250	26	0.7	459	4	AAK02234	Human bra
251	26	0.7	459	4	ABK27253	Human liv
252	26	0.7	459	4	AA102177	Probe #21
253	26	0.7	459	6	ABK02145	Human gen
254	26	0.7	462	4	ABL26941	Drosophill
255	26	0.7	463	5	AAH81556	Human dlf
256	26	0.7	476	2	AAZ32067	Human MET
257	26	0.7	476	2	AAC90324	AF001444
258	26	0.7	516	2	AAV06551	SCA2 gene
259	26	0.7	561	2	ABL22805	Drosophill
260	26	0.7	603	3	AAAF1492	Aspergill
261	26	0.7	623	2	AAV17229	SCA2 gene
262	26	0.7	625	4	AAI22504	Probe #12
263	26	0.7	625	4	ABK67580	Human foe
264	26	0.7	625	4	AA147796	Probe #16
265	26	0.7	625	4	ABK49677	Human bre
266	26	0.7	625	4	ABK34657	Probe #13
267	26	0.7	625	4	AAK41748	Human bon
268	26	0.7	625	4	AAK16002	Human bra
269	26	0.7	625	4	ABK41341	Human liv
270	26	0.7	625	5	AA108190	Probe #81
271	26	0.7	625	6	ABK15757	Human gen
272	26	0.7	792	4	AAK93622	Human CDN
273	26	0.7	792	4	AAK91954	Human CDN
274	26	0.7	793	2	AAK39688	Gastric c
275	26	0.7	800	2	AAQ32000	Encodes e
276	26	0.7	800	2	AAV31333	Bimelia a
277	26	0.7	801	2	ABL26399	Drosophill
278	26	0.7	924	4	ABL19283	Abv112923
279	26	0.7	936	2	AAV22213	Human Cdx
280	26	0.7	942	9	ADD36449	Human THA
281	26	0.7	945	9	ADD36362	Human THA
282	26	0.7	951	4	AB111357	Drosophill
283	26	0.7	990	4	AB105665	Drosophill
284	26	0.7	1002	4	AAK51628	Human pol
285	26	0.7	1010	5	AAK68262	DNA encod
286	26	0.7	1038	4	AB127667	Drosophill
287	26	0.7	1065	2	AAQ74149	Plasmid p
288	26	0.7	1068	4	AB123721	Drosophill
289	26	0.7	1082	3	AACT8047	Human can
290	26	0.7	1155	4	AB113431	Drosophill
291	26	0.7	1277	4	AB120961	Drosophill
292	26	0.7	1311	4	AB126093	Drosophill
293	26	0.7	1336	4	AB124591	Drosophill
294	26	0.7	1412	6	ABK84787	Human CDN
295	26	0.7	1492	7	ACC44604	Human CBF
296	26	0.7	1529	4	AB116653	Drosophill
297	26	0.7	1533	6	ABK90388	Drosophill
298	26	0.7	1545	4	AB127309	Drosophill
C 299	26	0.7	1547	6	ABK63761	Rat seque
C 300	26	0.7	1547	7	ABT42016	Toxicity-
C 301	26	0.7	1547	9	ABD58351	Toxicity-
C 302	26	0.7	1557	9	ADB52915	Primary r
303	26	0.7	1557	7	ABK94057	Bone and
304	26	0.7	1631	7	ACC44603	Human CBF
305	26	0.7	1680	7	AAQ74150	Plasmid p
306	26	0.7	1694	2	ACC44602	Human CBF
307	26	0.7	1725	6	ABK83820	Human CDN
308	26	0.7	1804	7	ABK94058	Bone and
309	26	0.7	1804	7	AAQ13573	Drosophill
310	26	0.7	1813	2	AB107931	Drosophill
311	26	0.7	1865	4	AB103353	Drosophill
312	26	0.7	1880	6	ABK60893	C1one MGC
313	26	0.7	1933	4	AB119239	Drosophill
314	26	0.7	1933	4	AA113269	Probe #32
315	26	0.7	1979	4	ABK13269	Probe #32
	316	26	0.7	1979	4	ABK54968
	317	26	0.7	1979	4	AA134622
	318	26	0.7	1979	4	ABK44526
	319	26	0.7	1979	4	ABK24732
	320	26	0.7	1979	4	AAK28693
	321	26	0.7	1979	4	AAK03239
	322	26	0.7	1979	4	ABK28293
	323	26	0.7	1979	5	AA103174
	324	26	0.7	1979	6	ABK03204
	325	26	0.7	2024	6	ABK69920
	326	26	0.7	2035	4	ABK19647
	327	26	0.7	2079	4	ABK16037
	328	26	0.7	2094	4	ABK15969
	329	26	0.7	2115	4	ABK25940
	330	26	0.7	2122	4	ABK17007
	331	26	0.7	2124	4	ABK16559
	332	26	0.7	2202	5	AAK87948
	333	26	0.7	2228	4	ABK27224
	334	26	0.7	2242	6	ABK61209
	335	26	0.7	2268	5	ABK08666
	336	26	0.7	2280	5	ABK82146
	337	26	0.7	2294	2	AAV80181
	338	26	0.7	2298	4	ABK18481
	339	26	0.7	2311	10	ADE52641
	340	26	0.7	2341	4	ABK07089
	341	26	0.7	2364	4	ABK15947
	342	26	0.7	2415	2	ABK86757
	343	26	0.7	2424	6	ABK55226
	344	26	0.7	2424	7	ABK11413
	345	26	0.7	2453	2	AAK86758
	346	26	0.7	2453	6	ABK41236
	347	26	0.7	2454	4	ABK14527
	348	26	0.7	2462	2	AAV35473
	349	26	0.7	2521	7	AAK08414
	350	26	0.7	2521	7	ACA64903
	351	26	0.7	2561	4	ABK22804
	352	26	0.7	2571	4	ABK30283
	353	26	0.7	2649	8	ACC70742
	354	26	0.7	2733	2	AAK84442
	355	26	0.7	2776	4	ABK07259
	356	26	0.7	2838	4	ABK09337
	357	26	0.7	2933	4	ABK26398
	358	26	0.7	2951	8	ABK11356
	359	26	0.7	3095	9	ACF03947
	360	26	0.7	3095	9	ADE31740
	361	26	0.7	3161	4	ABK27666
	C 362	26	0.7	3182	4	ABK05664
	363	26	0.7	3207	4	ABK11219
	364	26	0.7	3254	2	AAV32402
	365	26	0.7	3327	2	ADC59311
	366	26	0.7	3336	5	AAV80117
	367	26	0.7	3336	5	AAK87949
	368	26	0.7	3339	5	ABK01915
	369	26	0.7	3346	5	AAK79689
	370	26	0.7	3399	9	ADC59315
	371	26	0.7	3414	6	ABK07557
	372	26	0.7	3441	4	ABK20763
	373	26	0.7	3459	9	ADC59309
	374	26	0.7	3582	4	ABK24590
	375	26	0.7	3591	4	ABK16652
	376	26	0.7	3591	4	ABK10960
	377	26	0.7	3597	4	AAK94326
	378	26	0.7	3645	6	ABK94233
	379	26	0.7	3645	6	ABK12769
	380	26	0.7	3649	4	ABK08200
	381	26	0.7	3732	6	ABK94271
	382	26	0.7	3747	7	ACA03912
	383	26	0.7	3775	5	AAK81656
	384	26	0.7	3786	3	AAZ46153
	385	26	0.7	3798	2	AAZ40483
	386	26	0.7	3819	2	AAK014530
	387	26	0.7	3819	2	AAK063617
	388	26	0.7	3864	5	AAK81657
	ABK54968	Human foe				
	AA134622	Probe #33				
	ABK44526	Human bre				
	ABK24732	Probe #31				
	AAK28693	Human bon				
	AAK03239	Human bra				
	ABK28293	Human liv				
	AA103174	Probe #31				
	ABK03204	Human gen				
	ABK69920	Rat Tob c				
	ABK19647	Drosophill				
	ABK16037	Drosophill				
	ABK15969	Drosophill				
	ABK25940	Drosophill				
	ABK17007	Drosophill				
	ABK16559	Drosophill				
	AAK87948	Human lon				
	ABK27224	Drosophill				
	ABK61209	Unidentif				
	ABK82146	DNA encod				
	AAK82146	DNA encod				
	AAK80181	Alternat				
	ABK18481	Drosophill				
	ADE52641	Murine dn				
	ABK07089	Drosophill				
	ABK15947	Drosophill				
	ABK86757	CDNA of t				
	ABK55226	Human N-t				
	ABK11413	DNA encod				
	AAK86758	CDNA of t				
	ABK41236	Murine ne				
	ABK14527	Drosophill				
	AAV35473	Human hsk				
	AAK08414	Human sma				
	ACA64903	Human KCN				
	ABK22804	Drosophill				
	ABK30283	Drosophill				
	ACC70742	Mouse Jun				
	AAK84442	Mouse bra				
	ABK07259	Drosophill				
	ABK09337	Drosophill				
	ABK26398	Drosophill				
	ABK11356	Drosophill				
	ACF03947	Human SK-				
	ADE31740	Human 122				
	ABK27666	Drosophill				
	ABK05664	Drosophill				
	ABK11219	Drosophill				
	AAV32402	Drosophilla				
	ADC59311	DNA encod				
	AAV80117	Osf2/CDfa				
	AAK87949	Human sho				
	ABK01915	Drosophill				
	AAK79689	DNA encod				
	ADC59315	DNA encod				
	ABK07557	Human bre				
	ABK20763	Drosophill				
	ADC59309	DNA encod				
	ABK24590	Drosophill				
	ABK16652	Drosophill				
	ABK10960	Drosophill				
	AAK94326	Human ful				
	ABK94233	FLOT1 gen				
	ABK12769	Mouse CDN				
	ABK08200	Drosophill				
	ABK94271	Fungal ge				
	ACA03912	CDNA down				
	AAK81656	DNA encod				
	AAZ46153	CDNA equu				
	AAZ40483	Human ZC1				
	AAK014530	T cell pr				
	AAK063617	T-cell tr				
	AAK81657	DNA encod				

389	26	0.7	3864	6	AA18628	Human ins	C 462	26	0.7	9321	6	ABK15177	Abk15177 Human REP
390	26	0.7	3864	7	ABX08783	Angiogene	C 463	26	0.7	9931	7	ABL07088	ABL07088 Drosophill
391	26	0.7	3873	4	ABL26092	Drosophill	C 464	26	0.7	10531	4	ABE24268	ABE24268 Human GPC
392	26	0.7	3881	4	ABL16654	Drosophill	C 465	26	0.7	10882	4	ABL08678	ABL08678 Drosophill
393	26	0.7	3925	5	AAD08642	Human kin	C 466	26	0.7	10910	4	ABL03131	ABL03131 Drosophill
394	26	0.7	3925	5	AD825654	Human cDN	C 467	26	0.7	12363	4	ABL11218	ABL11218 Drosophill
395	26	0.7	3933	4	ABL19238	Drosophill	C 468	26	0.7	12713	4	ABL07608	ABL07608 Drosophill
396	26	0.7	3981	4	ABL08679	Drosophill	C 469	26	0.7	12749	2	AAK78032	AAK78032 Human Hum
397	26	0.7	4083	4	ABL09873	Drosophill	C 470	26	0.7	16975	4	ABL30282	ABL30282 Drosophill
398	26	0.7	4121	4	ABL13430	Drosophill	C 471	26	0.7	18495	4	AAK65235	AAK65235 Human imm
399	26	0.7	4122	4	ABL03706	Drosophill	C 472	26	0.7	18495	7	ABT16920	ABT16920 Human sec
400	26	0.7	4130	4	ABL27308	Drosophill	C 473	26	0.7	18495	7	ABE267561	ABE267561 Human sec
401	26	0.7	4177	4	ABL19282	Drosophill	C 474	26	0.7	18495	7	ABE73980	ABE73980 Secreted
402	26	0.7	4200	2	AA78912	Spinnocere	C 475	26	0.7	18877	4	ABL28632	ABL28632 Drosophill
403	26	0.7	4206	9	ADC30128	Human nov	C 476	26	0.7	19754	4	ABL07258	ABL07258 Drosophill
404	26	0.7	4266	5	AA881655	DNA encod	C 477	26	0.7	20377	4	ABM07231	ABM07231 Human pan
405	26	0.7	4266	5	AA881655	DNA encod	C 478	26	0.7	20377	4	AAK89872	AAK89872 Human dig
406	26	0.7	4298	6	ABK11027	DNA encod	C 479	26	0.7	24370	9	ADC86478	ADC86478 Human GPC
407	26	0.7	4367	2	AAV30270	Gene caus	C 480	26	0.7	31214	4	ABL16558	ABL16558 Drosophill
408	26	0.7	4481	2	AAV06552	Human SCA	C 481	26	0.7	31562	4	ABL03868	ABL03868 Drosophill
409	26	0.7	4481	2	AA23428	Human SCA	C 482	26	0.7	39746	4	ABL13398	ABL13398 Drosophill
410	26	0.7	4481	7	ABV75291	Human SCA	C 483	26	0.7	44456	4	ABL09862	ABL09862 Drosophill
411	26	0.7	4481	9	ADD18753	Human dis	C 484	26	0.7	49939	2	AA223895	AA223895
412	26	0.7	4569	4	ABL15968	Drosophill	C 485	26	0.7	110000	7	ABK16390	ABK16390_4
413	26	0.7	4631	4	ABL23720	Drosophill	C 486	26	0.7	268685	6	ABE56563	ABE56563 Human SUL
414	26	0.7	4655	4	ABL19646	Drosophill	C 487	25	0.6	153	2	AAT78907	AAT78907 Poly-glut
415	26	0.7	4685	5	AA587783	Drosophill	C 488	25	0.6	184	4	ABL23505	ABL23505 Drosophill
416	26	0.7	4777	4	ABL28633	DNA encod	C 489	25	0.6	195	4	ABL27913	ABL27913 Drosophill
417	26	0.7	4829	4	ABL13399	Drosophill	C 490	25	0.6	379	2	AAQ04602	AAQ04602 Cryptical
418	26	0.7	4852	4	ABL09963	Drosophill	C 491	25	0.6	402	2	AAT78906	AAT78906 Poly-glut
419	26	0.7	4920	4	ABL09461	Drosophill	C 492	25	0.6	548	9	ADD34150	ADD34150 Mouse mt
420	26	0.7	4959	6	ABSS5223	Mouse N-t	C 493	25	0.6	657	4	ABU10519	ABU10519 Drosophill
421	26	0.7	4959	6	ABX11410	DNA encod	C 494	25	0.6	668	3	AAE13154	AAE13154 Aspergill
422	26	0.7	4960	6	ABSS5228	Mouse myo	C 495	25	0.6	1109	2	AAZ24880	AAZ24880 Human sec
423	26	0.7	4960	7	ABX11415	DNA encod	C 496	25	0.6	1245	9	ADBE28660	ADBE28660 Human NOV
424	26	0.7	4961	5	AA581653	DNA encod	C 497	25	0.6	1396	2	AAZ21259	AAZ21259 Human cel
425	26	0.7	4981	4	ABL15946	Drosophill	C 498	25	0.6	1396	4	AA511583	AA511583 Human cDN
426	26	0.7	4989	7	AA54622	Human Mas	C 499	25	0.6	1396	6	ABK87047	ABK87047 Human cel
427	26	0.7	5025	4	ABL09336	Drosophill	C 500	25	0.6	1418	7	ACC79031	ACC79031 Human sec
428	26	0.7	5049	4	ABL18489	Drosophill	C 501	25	0.6	1478	4	ABL05963	ABL05963 Drosophill
429	26	0.7	5106	5	AA572419	DNA encod	C 502	25	0.6	1509	4	ABL24571	ABL24571 Drosophill
430	26	0.7	5139	4	ABL09373	Drosophill	C 503	25	0.6	1533	4	ABL27787	ABL27787 Drosophill
431	26	0.7	5178	4	ABL03152	Drosophill	C 504	25	0.6	1598	4	ABL09793	ABL09793 Drosophill
432	26	0.7	5252	4	ABL14526	Drosophill	C 505	25	0.6	1738	4	ABL30141	ABL30141 Drosophill
433	26	0.7	5377	4	ABL16036	Drosophill	C 506	25	0.6	1921	4	ABLO5597	ABLO5597 Drosophill
434	26	0.7	5419	7	ABA00947	Drosophill	C 507	25	0.6	1931	4	ABL30163	ABL30163 Drosophill
435	26	0.7	5556	4	ABU09460	Drosophill	C 508	25	0.6	1984	4	ABL17439	ABL17439 Drosophill
436	26	0.7	5568	5	AA587788	DNA encod	C 509	25	0.6	2048	6	AB576463	AB576463 CDNA enco
437	26	0.7	5895	6	ABT06294	Human NOV	C 510	25	0.6	2056	4	AAAD18037	AAAD18037 Human g1a
438	26	0.7	5970	2	AAK26546	Nucleic a	C 511	25	0.6	2075	6	AAAD35226	AAAD35226 Human TRN
439	26	0.7	6395	4	ABL09872	Drosophill	C 512	25	0.6	2090	7	ADA53234	ADA53234 Human cod
440	26	0.7	6463	3	AAZ45239	DNA encod	C 513	25	0.6	2184	4	ABL23504	ABL23504 Drosophill
441	26	0.7	6541	4	ABU04172	Drosophill	C 514	25	0.6	2223	6	ABK46531	ABK46531 Human PDZ
442	26	0.7	6558	3	AAZ45602	CNA sequ	C 515	25	0.6	2277	4	ABL27912	ABL27912 Drosophill
443	26	0.7	6577	4	ABL13777	Drosophill	C 516	25	0.6	2490	4	ABL26439	ABL26439 Drosophill
444	26	0.7	6832	6	AAAD30439	Human amp	C 517	25	0.6	2561	4	ABL02359	ABL02359 Drosophill
445	26	0.7	6835	9	AAV99915	Human ATB	C 518	25	0.6	2623	3	AAA62684	AAA62684 Human MYT
446	26	0.7	6845	9	AD876189	Human ATB	C 519	25	0.6	2657	4	ABL10518	ABL10518 Drosophill
447	26	0.7	7162	2	AAV22214	Mouse Cdk	C 520	25	0.6	2669	4	ABL08099	ABL08099 Drosophill
448	26	0.7	7188	7	AAAD55833	Human nuc	C 521	25	0.6	3012	4	ABL23891	ABL23891 Drosophill
449	26	0.7	7326	2	AAQ99456	Sequence	C 522	25	0.6	3154	6	AAAD30406	AAAD30406 Drosophill
450	26	0.7	7326	3	AAV10093	Cellular	C 523	25	0.6	3237	4	ABL03607	ABL03607 Drosophill
451	26	0.7	7326	3	AAV15554	Mouse nuc	C 524	25	0.6	3315	9	ADB78970	ADB78970 Rice tran
452	26	0.7	7326	3	AAA62948	CREB bind	C 525	25	0.6	3318	9	ADB78942	ADB78942 Rice tran
453	26	0.7	7568	5	AA587784	DNA encod	C 526	25	0.6	3402	4	ABL17455	ABL17455 Drosophill
454	26	0.7	7568	5	AA572421	DNA encod	C 527	25	0.6	3475	4	ABL03103	ABL03103 Drosophill
455	26	0.7	7593	7	ABX74469	Human cDN	C 528	25	0.6	3708	7	AA151458	AA151458 Rat IRSAL
456	26	0.7	7593	4	ABL07930	Human cDN	C 529	25	0.6	3795	4	ABL23829	ABL23829 Drosophill
457	26	0.7	7680	4	AA159276	Human pol	C 530	25	0.6	3857	4	AAAF85148	AAAF85148 DNA encod
458	26	0.7	7967	4	ABL18498	Drosophill	C 531	25	0.6	3868	4	ABL04755	ABL04755 Drosophill
459	26	0.7	8043	8	AAAD57227	Human CDP	C 532	25	0.6	3884	4	ABL24570	ABL24570 Drosophill
460	26	0.7	8772	4	AA511678	Human Flt	C 533	25	0.6	3973	4	ABL05717	ABL05717 Drosophill
461	26	0.7	8871	4	AA511677	Human Flt	C 534	25	0.6	4067	4	ABL05962	ABL05962 Drosophill

C 535	25	0.6	4141	4	ABL055596	Abi05596	Drosophila	608	24	0.6	109	5	AAI07188	Aai07188	Probe #71
536	25	0.6	4172	4	ABL13509	Abi13509	Drosophila	609	24	0.6	109	6	ABSI4687	Abi14687	Human gen
537	25	0.6	4341	4	AAH49494	Aai49494	D. melano	610	24	0.6	253	4	AAI21383	Aai21383	Probe #11
538	25	0.6	4510	4	ABL20209	Abi20209	Drosophila	611	24	0.6	253	4	ABAA66465	AbA66465	Human toe
539	25	0.6	4621	2	AAV99919	Aav99919	Murine pc	612	24	0.6	253	4	AAI46664	Aai46664	Probe #15
540	25	0.6	4785	4	ABL13743	Abi13743	Drosophila	613	24	0.6	253	4	ABAA48552	AbA48552	Human bre
541	25	0.6	4826	4	ABL17497	Abi17497	Drosophila	614	24	0.6	253	4	ABAA33525	AbA33525	Probe #11
542	25	0.6	4949	4	ABL08615	Abi08615	Drosophila	615	24	0.6	253	4	AAK40618	Aak40618	Human bon
543	25	0.6	4984	4	ABL0778	Abi0778	Drosophila	616	24	0.6	253	4	AAK14884	Aak14884	Human bra
544	25	0.6	5125	2	AAQ29703	Aaq29703	IRS-1, 3/	617	24	0.6	253	4	ABSA40185	AbS40185	Human liv
545	25	0.6	5138	4	ABL17438	Abi17438	Drosophila	618	24	0.6	253	5	AAI07078	Aai07078	Probe #70
546	25	0.6	5175	2	AAZ00022	Aaz00022	osl DNA n	619	24	0.6	253	6	ABSI4585	AbS14585	Human gen
547	25	0.6	5257	6	ABV94246	Abv94246	Breast ca	620	24	0.6	414	3	AAA31507	Aaa31507	Plant mic
548	25	0.6	5286	4	ABL05391	Abi05391	Drosophila	621	24	0.6	427	2	AAV89806	Aav89806	EST clone
C 549	25	0.6	5330	4	ABL13318	Abi13318	Drosophila	622	24	0.6	455	4	AAI12184	Aai12184	Probe #21
550	25	0.6	5508	8	AAD57441	Aad57441	Fruit fly	623	24	0.6	455	4	ABAS3889	AbA3889	Human toe
551	25	0.6	5618	4	ABL27786	Abi27786	Drosophila	624	24	0.6	455	4	AAI33530	Aai33530	Probe #22
552	25	0.6	5697	2	AAZ00023	Aaz00023	osl genom	625	24	0.6	455	4	ABAA43438	AbA43438	Human bre
553	25	0.6	5718	4	ABL04853	Abi04853	Drosophila	626	24	0.6	455	4	ABAA23636	AbA23636	Probe #21
554	25	0.6	5718	4	AAAS57077	Aas57077	CDNA enco	627	24	0.6	455	4	AAK27602	Aak27602	Human bon
555	25	0.6	5718	9	ADC35756	Adc35756	Drosophila	628	24	0.6	455	4	AAK02154	Aak02154	Human bra
556	25	0.6	5868	4	ABL04754	Abi04754	Drosophila	629	24	0.6	455	4	ABSA27173	AbS27173	Human liv
557	25	0.6	5959	6	ABL66686	Abi66686	Lung canc	630	24	0.6	455	5	AAI02097	Aai02097	Probe #20
558	25	0.6	5959	6	ABK84651	Abk84651	Human CDN	631	24	0.6	455	6	ABSO02070	AbS02070	Human gen
C 559	25	0.6	6039	4	ABL07844	Abi07844	Drosophila	632	24	0.6	472	4	AAI13295	Aai13295	Probe #22
560	25	0.6	6101	4	ABL05716	Abi05716	Drosophila	633	24	0.6	472	4	ABAS5398	AbA5398	Human foe
561	25	0.6	6110	4	ABL23890	Abi23890	Drosophila	634	24	0.6	472	4	AAI33651	Aai33651	Probe #23
562	25	0.6	6333	7	AAD54620	Aad54620	Drosophila	635	24	0.6	472	4	ABAA43548	AbA43548	Human bre
563	25	0.6	6523	4	AACT6548	Aac76548	Human ORF	636	24	0.6	472	4	ABAA23750	AbA23750	Probe #22
564	25	0.6	6545	2	AAZ00020	Aaz00020	osl + DNA	637	24	0.6	472	4	AAK27715	Aak27715	Human bon
565	25	0.6	6912	4	ABL23828	Abi23828	Drosophila	638	24	0.6	472	4	AAK02268	Aak02268	Human bra
566	25	0.6	7005	4	ABL15355	Abi15355	Drosophila	639	24	0.6	472	4	ABSA27290	AbS27290	Human liv
C 567	25	0.6	7144	4	ABL08098	Abi08098	Drosophila	640	24	0.6	472	5	AAI02210	Aai02210	Probe #22
568	25	0.6	7521	4	ABL18831	Abi18831	Drosophila	641	24	0.6	472	6	ABSO2175	AbS02175	Human gen
569	25	0.6	7737	4	ABL02204	Abi02204	Drosophila	642	24	0.6	597	6	ABK33107	AbK33107	DNA enco
C 570	25	0.6	7766	4	ABL17496	Abi17496	Drosophila	643	24	0.6	970	4	ABL13259	Abi13259	Probe #11
C 571	25	0.6	7807	4	ABL17454	Abi17454	Drosophila	644	24	0.6	1018	4	AAI22494	Aai22494	Probe #12
572	25	0.6	8113	4	ABL06899	Abi06899	Drosophila	645	24	0.6	1018	4	ABAA67570	AbA67570	Human foe
573	25	0.6	8303	4	ABL05390	Abi05390	Drosophila	646	24	0.6	1018	4	AAI47786	Aai47786	Probe #16
574	25	0.6	9330	4	ABL13508	Abi13508	Drosophila	647	24	0.6	1018	4	ABAA49667	AbA49667	Human bre
C 575	25	0.6	9400	4	ABL04852	Abi04852	Drosophila	648	24	0.6	1018	4	ABAA34647	AbA34647	Probe #13
C 576	25	0.6	9400	4	AAAS57076	Aas57076	DNA enco	649	24	0.6	1018	4	AAK41738	Aak41738	Human bon
C 577	25	0.6	9400	9	ADC35755	Adc35755	Drosophila	650	24	0.6	1018	4	AAK15992	Aak15992	Human bra
578	25	0.6	9673	4	ABL26438	Abi26438	Drosophila	651	24	0.6	1018	4	ABSA41331	AbS41331	Human liv
579	25	0.6	10072	4	ABL10828	Abi10828	Drosophila	652	24	0.6	1018	5	AAI08180	Aai08180	Probe #81
580	25	0.6	10620	4	ABL17327	Abi17327	Drosophila	653	24	0.6	1018	6	ABSI5747	AbS15747	Human gen
581	25	0.6	10868	4	ABL02358	Abi02358	Drosophila	654	24	0.6	1235	4	ABL08663	Abi08663	Drosophila
582	25	0.6	11133	4	ABL18830	Abi18830	Drosophila	655	24	0.6	1273	7	ABZ36212	AbZ36212	Human sec
583	25	0.6	11961	4	ABL09792	Abi09792	Drosophila	656	24	0.6	1329	4	ABL27023	AbL27023	Drosophila
584	25	0.6	12748	4	ABL17326	Abi17326	Drosophila	657	24	0.6	1350	4	ABL06633	AbL06633	Drosophila
C 585	25	0.6	13015	4	AAAF5571	Aaf5571	Drosophila	658	24	0.6	1417	3	AAZ33343	Aaz33343	Human sec
586	25	0.6	13075	4	ABL15354	Abi15354	Drosophila	659	24	0.6	1464	5	ABAD08651	AbA08651	Mouse can
587	25	0.6	16969	4	ABL26778	Abi26778	Drosophila	660	24	0.6	1578	2	AAAX19960	Aax19960	Human Tan
588	25	0.6	20990	4	ABL03102	Abi03102	Drosophila	661	24	0.6	1593	4	ABL30175	AbL30175	Drosophila
589	25	0.6	21379	4	ABL30162	Abi30162	Drosophila	662	24	0.6	1981	3	AAFI4618	Aafi4618	Aspergill
590	25	0.6	21409	4	ABL30140	Abi30140	Drosophila	663	24	0.6	2104	4	ABL09709	AbL09709	Drosophila
C 591	25	0.6	21475	4	ABL08614	Abi08614	Drosophila	664	24	0.6	2138	4	ABL24940	AbL24940	Drosophila
592	25	0.6	22788	4	ABL20208	Abi20208	Drosophila	665	24	0.6	2240	4	ABL07261	AbL07261	Drosophila
C 593	25	0.6	23306	4	ABL13338	Abi13338	Drosophila	666	24	0.6	2295	5	AAAS72219	Aas72219	DNA enco
C 594	25	0.6	28660	4	ABL03606	Abi03606	Drosophila	667	24	0.6	2295	5	AAAS91825	Aas91825	DNA enco
C 595	25	0.6	31449	4	ABL09172	Abi09172	Drosophila	668	24	0.6	2435	4	ABLI4691	AbL14691	Drosophila
596	25	0.6	37322	4	ABL06898	Abi06898	Drosophila	669	24	0.6	2435	4	ABLI24360	AbL24360	Drosophila
597	25	0.6	44242	4	ABL19930	Abi19930	Drosophila	670	24	0.6	2485	4	ABLI06332	AbL06332	Drosophila
598	25	0.6	49431	4	ABL13742	Abi13742	Drosophila	671	24	0.6	2656	4	ABLI08375	AbL08375	Drosophila
C 599	25	0.6	171936	6	ABSS5655	Abss5655	Human SUV	672	24	0.6	2706	4	ABLI12001	AbL12001	Drosophila
600	24	0.6	109	4	AAI21491	Aai21491	Probe #11	673	24	0.6	2879	4	ABLI02847	AbL02847	Drosophila
601	24	0.6	109	4	ABAA6571	AbA6571	Human foe	674	24	0.6	2909	5	AAAS72220	Aas72220	DNA enco
602	24	0.6	109	4	AAI46782	Abi46782	Probe #15	675	24	0.6	3042	4	ABLI28445	AbL28445	Drosophila
603	24	0.6	109	4	ABAA48659	AbA48659	Human bre	676	24	0.6	3099	4	ABLI23050	AbL23050	Drosophila
604	24	0.6	109	4	ABAA33636	AbA33636	Probe #12	677	24	0.6	3104	4	ABLI04869	AbL04869	Drosophila
605	24	0.6	109	4	AAK40728	Aak40728	Human bon	678	24	0.6	3216	4	ABLI07525	AbL07525	Drosophila
606	24	0.6	109	4	AAK14995	Aak14995	Human bra	679	24	0.6	3423	6	AAAD6318	Aad6318	Human EGF
607	24	0.6	109	4	ABSA40299	AbS40299	Human liv	680	24	0.6	3570	4	ABLI19381	AbL19381	Drosophila

C 681	24	0.6	3593	4	ABL30174	Ab130174 Drosophila	C 754	23	0.6	351	9	ADB95017	Ad95017 A. thaliana
C 682	24	0.6	3679	4	ABL04099	Ab104099 Drosophila	755	23	0.6	360	4	ABL25081	Ab125081 Drosophila
C 683	24	0.6	3820	4	ABL27022	Ab127022 Drosophila	756	23	0.6	362	8	ACL18963	ACL18963 DNA clone
C 684	24	0.6	4110	4	ABL06447	Ab106447 Drosophila	C 757	23	0.6	466	3	AAC42435	AAC42435 Arabidopsis
C 685	24	0.6	4251	4	ABL17365	Ab117365 Drosophila	758	23	0.6	477	4	ABL07485	Ab107485 Drosophila
C 686	24	0.6	4443	4	ABL04821	Ab104821 Drosophila	759	23	0.6	486	4	AAF75507	AAF75507 Polyglutera
C 687	24	0.6	4455	7	ABT17054	Abt17054 Human MP2	760	23	0.6	562	5	AAS05415	AAS05415 Mammalian
C 688	24	0.6	4656	4	ABL08374	Ab108374 Drosophila	761	23	0.6	569	8	ACL18962	ACL18962 DNA clone
C 689	24	0.6	4826	4	ABL07260	Ab107260 Drosophila	762	23	0.6	577	4	AA118861	AA118861 Probe #87
C 690	24	0.6	4835	2	AA137050	AA137050 Drosophila	763	23	0.6	577	4	ABR63860	ABR63860 Human fce
C 691	24	0.6	4994	7	ACC44331	ACC44331 Gene enco	764	23	0.6	577	4	AA143983	AA143983 Probe #12
C 692	24	0.6	5101	4	ABL28057	Ab128057 Drosophila	765	23	0.6	577	4	ABR31040	ABR31040 Human bon
C 693	24	0.6	5109	4	ABL17409	Ab117409 Drosophila	766	23	0.6	577	4	AAK38087	AAK38087 Human bra
C 694	24	0.6	5184	9	ADZ55651	Adz55651 Human cDN	767	23	0.6	577	4	AAK12370	AAK12370 Human liv
C 695	24	0.6	5215	4	ABL28444	Ab128444 Drosophila	768	23	0.6	577	4	ABS37704	ABS37704 Human liv
C 696	24	0.6	5227	4	ABL06175	Ab106175 Drosophila	769	23	0.6	577	6	ABS12099	ABS12099 Human gen
C 697	24	0.6	5337	4	ABL06529	Ab106529 Drosophila	770	23	0.6	602	8	ACL18964	ACL18964 DNA clone
C 698	24	0.6	5407	4	ABL08765	Ab108765 Drosophila	771	23	0.6	616	4	AA193709	AA193709 Human pol
C 699	24	0.6	5448	4	ABL12000	Ab112000 Drosophila	772	23	0.6	762	4	ABL28195	ABL28195 Drosophila
C 700	24	0.6	6033	4	ABL23051	Ab123051 Drosophila	C 773	23	0.6	790	6	ABL01400	ABL01400 Murine ap
C 701	24	0.6	6186	4	ABL29885	Ab129885 Drosophila	774	23	0.6	811	4	ABL10185	ABL10185 Drosophila
C 702	24	0.6	6223	4	ABL14630	Ab114630 Drosophila	775	23	0.6	921	4	ABL17215	ABL17215 Drosophila
C 703	24	0.6	6307	4	ABL05643	Ab105643 Drosophila	776	23	0.6	923	4	ABL10189	ABL10189 Drosophila
C 704	24	0.6	6325	4	AAK80005	AAK80005 Human imm	777	23	0.6	927	6	ABG94265	ABG94265 Fungal ZB
C 705	24	0.6	6359	4	ABL04098	Ab104098 Drosophila	778	23	0.6	927	6	ABN79906	ABN79906 Human sec
C 706	24	0.6	6593	4	ABL02645	Ab102645 Drosophila	779	23	0.6	930	4	ABL21657	ABL21657 Drosophila
C 707	24	0.6	6915	4	ABL07524	Ab107524 Drosophila	780	23	0.6	939	4	ABL28527	ABL28527 Drosophila
C 708	24	0.6	7101	4	ABR28056	Ab128056 Drosophila	781	23	0.6	996	4	ABL12371	ABL12371 Drosophila
C 709	24	0.6	7243	4	ABL02521	Ab102521 Drosophila	782	23	0.6	1080	4	ABL22295	ABL22295 Drosophila
C 710	24	0.6	7278	4	ABL09708	Ab109708 Drosophila	783	23	0.6	1089	4	ABL18089	ABL18089 Human sec
C 711	24	0.6	7314	4	ABL17364	Ab117364 Drosophila	784	23	0.6	1144	7	ABY41973	ABY41973 Toxicity
C 712	24	0.6	7522	9	ADD18689	Add18689 Human dis	785	23	0.6	1353	3	ADB58275	ADB58275 DNA encod
C 713	24	0.6	7887	4	ADZ71243	Adz71243 Novel hum	786	23	0.6	1686	5	AA574183	AA574183 Toxicity
C 714	24	0.6	8100	4	ABL08652	Ab108652 Drosophila	787	23	0.6	1715	4	ABL27703	ABL27703 Drosophila
C 715	24	0.6	8147	4	ABL13276	Ab113276 Drosophila	788	23	0.6	1726	4	ABL13809	ABL13809 Drosophila
C 716	24	0.6	8147	4	ABL04820	Ab104820 Drosophila	789	23	0.6	1745	4	AA129497	AA129497 CDX2 cDNA
C 717	24	0.6	8147	6	AB573313	Ab573313 DNA encod	790	23	0.6	1745	6	AA172629	AA172629 Human col
C 718	24	0.6	8357	4	ABL06174	Ab106174 Drosophila	791	23	0.6	1745	3	AB233683	AB233683 Soybean a
C 719	24	0.6	9105	4	ABL29884	Ab129884 Drosophila	792	23	0.6	1795	3	AA550065	AA550065 Soybean a
C 720	24	0.6	9165	4	ABL06528	Ab106528 Drosophila	793	23	0.6	1875	4	AB127163	AB127163 Drosophila
C 721	24	0.6	9555	7	ABX34542	Abx34542 Human mdd	794	23	0.6	1967	4	ABL07527	ABL07527 Drosophila
C 722	24	0.6	9936	4	ABL13258	Ab113258 Drosophila	795	23	0.6	2062	6	ABN85850	ABN85850 Human ful
C 723	24	0.6	10558	4	ABL06446	Ab106446 Drosophila	C 796	23	0.6	2112	4	ABL13587	ABL13587 Drosophila
C 724	24	0.6	10558	4	ABL02846	Ab102846 Drosophila	797	23	0.6	2146	4	AAK94825	AAK94825 Human ful
C 725	24	0.6	10979	4	ABL02644	Ab102644 Drosophila	798	23	0.6	2160	4	AA166703	AA166703 A. gossyp
C 726	24	0.6	11439	4	ABL14258	Ab114258 Drosophila	799	23	0.6	2210	4	ABL26748	ABL26748 Drosophila
C 727	24	0.6	11613	4	ABL05642	Ab105642 Drosophila	C 800	23	0.6	2309	4	ABL13298	ABL13298 Drosophila
C 728	24	0.6	17841	4	ABL04868	Ab104868 Drosophila	C 801	23	0.6	2324	4	ABL26618	ABL26618 Drosophila
C 729	24	0.6	18977	4	ABL19380	Ab119380 Drosophila	C 802	23	0.6	2331	4	ABL24927	ABL24927 Drosophila
C 730	24	0.6	21748	4	ABL02520	Ab102520 Drosophila	803	23	0.6	2339	4	ABL20445	ABL20445 Drosophila
C 731	24	0.6	26767	4	ABL08654	Ab108654 Drosophila	804	23	0.6	2405	5	AA574184	AA574184 DNA encod
C 732	24	0.6	26960	4	ABL08712	Ab108712 Drosophila	805	23	0.6	2453	4	AB102487	AB102487 Drosophila
C 733	24	0.6	36336	4	ABL08764	Ab108764 Drosophila	806	23	0.6	2453	4	ABL22239	ABL22239 Drosophila
C 734	24	0.6	40152	4	ABL17408	Ab117408 Drosophila	807	23	0.6	2529	4	ABL15638	ABL15638 Drosophila
C 735	24	0.6	81440	6	ABQ76617	Abq76617 C. albica	C 808	23	0.6	2552	4	ABL18372	ABL18372 Drosophila
C 736	24	0.6	106323	7	ABX14591	Abx14591 Human chl	C 809	23	0.6	2552	4	ABL07484	ABL07484 Drosophila
C 737	24	0.6	106323	9	AAD58821	AAZ58821 Human txa	C 810	23	0.6	2682	4	ABL25080	ABL25080 Drosophila
C 738	23	0.6	23	2	AAZ40517	AAZ40517 Human STE	C 811	23	0.6	2756	4	ABL27702	ABL27702 Drosophila
C 739	23	0.6	23	2	AAZ40518	AAZ40518 Human STE	C 812	23	0.6	2847	4	ABL28194	ABL28194 Drosophila
C 740	23	0.6	23	6	ABL19570	Ab119570 Human can	C 813	23	0.6	2860	2	AAK91533	AAK91533 Drosophila
C 741	23	0.6	23	6	AA127788	AA127788 Probe #17	C 814	23	0.6	2988	4	ADAO0895	ADAO0895 Mouse oet
C 742	23	0.6	23	6	ABA76100	AbA76100 Human fce	C 815	23	0.6	2997	7	ABL24827	ABL24827 Drosophila
C 743	23	0.6	23	6	AA156760	AA156760 Probe #25	C 816	23	0.6	3048	4	ABL24827	ABL24827 Drosophila
C 744	23	0.6	23	6	ABA40655	AbA40655 Probe #19	C 817	23	0.6	3057	4	AAAD08348	AAAD08348 Human sec
C 745	23	0.6	23	6	AAK50771	AAK50771 Human bon	C 818	23	0.6	3125	4	ABL28526	ABL28526 Drosophila
C 746	23	0.6	23	6	AAK24774	AAK24774 Human bra	C 819	23	0.6	3236	4	ABL15799	ABL15799 Drosophila
C 747	23	0.6	23	6	ABS50361	ABS50361 Human liv	C 820	23	0.6	3263	4	ABL10403	ABL10403 Drosophila
C 748	23	0.6	23	6	ABS24250	ABS24250 Human gen	C 821	23	0.6	3269	4	ABL30322	ABL30322 Drosophila
C 749	23	0.6	23	6	AAAF75506	AAAF75506 Polyglutera	C 822	23	0.6	3282	7	ADA70873	ADA70873 Rice gene
C 750	23	0.6	23	6	AAH62144	AAH62144 Rat diffe	C 823	23	0.6	3332	4	AB120171	AB120171 Drosophila
C 751	23	0.6	23	6	ABX90681	AbX90681 Murine ge	C 824	23	0.6	3355	4	ABL06009	ABL06009 Drosophila
C 752	23	0.6	23	6	ABL13299	Ab113299 Drosophila	C 825	23	0.6	3373	4	ABL17214	ABL17214 Drosophila
C 753	23	0.6	23	6	ABL26619	Ab126619 Drosophila	C 826	23	0.6	3373	4	ABL17214	ABL17214 Drosophila

827	23	0.6	3407	4	ABL1088	Ab118088	Drosophila	c 900	23	0.6	10194	4	ABL08154	Ab108154	Drosophila
828	23	0.6	3455	3	AAA96703	AAA96703	Reporter	c 901	23	0.6	10230	4	ABL15505	Ab115505	Drosophila
829	23	0.6	3462	4	AA25378	AA25378	Nucleic acid	c 902	23	0.6	11029	4	ABL20444	Ab120444	Drosophila
830	23	0.6	3483	4	ABL14095	ABL14095	Drosophila	c 903	23	0.6	11693	4	ABL30327	Ab130327	Drosophila
831	23	0.6	3584	4	ABL07253	ABL07253	Drosophila	c 904	23	0.6	12099	4	ABL16890	Ab116890	Drosophila
832	23	0.6	3598	4	ABL27843	ABL27843	Drosophila	c 905	23	0.6	12155	4	ABL06590	Ab106590	Drosophila
833	23	0.6	3756	4	ABL08875	ABL08875	Drosophila	c 906	23	0.6	12260	4	ABL08874	Ab108874	Drosophila
834	23	0.6	3762	4	ABL14087	ABL14087	Drosophila	c 907	23	0.6	13531	4	ABL07252	Ab107252	Drosophila
835	23	0.6	3790	4	ABL14101	ABL14101	Drosophila	c 908	23	0.6	15405	4	ABL03146	Ab103146	Drosophila
836	23	0.6	3791	4	ABL04336	ABL04336	Drosophila	c 909	23	0.6	15648	4	ABL03036	Ab103036	Drosophila
837	23	0.6	3801	4	ABL07597	ABL07597	Drosophila	c 910	23	0.6	15923	4	ABL07596	Ab107596	Drosophila
838	23	0.6	3951	4	ABL24893	ABL24893	Drosophila	c 911	23	0.6	16962	4	ABL10402	Ab110402	Drosophila
839	23	0.6	3959	4	ABL08865	ABL08865	Drosophila	c 912	23	0.6	18506	4	ABL05592	Ab105592	Drosophila
840	23	0.6	3967	4	ABL07526	ABL07526	Drosophila	c 913	23	0.6	19399	4	ABL05146	Ab105146	Drosophila
841	23	0.6	3998	4	ABL27162	ABL27162	Drosophila	c 914	23	0.6	19399	4	ABL06008	Ab106008	Drosophila
842	23	0.6	4014	4	ABL21656	ABL21656	Drosophila	c 915	23	0.6	20245	4	ABL15504	Ab115504	Drosophila
843	23	0.6	4203	6	ABX97119	ABX97119	Human NOV	c 916	23	0.6	20892	4	ABL22310	Ab122310	Drosophila
844	23	0.6	4229	6	ABK91051	ABK91051	Genomic D	c 917	23	0.6	30143	4	ABL18664	Ab118664	Drosophila
845	23	0.6	4233	4	ABL25099	ABL25099	Drosophila	c 918	23	0.6	37687	4	ABL29366	Ab129366	Drosophila
846	23	0.6	4331	4	ABL24926	ABL24926	Drosophila	c 919	23	0.6	44577	8	ADA03038	Ada03038	Human ROR
847	23	0.6	4336	2	AAQ37543	AAQ37543	Cardiac a	c 920	23	0.6	44577	8	ADA66322	Ada66322	Human ROR
848	23	0.6	4356	2	AAQ95540	AAQ95540	Cardiac a	c 921	23	0.6	44577	9	ADB72776	ADB72776	Human ROR
849	23	0.6	4387	6	ABN59837	ABN59837	Novel hum	c 922	23	0.6	56686	4	ABL18488	Ab118488	Drosophila
850	23	0.6	4400	4	ABL18665	ABL18665	Drosophila	c 923	23	0.6	25	9	ADC38187	ADC38187	Human AML
851	23	0.6	4409	4	ABL17895	ABL17895	Drosophila	c 924	23	0.6	25	9	ADC38189	ADC38189	Human AML
852	23	0.6	4629	4	ABL29279	ABL29279	Drosophila	c 925	23	0.6	25	9	ADC38186	ADC38186	Human AML
853	23	0.6	4662	4	ABL18808	ABL18808	Drosophila	c 926	23	0.6	25	9	ADC38188	ADC38188	Human AML
854	23	0.6	4705	4	ABL10184	ABL10184	Drosophila	c 927	23	0.6	30	7	ABZ81777	ABZ81777	Human lnt
855	23	0.6	4916	4	ABL18373	ABL18373	Drosophila	c 928	23	0.6	52	7	ABZ81774	ABZ81774	Oligonucle
856	23	0.6	5021	4	ABL11783	ABL11783	Drosophila	c 929	23	0.6	52	7	ABZ81756	ABZ81756	Human lnt
857	23	0.6	5054	4	ABA09272	ABA09272	Human dlt	c 930	23	0.6	138	3	AAA15871	AAA15871	DNA encod
858	23	0.6	5054	4	AAK52712	AAK52712	Human pol	c 931	23	0.6	172	7	ACC83027	ACC83027	Human lnt
859	23	0.6	5083	3	AAK22393	AAK22393	Human sec	c 932	23	0.6	172	7	ACC83027	ACC83027	Human lnt
860	23	0.6	5123	4	ABL27842	ABL27842	Drosophila	c 933	23	0.6	196	6	AAZ99412	AAZ99412	Trans-epi
861	23	0.6	5264	4	ABL22294	ABL22294	Drosophila	c 934	23	0.6	196	6	ABQ73501	ABQ73501	Human CG
862	23	0.6	5360	8	AAAD5168	AAAD5168	Drosophila	c 935	23	0.6	267	2	AAZ31736	AAZ31736	Human CG
863	23	0.6	5418	4	ABL16891	ABL16891	Drosophila	c 936	23	0.6	267	2	AAZ31735	AAZ31735	Human CG
864	23	0.6	5482	5	AAK63955	AAK63955	Drosophila	c 937	23	0.6	294	3	AAA15879	AAA15879	DNA encod
865	23	0.6	5484	4	ABL08155	ABL08155	Drosophila	c 938	23	0.6	300	2	AAZ13093	AAZ13093	Human gen
866	23	0.6	5564	4	ABL28214	ABL28214	Drosophila	c 939	23	0.6	316	4	AAI20017	AAI20017	Probe #99
867	23	0.6	5710	4	ABL18813	ABL18813	Drosophila	c 940	23	0.6	316	4	ABA65045	ABA65045	Human lnt
868	23	0.6	5718	4	ABL04853	ABL04853	Drosophila	c 941	23	0.6	316	4	AAI45215	AAI45215	Probe #13
869	23	0.6	5718	4	AAAS7077	AAAS7077	DNA encod	c 942	23	0.6	316	4	ABA47161	ABA47161	Human bre
870	23	0.6	5718	4	ADC35756	ADC35756	Drosophila	c 943	23	0.6	316	4	ABA32153	ABA32153	Probe #10
871	23	0.6	5720	2	AAAT4217	AAAT4217	Lacta gene	c 944	23	0.6	316	4	AAK39207	AAK39207	Human bon
872	23	0.6	5720	8	AAZ51508	AAZ51508	Drosophila	c 945	23	0.6	316	4	AAK33469	AAK33469	Human bra
873	23	0.6	5720	8	AAZ51508	AAZ51508	Drosophila	c 946	23	0.6	316	4	AAK38793	AAK38793	Human lnt
874	23	0.6	5910	4	AAK51728	AAK51728	Human pol	c 947	23	0.6	316	5	AAI05725	AAI05725	Probe #57
875	23	0.6	5975	4	ABL12270	ABL12270	Drosophila	c 948	23	0.6	316	6	ABSI3291	ABSI3291	Human gen
876	23	0.6	6034	4	ABL22516	ABL22516	Drosophila	c 949	23	0.6	358	2	AAV87567	AAV87567	EST clone
877	23	0.6	6129	4	ABL22298	ABL22298	Drosophila	c 950	23	0.6	362	3	AAI15880	AAI15880	DNA encod
878	23	0.6	6177	4	ABL14094	ABL14094	Drosophila	c 951	23	0.6	387	4	ABL28401	ABL28401	Drosophila
879	23	0.6	6284	4	ABL15798	ABL15798	Drosophila	c 952	23	0.6	387	9	ADC37658	ADC37658	Human ang
880	23	0.6	6416	4	ABL13586	ABL13586	Drosophila	c 953	23	0.6	396	6	ABO98092	ABO98092	Mouse ES
881	23	0.6	6416	4	ABL20170	ABL20170	Drosophila	c 954	23	0.6	399	3	AAZ94093	AAZ94093	Haemacopo
882	23	0.6	6594	4	ABL16539	ABL16539	Drosophila	c 955	23	0.6	426	1	AAK60524	AAK60524	Sequence
883	23	0.6	6693	4	ABL29278	ABL29278	Drosophila	c 956	23	0.6	436	1	AAI10775	AAI10775	Probe #70
884	23	0.6	6776	4	ABL04337	ABL04337	Drosophila	c 957	23	0.6	436	4	ABA54225	ABA54225	Human foe
885	23	0.6	6895	4	ABL10188	ABL10188	Drosophila	c 958	23	0.6	436	4	AAI33033	AAI33033	Probe #71
886	23	0.6	6919	4	ABL05593	ABL05593	Drosophila	c 959	23	0.6	436	4	ABA22220	ABA22220	Probe #68
887	23	0.6	7008	4	ABL24826	ABL24826	Drosophila	c 960	23	0.6	436	4	AAK26145	AAK26145	Human bon
888	23	0.6	7179	4	ABL25098	ABL25098	Drosophila	c 961	23	0.6	436	4	AAK00694	AAK00694	Human bra
889	23	0.6	7394	4	ABL17894	ABL17894	Drosophila	c 962	23	0.6	436	4	ABSI25735	ABSI25735	Human lnt
890	23	0.6	7529	4	ABL02486	ABL02486	Drosophila	c 963	23	0.6	436	5	AAI00701	AAI00701	Probe #69
891	23	0.6	7614	4	ABL11782	ABL11782	Drosophila	c 964	23	0.6	436	6	ABSI00730	ABSI00730	Human gen
892	23	0.6	7669	4	ABL07263	ABL07263	Drosophila	c 965	23	0.6	500	9	ADC37673	ADC37673	Human ang
893	23	0.6	8974	4	ABL14100	ABL14100	Drosophila	c 966	23	0.6	503	7	ABO80312	ABO80312	Full leng
894	23	0.6	8984	4	ABL24892	ABL24892	Drosophila	c 967	23	0.6	503	7	ACC83026	ACC83026	Human lnt
895	23	0.6	9283	4	ABL14086	ABL14086	Drosophila	c 968	23	0.6	508	2	AAZ31752	AAZ31752	Human CG
896	23	0.6	9400	4	ABL04852	ABL04852	Drosophila	c 969	23	0.6	512	9	ADBE81405	ADBE81405	Ataxidops
897	23	0.6	9400	4	AAAS7076	AAAS7076	DNA encod	c 970	23	0.6	526	6	AAI199619	AAI199619	Mouse lsc
898	23	0.6	9400	9	ADC35755	ADC35755	Drosophila	c 971	23	0.6	539	2	AAV04780	AAV04780	Human cho
899	23	0.6	9907	4	ABL08864	ABL08864	Drosophila	c 972	23	0.6	539	2	AAV18517	AAV18517	Human bet

c 973	22	0.6	539	2	AAV04779	Human cho
c 974	22	0.6	539	2	AAx25387	Human cho
c 975	22	0.6	539	3	AAx73833	Human cho
c 976	22	0.6	543	2	AAQ23092	Antigen t
c 977	22	0.6	549	4	AAO08808	Human sin
c 978	22	0.6	575	2	AAO03240	Human CG
c 979	22	0.6	575	4	AAO08507	DNA encod
c 980	22	0.6	575	4	AAO08807	Human sin
c 981	22	0.6	587	2	AAz31734	Human cho
c 982	22	0.6	595	5	AAx80859	DNA encod
c 983	22	0.6	627	4	ABU23497	Drosophill
c 984	22	0.6	633	4	ABU27793	Drosophill
c 985	22	0.6	686	6	ABs77041	Frog embry
c 986	22	0.6	717	4	AAO08788	Human sin
c 987	22	0.6	717	4	AAO08800	Human sin
c 988	22	0.6	717	4	AAO08798	Human sin
c 989	22	0.6	718	4	AAO08790	Human sin
c 990	22	0.6	725	2	AAz31742	Human CG
c 991	22	0.6	725	2	AAz31751	Human CG
c 992	22	0.6	725	2	AAz31750	Human CG
c 993	22	0.6	726	4	AAO08796	Human sin
c 994	22	0.6	726	4	AAO08794	Human sin
c 995	22	0.6	729	2	AAz31748	Human CG
c 996	22	0.6	729	2	AAz31741	Human CG
c 997	22	0.6	729	2	AAz31749	Human CG
c 998	22	0.6	731	6	ABA90389	Single ch
c 999	22	0.6	743	2	AAO03233	Single ch
c1000	22	0.6	743	2	AAO03231	Single ch

## ALIGNMENTS

## RESULT 1

ADE34151 standard; DNA; 3951 BP.

ADE34151;

29-JAN-2004 (first entry)

Human DNA encoding mishapen/NIKs-related kinase, Mink3a.

Human; mishapen/NIKs-related kinase; Mink3a; ds; antiinflammatory;  
 immunosuppressive; cytoskeletal; germinal centre kinase;  
 c-JUN N-terminal kinase; JNK; extracellular signal response kinase; ERK;  
 growth factor induced-ERK activation; proliferation;  
 cell proliferation disorder; cell survival;  
 intracellular signal transduction; apoptosis; morphological change;  
 cell migration; gene therapy; inflammatory disease; autoimmune disease;  
 immunodeficiency; cancer.

Homo sapiens.

Key Location/Qualifiers

CDS 7..3945

FT /tag= a

FT /product= "Mink3a"

US2003077597-A1.

24-APR-2003.

19-OCT-2001; 2001US-00029115.

19-OCT-2001; 2001US-00029115.

(LUOY/) LUO Y.

(FUCA/) FU C A.

(SHEN/) SHEN M.

Luo Y, Fu CA, Shen M;

WPI, 2003-635076/60.  
 P-PSDB; ADE34150.  
 New mishapen/NIKs-related kinase nucleic acids and proteins useful in  
 gene therapy and for treating disorders, e.g. acute and chronic  
 inflammatory diseases.  
 Claim 3; SEQ ID NO 1; 53bp; English.

The invention relates to a recombinant nucleic acid capable of  
 hybridising to a Human DNA encoding mishapen/NIKs-related kinase  
 (Mink3a, 3b and 3c, germinal centre kinase proteins) appearing as  
 ADE34151, ADE34153 and ADE34155, or at least 90% identity to them, or  
 their complements. Also included are a recombinant polypeptide at least  
 95 % sequence identity to Mink3a, 3b or 3c (appearing as ADE34150,  
 ADE34152 and ADE34154), screening for a candidate bioactive agent capable  
 of modulating c-JUN N-terminal kinase (JNK) or extracellular signal  
 response kinase (ERK) phosphorylation or activity, screening for a  
 candidate bioactive agent capable of modulating growth factor induced-ERK  
 activation in a mammalian cell, screening for a candidate bioactive agent  
 capable of modulating proliferation in a mammalian cell, diagnosing a  
 mammalian cell proliferation disorder, a medicament for treating a  
 mammalian cell proliferation disorder and screening for a candidate agent  
 capable of modulating cell survival. The MINK3 (mishapen/NIKs-related  
 kinase) nucleic acids are useful in the modulation of intracellular  
 signal transduction, cell proliferation, apoptosis, morphological change  
 and migration of mammalian cells. MINK3 nucleic acids and proteins are  
 specifically useful in gene therapy, and for treating, preventing or  
 diagnosing acute and chronic inflammatory diseases, autoimmune diseases  
 and diseases characterised by immunodeficiency. The compositions may also  
 be used to treat MINK3 dysfunction related disorders, e.g. cancer. The  
 CC nucleotide sequences may also be used as hybridisation probes, in  
 CC chromosome and gene mapping, and in generating antisense RNA and DNA. The  
 CC present sequence encodes Mink3a.

SQ Sequence 3951 BP; 928 A; 1196 C; 1199 G; 628 T; 0 U; 0 Other;

Query Match 100.0%; Score 3951; DB 9; Length 3951;

Best Local Similarity 100.0%; Pred. No. 0; Matches 3951; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGCTTATGGGCGATCCAGCCCCCGCGAGCTGAGACGACATGACTGTCCGCCCTG	60
DB	1	GGCTTATGGGCGAGCCAGCCCCCGCGAGCTGAGACGACATGACTGTCCGCCCTG	60
QY	61	CGGAGCCCTGCTGGGATCTTGAAGTTGAGAGGTGCGGATGAGAACCTACGACAG	120
DB	61	CGGAGCCCTGCTGGGATCTTGAAGTTGAGAGGTGCGGATGAGAACCTACGACAG	120
QY	121	GTGTCAAGAGGTGCGATGTCAAGACGGGCGAGCTGCTGCCATCAAGGTCAATGTC	180
DB	121	GTGTCAAGAGGTGCGATGTCAAGACGGGCGAGCTGCTGCCATCAAGGTCAATGTC	180
QY	181	ACGAGAGCAGAGAGAGAGATCAACAGAGATCAACATCTGTAAGAAAGTCTCTAC	240
DB	181	ACGAGAGCAGAGAGAGAGATCAACAGAGATCAACATCTGTAAGAAAGTCTCTAC	240
QY	241	CACCGCAACATGCGACCTACGAGAGCTTCAATCAAGAGAGCCCGCGGAACGAT	300
DB	241	CACCGCAACATGCGACCTACGAGAGCTTCAATCAAGAGAGCCCGCGGAACGAT	300
QY	301	GACCACTCTGCTGTGTATGAGATTTCTGTGCTGTGTTCAAGTACGACCTGTAAAG	360
DB	301	GACCACTCTGCTGTGTATGAGATTTCTGTGCTGTGTTCAAGTACGACCTGTAAAG	360
QY	361	AAACAAGAGCAAGCCCTGAAGAGACTGTATTCGCTATATTCGAGGAGATCTTC	420
DB	361	AAACAAGAGCAAGCCCTGAAGAGACTGTATTCGCTATATTCGAGGAGATCTTC	420
QY	421	AGGGGTGCGCCATCTCATGCGCAAGAGGATTCATCGAGATCAAGGGGAGAAAT	480
DB	421	AGGGGTGCGCCATCTCATGCGCAAGAGGATTCATCGAGATCAAGGGGAGAAAT	480



QY 481 GTGCTGCTGACAGAAATGCTGAGGTCAAGCTAGTGAATTTGGGGTGAAGTCTCAGCTG 540  
DB 481 GTGCTGCTGACAGAAATGCTGAGGTCAAGCTAGTGAATTTGGGGTGAAGTCTCAGCTG 540  
QY 541 GACCGCACCGTGGGACAGACGAAACACTTTCATTTGGGACTCCCTACTGGATGGCTCAGAG 600  
DB 541 GACCGCACCGTGGGACAGACGAAACACTTTCATTTGGGACTCCCTACTGGATGGCTCAGAG 600  
QY 601 GTCATCCGCTGTGTATGAGAACCTGTATGCCACTATGTATTAACAGAGATGATATTTGGTCT 660  
DB 601 GTCATCCGCTGTGTATGAGAACCTGTATGCCACTATGTATTAACAGAGATGATATTTGGTCT 660  
QY 661 CTAGAATCAACAGCATCGAATGGCAGAGGGAGCCCCCTGTGTGATGATGACACCC 720  
DB 661 CTAGAATCAACAGCATCGAATGGCAGAGGGAGCCCCCTGTGTGATGATGACACCC 720  
QY 721 ATGGAGGCCCCCTTCTCTCATTTCTGGAACTCTCGCCCAAGGCTCAAGTCCAGAGAGTGG 780  
DB 721 ATGGAGGCCCCCTTCTCTCATTTCTGGAACTCTCGCCCAAGGCTCAAGTCCAGAGAGTGG 780  
QY 781 TCTAAGAAATTGATGACTTGAATGACATGTCTCATCAAGACTTACCTGAGCCGCCA 840  
DB 781 TCTAAGAAATTGATGACTTGAATGACATGTCTCATCAAGACTTACCTGAGCCGCCA 840  
QY 841 CCCACGGACGACTGAAATTTCCCTTCATCCGGGACCAAGCCACGGAGCGGAGGTC 900  
DB 841 CCCACGGACGACTGAAATTTCCCTTCATCCGGGACCAAGCCACGGAGCGGAGGTC 900  
QY 901 CGCATCCAGCTTAAAGACCAATTTGACGATCCCGAAGAAAGCGGGGTGAAGAGAGAG 960  
DB 901 CGCATCCAGCTTAAAGACCAATTTGACGATCCCGAAGAAAGCGGGGTGAAGAGAGAG 960  
QY 961 ACAGAAATATGATGACAGCGGACCGAGGAGGAAGATGACAGCCATGAGAGAGAGAGAG 1020  
DB 961 ACAGAAATATGATGACAGCGGACCGAGGAGGAAGATGACAGCCATGAGAGAGAGAGAG 1020  
QY 1021 CCAAGCTCCATCAATGAAGTGTGCTGGAGAGTGTGATCAAGCCGGGAACTTCTCCGGGTC 1080  
DB 1021 CCAAGCTCCATCAATGAAGTGTGCTGGAGAGTGTGATCAAGCCGGGAACTTCTCCGGGTC 1080  
QY 1081 CAGACGAAATTAAGAGCAATCAGAGGCTTTAAACAGACAGACAGCTCAGACAGAG 1140  
DB 1081 CAGACGAAATTAAGAGCAATCAGAGGCTTTAAACAGACAGACAGCTCAGACAGAG 1140  
QY 1141 CAGACGCGAGACCCCGAGGCAACATCAAAACCTGTGACACAGCGGACAGCGGCGCAT 1200  
DB 1141 CAGACGCGAGACCCCGAGGCAACATCAAAACCTGTGACACAGCGGACAGCGGCGCAT 1200  
QY 1201 GAGAGAGGAAGAGAGAGCGGCGCTGTGAGAGGACACAGCGGCGGAGCGGAGAGAG 1260  
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DB 1381 CAGCGGCGGTCAAGACGTCTCAAGAGGACGTGACGAGAGCAAGCTTACCTCAAGTCC 1440  
QY 1441 CTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1500  
DB 1441 CTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1500  
QY 1501 GGGGACAGAGAGCCCTGTACATTTATGCTGCGGCGATGAATCCCGTGAACAAACAGCC 1560  
DB 1501 GGGGACAGAGAGCCCTGTACATTTATGCTGCGGCGATGAATCCCGTGAACAAACAGCC 1560  
QY 1561 TGGGCCCCGAGAGGTGAAGAGAGAAAGAGATGAACAGCAGACGACGACGACGACGACGAC 1620

DB 1561 TGGGCCCCGAGAGGTGAAGAGAGAAAGAGATGAACAGCAGACGACGACGACGACGACGAC 1620  
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DB 1681 CCAAGAACCCCTTCCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1740  
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DB 2521 GATACAGACAGCGTCAAGCAGATGAGTGTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2580  
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DB 2581 CCCCCTATGAG 2640  
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 Qy 2701 CCCACCGAAGAGAGCAAAAGCCCAACCTCGAAGATGGAGTGTGACTACAG 2760  
 Db 2701 CCCACCGAAGAGAGCAAAAGCCCAACCTCGAAGATGGAGTGTGACTACAG 2760  
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 Db 2941 CCCACCAACACCGGGGCCACAGTGAAGCCCTGAGATCCGGAAGTACAAAGAGCATTC 3000  
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 Qy 3901 GTTACTTCAATGACTGAAACCGTAACATGATGAATGAGTGAAGAGGC 3951  
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 RESULT 2  
 ADEB34155  
 ID ADEB34155 standard; DNA; 4033 BP.  
 AC ADEB34155;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human DNA encoding misshapen/NIKs-related kinase, Mink3c.  
 XX  
 KW Human; misshapen/NIKs-related kinase; Mink3c; ds; antiinflammatory;  
 KW immunosuppressive; cytoskeletal; germinal centre kinase;  
 KW c-JUN N-terminal kinase; JNK; extracellular signal response kinase; ERK;  
 KW growth factor induced-ERK activation; proliferation;  
 KW cell proliferation disorder; cell survival;  
 KW intracellular signal transduction; apoptosis; morphological change;  
 KW cell migration; gene therapy; inflammatory disease; autoimmune disease;  
 KW immunodeficiency; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 203..4033  
 FT /tag= a  
 FT /product= "Mink3c"  
 XX  
 PN US2003077597-A1.  
 XX  
 PD 24-APR-2003.  
 XX  
 PF 19-OCT-2001; 2001US-00029115.  
 XX  
 PR 19-OCT-2001; 2001US-00029115.  
 XX  
 PA (LDOY/) LDO Y.  
 PA (FUCA/) FU C A.  
 PA (SHEN/) SHEN M.  
 XX  
 PI Luo Y, Fu CA, Shen M;  
 XX  
 DR WPI; 2003-635076/60.  
 DR P-PSDB; ADEB34154.  
 XX  
 PT New misshapen/NIKs-related kinase nucleic acids and proteins useful in  
 PT gene therapy and for treating disorders, e.g. acute and chronic  
 PT inflammatory diseases.  
 XX  
 PS Claim 3; SEQ ID NO 5; 53bp; English.  
 XX  
 CC The invention relates to a recombinant nucleic acid capable of  
 CC hybridizing to a Human DNA encoding misshapen/NIKs-related kinase  
 CC (Mink3a, 3b and 3c, germinal centre kinase proteins) appearing as  
 CC ADEB34151, ADEB34153 and ADEB34155, or at least 90% identity to them, or  
 CC their complements. Also included are a recombinant polypeptide at least  
 CC 95% sequence identity to Mink3a, 3b or 3c (appearing as ADEB34150,  
 CC ADEB34152 and ADEB34154), screening for a candidate bioactive agent capable  
 CC of modulating c-JUN N-terminal kinase (JNK) or extracellular signal  
 CC response kinase (ERK) phosphorylation or activity, screening for a  
 CC candidate bioactive agent capable of modulating growth factor induced-ERK

CC activation in a mammalian cell, screening for a candidate bioactive agent  
CC capable of modulating proliferation in a mammalian cell, diagnosing a  
CC mammalian cell proliferation disorder, a medicament for treating a  
CC mammalian cell proliferation disorder and screening for a candidate agent  
CC capable of modulating cell survival. The MINK3 (mishapen/NIN3-related  
CC kinase) nucleic acids are useful in the modulation of intracellular  
CC signal transduction, cell proliferation, apoptosis, morphological change  
CC and migration of mammalian cells. MINK3 nucleic acids and proteins are  
CC specifically useful in gene therapy, and for treating, preventing or  
CC diagnosing acute and chronic inflammatory diseases, autoimmune diseases  
CC and diseases characterized by immunodeficiency. The compositions may also  
CC be used to treat MINK3 dysfunction related disorders, e.g. cancer. The  
CC nucleotide sequences may also be used as hybridisation probes, in  
CC chromosome and gene mapping, and in generating antisense RNA and DNA. The  
CC present sequence encodes MINK3c.

XX Sequence 4033 BP; 959 A; 1213 C; 1210 G; 651 T; 0 U; 0 Other;

Query Match 48.3%; Score 1907; DB 9; Length 4033;

Best Local Similarity 99.8%; Pred. No. 0; Mismatches 1; Indels 3; Gaps 1;

Matches 2197; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Qy 1745 AGTCCCTGCAGAGACAGCCCACTGAGCTGCTTCCAGCTCCCATGACCCCG 1804  
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Qy 1805 ACCCTGCCATCCCGACACCTGACAGCTGCTCCGAGAGCTTCATCCGCGCA 1864  
Db 1896 ACCCTGCCATCCCGACACCTGACAGCTGCTCCGAGAGCTTCATCCGCGCA 1955  
Qy 1865 ATTGAGACCCCACTGAGAGAGCTGAGCTGCTCCAGCTGCTCCGAGCTGCTCC 1924  
Db 1956 ATTGAGACCCCACTGAGAGAGCTGAGCTGCTCCAGCTGCTCCGAGCTGCTCC 2015  
Qy 1925 CAGATTAAGAGAGCCCACTGAGAGAGCTGAGCTGCTCCAGCTGCTCCGAGCT 1984  
Db 2016 CAGATTAAGAGAGCCCACTGAGAGAGCTGAGCTGCTCCAGCTGCTCCGAGCT 2075  
Qy 1985 ACACAGTGGGGCGGAGAGGTCCTGCGGACAGCCAGGAGCTGCTGCGAGAGCA 2044  
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Qy 2045 ACTCGGCTGCAATATCTATGCAAGAGGCGGAGAGGAGGAGCCCAAGGCTCAG 2104  
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Qy 2105 GGGCCCTGCTCAGCCCTGAGCCGCGCCCAAGCTTCTAGTAACCCCGAGCTCAGAGGA 2164  
Db 2196 GGGCCCTGCTCAGCCCTGAGCCGCGCCCAAGCTTCTAGTAACCCCGAGCTCAGAGGA 2255  
Qy 2165 GCGACCTGCTGAGAAAGCTGCGAGCAGCTTCTCAGCTTCAAGGAGCACTTCCCCC 2224  
Db 2256 GCGACCTGCTGAGAAAGCTGCGAGCAGCTTCTCAGCTTCAAGGAGCACTTCCCCC 2315  
Qy 2225 AGGCTGCTCAGCTGAGAGCGGAAAGCGGCGGAGGCTCTCCAACTGAGAGCTCCCCG 2284  
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Db 2376 TGCTCTCCCTGAGATTAAGAGCGAGACTGAGAGAGCCCTGCGGCTTCCAGAGAG 2435  
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Qy 2405 CCAATGAGCTACTGCTGCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2464  
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Db 2556 GCGAGAGCGGCGCAGAGAGGAGGAGAGATACCCCTGAGGAGCGGAGGAGGAGTA 2612

Qy 2525 CAGACAGCTGAGAGACCATGCTGCTCCAGAGCGTGCAGAGATGACCGGAGCCAGGCC 2584  
Db 2613 CAGACAGCTGAGAGACCATGCTGCTCCAGAGCGTGCAGAGATGACCGGAGCCAGGCC 2672  
Qy 2585 CATACGGGGGCGGAGCATGCTGCTCAGAGCACCCCTGAGAGAGAGAGAGAGCTGCTGC 2644  
Db 2673 CATACGGGGGCGGAGCATGCTGCTCAGAGCACCCCTGAGAGAGAGAGAGAGCTGCTGC 2732  
Qy 2645 ATGCTGACAGATGAGTACCAAACTGCTGACGCTGCTCAGAGCCAGAGCATCAGCCCA 2704  
Db 2733 ATGCTGACAGATGAGTACCAAACTGCTGACGCTGCTCAGAGCCAGAGCATCAGCCCA 2792  
Qy 2705 CCGAGAAACAGAAAGGCGCAAGCCCACTGAGAGAGTGGAGAGGAGTGCATCAGCTC 2764  
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Db 2913 ACCAGCTGAGAGGAGTGGAGACAGATCCCATCAAGCCCTAGTGGTGGAGAGGCA 2972  
Qy 2885 CTGGCTGCAACAGCTGCAAGAGAGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 2944  
Db 2973 CTGGCTGCAACAGCTGCAAGAGAGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 3032  
Qy 2945 CCAACACCCGGGCGCAGAGTGAAGACCCCTGAGATCCGGAAGTACAGAGAGGATTCAC 3004  
Db 3033 CCAACACCCGGGCGCAGAGTGAAGACCCCTGAGATCCGGAAGTACAGAGAGGATTCAC 3092  
Qy 3005 CCGAGATCTCTGTCAGAGCTTGTGGGGGAGTCAACTGCTGCTGAGGAGCAGAGAG 3064  
Db 3093 CCGAGATCTCTGTCAGAGCTTGTGGGGGAGTCAACTGCTGCTGAGGAGCAGAGAG 3152  
Qy 3065 TGAATGTCGAGACCGAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3124  
Db 3153 TGAATGTCGAGACCGAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3212  
Qy 3125 TCCAGCAGATGATGCTGAGAGGAGGAGTCAACTGCTCATCAACCATCTCAGGAGAGAG 3184  
Db 3213 TCCAGCAGATGATGATGCTGAGAGGAGGAGTCAACTGCTCATCAACCATCTCAGGAGAGAG 3272  
Qy 3185 ACAACCTGCGGAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3244  
Db 3273 ACAACCTGCGGAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3332  
Qy 3245 AAGTGAAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3304  
Db 3333 AAGTGAAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3392  
Qy 3305 GTGTTGTAATTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3364  
Db 3393 GTGTTGTAATTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3452  
Qy 3365 TGTATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3424  
Db 3453 TGTATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3512  
Qy 3425 TCCGCCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3484  
Db 3513 TCCGCCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3572  
Qy 3485 TCTATGCTGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3544  
Db 3573 TCTATGCTGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3632  
Qy 3545 TCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3604  
Db 3633 TCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3692

Qy	3 605	ACACCGAAGCGATGAGAGTGCCTGCTGCTGCTGAGAGAGAGAGGCTCAGCGTCAACACAGT	3 665
Db	3 693	ACACCGAAGCGATGAGAGTGCCTGCTGCTGCTGAGAGAGAGAGGCTCAGCGTCAACACAGT	3 752
Qy	3 665	ACGGGCGCATCATTTAAGATGAGTGCGTGCAGAGAGAGAGGAGATGCGCTACTTCTGAGCGCT	3 724
Db	3 753	ACGGGCGCATCATTTAAGATGAGTGCGTGCAGAGAGAGAGGAGATGCGCTACTTCTGAGCGCT	3 812
Qy	3 725	ACATCTGCTCCAAACCGATTAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG	3 784
Db	3 813	ACATCTGCTCCAAACCGATTAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGG	3 872
Qy	3 785	AGACGGGCGCACTCGACGGGGCTTTCATGCAACAAGAGCTCAGAGGCTCAAGTTCCGT	3 844
Db	3 873	AGACGGGCGCACTCGACGGGGCTTTCATGCAACAAGAGCTCAGAGGCTCAAGTTCCGT	3 932
Qy	3 845	GTGAGCGGAATGACAAAGTGTCTTTCCTCAGTCCGCTCTGGGGGACAGCCAAAGTTT	3 904
Db	3 933	GTGAGCGGAATGACAAAGTGTCTTTCCTCAGTCCGCTCTGGGGGACAGCCAAAGTTT	3 992
Qy	3 995	ACTTCATGACTCTGAACCGTAACTGACATCATGAACTGGGGA	3 945
Db	3 993	ACTTCATGACTCTGAACCGTAACTGACATCATGAACTGGGGA	4 003

RESULT 3	
AA148627	
ID	AA148627 standard; cDNA, 3888 BP.
XX	
AC	AA148627;
XX	
DT	11-OCT-2002 (first entry)
XX	
DE	Human insulin receptor signaling modifier cDNA SEQ ID NO: 37.
XX	
KW	Human; insulin receptor signaling; insulin receptor signaling modifier
KW	ISM; diabetes; metabolic syndrome; antidiabetic; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200255664-A2.
XX	
PD	18-JUL-2002.
XX	
PF	11-JAN-2002; 2002WO-US001048.
XX	
FR	12-JAN-2001; 2001US-0261226P.
PR	12-JAN-2001; 2001US-0261303P.
PR	12-JAN-2001; 2001US-0261304P.
PR	12-JAN-2001; 2001US-0261335P.
PR	12-JAN-2001; 2001US-0261336P.
PR	12-JAN-2001; 2001US-0261361P.
PR	12-JAN-2001; 2001US-0261456P.
PR	12-JAN-2001; 2001US-0261457P.
PR	12-JAN-2001; 2001US-0261458P.
PR	12-JAN-2001; 2001US-0261459P.
PR	12-JAN-2001; 2001US-0261461P.
PR	12-JAN-2001; 2001US-0261518P.
PR	12-JAN-2001; 2001US-0261531P.
PR	12-JAN-2001; 2001US-0261532P.
PR	12-JAN-2001; 2001US-0261589P.
PR	12-JAN-2001; 2001US-0261590P.
PR	12-JAN-2001; 2001US-0261694P.
PR	12-JAN-2001; 2001US-0261695P.
PR	12-JAN-2001; 2001US-0261697P.
XX	
PA	(EXEL-) EXELIXIS INC.
XX	
PI	Seidel-Dugan C, Ferguson KC, Kidd T;
XX	
WI	WPI; 2002-599664/64.
DR	P-PSDB; AAO18508.
XX	

PT Identifying an insulin receptor signaling modulator, useful as drug  
PT targets for treating diabetes or metabolic disorders, comprises  
PT contacting an assay system comprising insulin receptor signaling  
PT modifiers with a test agent.

Disclosure; Page 118-120; 232pp; English.

The present invention relates to a method of identifying a candidate insulin receptor (INR) signaling modulating agent, involving contacting an assay system comprising an insulin receptor signaling modifier (ISM) polypeptide or nucleic acid with a test agent, and detecting a test agent's biased activity of the assay system. The method is useful for identifying candidate INR signaling modulating agents. ISM genes may be used as drug targets for treatment of disorders related to INR signaling such as diabetes or metabolic syndrome. ISM nucleic acids and polypeptides are useful for identifying and testing agents that modulate ISM function and for other applications related to the involvement of ISM in INR signaling, and for identifying subjects having a predisposition to such diseases associated with INR signaling. The present sequence is an ISM coding sequence described in the exemplification of the invention

Sequence 3888 BP; 917 A; 1168 C; 1182 G; 621 T; 0 U; 0 Other;

every match 43.1%; Score 1701; DB 6; Length 3888;

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best local similarity: 0.99; 100% identity
Matches 1801; Conservative 0; Mismatches 2; Indels 0; Gaps 0

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2143 AGTAACCCGACCTCAGGAGGAGCGACCTGGCTGGGAACGCTCGACAGCGTCTTCCA 2202

Db 2086 AGTAACCCGACCTCAGGAGGAGCGACCTGGCTGGGAACGCTCGGACAGCGTCTTCCA 2145

2203 GCCTTCACGGCACCTCCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGAGCCTCC 2267

Db 2146 GCCTCTCACGGGCACTCCCCCAGGCTGGCTCACTGGAGCGGAACCGGTGGAGTCTCC 2205

2263 TCCTAACTGGACAGCTCCCTGTGCTCTCCCTGGGATAAGCCAGCCGACGACCAC 2322

Db 2206 TCCAAACCGACAGCTCCCTGTGCTCTCCCTGGGATAAGCCAGCCCGACGACCCAC 2265

2323 CGCTCAGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTGAAGAGCGGACTCTGGACGAG 2381

Db 2266 CGCTACGGCCAGGCCGGCCCGCAGACTTGTGTTGCTGALAGAGCGGACTCTGACGAG 232:

2383 GCCCCTGGCCTCCCAAGAGGCCATGGA CTACTGTCGTCACGAGGAGGTGGAAGC 244:

Db 2326 GCCCCTGGCTCCCAAGAGGCCATGACTACTCGTCGTCCAGCGAGGAGTGGAAGC 2381

2443 AGTGAGGACGACGAGGAGGAAGGCCGAAGCGGGCCAGCAGAGGGGAGCAGAGATACCCCT 250

Db 2386 AGTGAGGACGACGAGGAGGCGAAGCGCGGCCAGCAGAGGGGAGCAGAGATACCCCT 244

2503 GGGGGCCGACGATGGGATACAGACAGCGTCAGCACCATGGTGTCCACGACGTCGAG 256

Db 2446 GGGGGCCGACGATGGGATACAGACAGCGTCAGCACCATGTGTCCACGACGTCGAG 250

2563 GAGATCACC GGACCCAGCCCCCATAACGGGGCGGCACCATGTGTTCAGCGACCCCT 262

Db 2506 GAGATCACCGGACCCAGCCCCCATACGGGGGGCGGACCATGTGTTCAGCGCACCCCT 256

2623 GAAGAGGAGCGAACCTGCTGCATGCTGACAGCAATGGGTACACAACCTGCCTGACGTG 268

Db 2566 GAAGAGGAGCGAACCTGCTGCATGCTGACAGCAATGGGTACACAACCTGCCTGACGTG 262

2683 GTCCAGCCAGCCTCACCACCGAGAACGCAAGGCCAAGCCACCTCGAAGGAT 274

Db 2626 GTCCAGCCCACTCAACCGAGAACAGCAAGGCCCACTCGAAGGAT 268

2743 GGGAGTGGTGA CTACCA GTCTCCGTGGCTGGTAAAGGCCCTGGCAAGAGCTCGTTCACG 280

Db 2686 GGGAGTGTGACTACCACTCTCGTGGCTGGTAAAGCCCTGGCAAGAGCTCGTTCACG 274

2803 ATGTTTGATCTAGGATCTACCAGCCTGGAGGCA GTGGGACAGCATCCCATCACA 286

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Db      2746 ATGTTTGATCTAGGGATCTACAGCGCTGGAGGCACTGGGGACAGATCCCATCA 2805
Qy      2863 GCCCTAGTGGTGGAGAGGGCACTGGGCTGCACCACTGCACTAGAGAGTGAAGAGGT 2922
Db      2806 GCCCTAGTGGTGGAGAGGGCACTGGGCTGCACCACTGCACTAGAGAGTGAAGAGGT 2865
Qy      2923 TCTGTGGTCAAGTGAATCCACCAACAACCGGGGCCCACTGAGAGACCCCTGAGATCCGG 2982
Db      2866 TCTGTGGTCAAGTGAATCCCAACCAACAACCGGGGCCCACTGAGAGAGTGAAGAGGT 2925
Qy      2983 AAGTACAAGAGCAGATTCACTCCGAGATCTCTGTGAGCCCTTTGGGGGGTCAACTG 3042
Db      2926 AAGTACAAGAGCAGATTCACTCCGAGATCTCTGTGAGCCCTTTGGGGGGTCAACTG 2985
Qy      3043 CTGGTGGGCAACGAGAACGGGCTGATGTTGCTGACCGAGTGGGCAAGGTTAT 3102
Db      2986 CTGGTGGGCAACGAGAACGGGCTGATGTTGCTGACCGAGTGGGCAAGGTTAT 3045
Qy      3103 GGAATCAATGGGCGGCGCACTTCACAGAGATGATGCTGAGGGGGCTCAACTGCTC 3162
Db      3046 GGAATCAATGGGCGGCGCACTTCACAGAGATGATGCTGAGGGGGCTCAACTGCTC 3105
Qy      3163 ATCAACCACTTCAGAGGAAAGAGAACAACTGGGGGTGTTACTCTGCTGCTCCGAGAC 3222
Db      3106 ATCAACCACTTCAGAGGAAAGAGAACAACTGGGGGTGTTACTCTGCTGCTCCGAGAC 3165
Qy      3223 AAGATTCTGCACATGACCCAGAAAGTGAAGAAAGAGGAGGCTGAGACCACTGGGGGAGC 3282
Db      3166 AAGATTCTGCACATGACCCAGAAAGTGAAGAAAGAGGAGGCTGAGACCACTGGGGGAGC 3225
Qy      3283 ATGAGAGGCTGGCGGGCACTACCGTGTGTGAATACGAGCGGATTAATCTCTGCTATC 3342
Db      3226 ATGAGAGGCTGGCGGGCACTACCGTGTGTGAATACGAGCGGATTAATCTCTGCTATC 3285
Qy      3343 GCCCTCAAGAGCTCGTGAAGGTGTATGCTGGGCGCCCAACCTCAACAATAATCATG 3402
Db      3286 GCCCTCAAGAGCTCGTGAAGGTGTATGCTGGGCGCCCAACCTCAACAATAATCATG 3345
Qy      3403 GCCTTCAAGTCTTTGCCGACCTCCGCCACCGGCTCTGCTGTGACCTGACAGTGAAG 3462
Db      3346 GCCTTCAAGTCTTTGCCGACCTCCGCCACCGGCTCTGCTGTGACCTGACAGTGAAG 3405
Qy      3463 GAGGGGAGCGGCTCAAGGTATCTATGAGCTGAGTGTGCTTCATGCTGAGAGTGAAGTGC 3522
Db      3406 GAGGGGAGCGGCTCAAGGTATCTATGAGCTGAGTGTGCTTCATGCTGAGAGTGAAGTGC 3465
Qy      3523 GACTCGGGGAAACAGTATGACATCTACATCCCTGTGACATCCAGAGCAGATCAGCGCC 3582
Db      3466 GACTCGGGGAAACAGTATGACATCTACATCCCTGTGACATCCAGAGCAGATCAGCGCC 3525
Qy      3583 CAGGCATCATCTTCTCCCAACACCGAGCGCATGAGATGCTGCTGTACGAGGAC 3642
Db      3526 CAGGCATCATCTTCTCCCAACACCGAGCGCATGAGATGCTGCTGTACGAGGAC 3585
Qy      3643 GAGGGTGTCTACGTCACACCTAGAGGGGCACTATTAGAGATGTGTGCTGCACTGGGG 3702
Db      3586 GAGGGTGTCTACGTCACACCTAGAGGGGCACTATTAGAGATGTGTGCTGCACTGGGG 3645
Qy      3703 GAGATGCTACTTCTGTGGGCTCAATCTGCTCAACAGCATATGAGGTGGGGTGAGAAA 3762
Db      3646 GAGATGCTACTTCTGTGGGCTCAATCTGCTCAACAGCATATGAGGTGGGGTGAGAAA 3705
Qy      3763 GCCATTGAGATCCGCTCTGTGAGAACGGGCACTCGACGGGGTCTTTCATGACAAAAGA 3822
Db      3706 GCCATTGAGATCCGCTCTGTGAGAACGGGCACTCGACGGGGTCTTTCATGACAAAAGA 3765
Qy      3823 GCTTAGAGGCTCAAGTTCCTGTGTGAGAGGAAATGACAAAGGTGTTTTTGCTCACTCCG 3882
Db      3766 GCTTAGAGGCTCAAGTTCCTGTGTGAGAGGAAATGACAAAGGTGTTTTTGCTCACTCCG 3825
Qy      3883 TCTGGGGGAGCAGCAGATTACTTCACTGACTGTAACCTGATCATGAACTGG 3942
Db      3826 TCTGGGGGAGCAGCAGATTACTTCACTGACTGTAACCTGATCATGAACTGG 3885

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Qy      3943 TGA 3945
Db      3886 TGA 3888

RESULT 4
AA240485
ID   AA240485 standard; DNA, 4133 BP.
XX
AC   AA240485;
XX
DT   18-FEB-2000 (first entry)
XX
DE   Human ZC3 DNA.
XX
KW   Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;
KW   antiprosthetic; antiarteriosclerotic; antiasthmatic; immunosuppressive;
KW   neuroprotective; cardiac; cerebroprotective; cytoskeletal; antidiabetic;
KW   vulnery; STE20; protein kinase; STIK2; STIK3; STIK4; STIK5; STIK6; STIK7;
KW   ZC1; ZC2; ZC3; ZC4; KHS2; SUDU1; SUDU3; GEX2; PAK4; PAK5; antagonist;
KW   antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;
KW   inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
KW   rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
KW   myocardial infarction; cardiovascular disease; stroke; renal failure;
KW   oxidative stress-related neurodegenerative disorder; Parkinson's disease;
KW   amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
KW   ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
KW   menageal disorder; growth regulation; wound healing; T cell activation;
KW   immunosuppressant; ss.
XX
OS   Homo sapiens.
XX
PN   W09953036-A2.
XX
PD   21-OCT-1999.
XX
PF   13-APR-1999; 99MO-US008150.
XX
PR   14-APR-1998; 98US-0081784P.
XX
PA   (SUGB-) SUGEN INC.
XX
PI   Plowman G, Martinez R, Whyte D;
XX
DR   WPI; 1999-611301/52.
XX
PT   P-PSDB; AAY55933.
XX
FT   Novel kinase-related polypeptides used for the diagnosis and treatment of
XX   kinase-related diseases and disorders.
XX
PS   Disclosure; Page 267-269; 387pp; English.
XX
CC   This sequence represents the coding sequence for a novel STE20-related
CC   protein kinase. The invention relates to nucleic acid molecule encoding a
CC   kinase polypeptide selected from STIK2, STIK3, STIK4, STIK5, STIK6,
CC   STIK7, ZC1, ZC2, ZC3, ZC4, KHS2, SUDU1, SUDU3, GEX2, PAK4 and PAK5. The
CC   proteins are used to identify agonists and antagonists, and to raise
CC   antibodies. The polynucleotides are useful in gene therapy protocols. The
CC   polynucleotides, polypeptides, antibodies, antagonists and agonists may
CC   be used to treat diseases such as immune-related disorders and diseases
CC   (e.g. Rheumatoid arthritis, artherosclerosis, chronic inflammatory bowel
CC   disease (e.g. Crohn's disease), asthma, osteoarthritis, psoriasis,
CC   atherosclerosis, rhinitis, autoimmunity, and organ transplantation,
CC   chronic inflammatory pelvic disease, multiple sclerosis, organ
CC   transplantation, myocardial infarction, cardiovascular disease, stroke,
CC   renal failure, oxidative stress-related neurodegenerative disorders (e.g.
CC   amyotrophic lateral sclerosis, Parkinson's disease and Leigh syndrome),
CC   cancer, cardiomyopathies, ischemic disorders, inflammatory disorders,
CC   diabetes mellitus, fibrotic and menageal disorders. The proteins may
CC   also be useful for cell growth regulation (e.g. in wound healing), T cell
CC   activation, mitosis control, and as immunosuppressants
XX

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SQ Sequence 4133 BP; 960 A; 1258 C; 1246 G; 669 T; 0 U; 0 Other;  
Query Match 42.9%; Score 1694; DB 2; Length 4133;  
Beet Local Similarity 99.7%; Pred. No. 0;  
Matches 2084; Conservative 0; Mismatches 3; Indels 3; Gaps 1;  
QY 1745 AGTCCCTGAGAGACAGCCCAACCCGAAACCTGCTGCTTCCCAAGCTTCCCAAGACCCG 1804  
DB 1784 AGTCCCTGAGAGACAGCCCAACCCGAAACCTGCTGCTTCCCAAGCTTCCCAAGACCCG 1843  
QY 1805 ACCCTGCAATCCCGGACCCCACTGCGACGCCCAAGTCCCGAGAGCTGCTCATCCGCA 1864  
DB 1844 ACCCTGCAATCCCGGACCCCACTGCGACGCCCAAGTCCCGAGAGCTGCTCATCCGCA 1903  
QY 1865 ATTCAAGCCCACTGTAAGAGACCTGCGCCGACCCGAAATCCCAAGCTGAGTCCGCG 1924  
DB 1904 ATTCAAGCCCACTGTAAGAGACCTGCGCCGACCCGAAATCCCAAGCTGAGTCCGCG 1963  
QY 1925 CAGATACAGAGGCCCAACCCCAAGTGCCTCAGAGGACCTCATCTATCCGCACTGCTT 1984  
DB 1964 CAGATACAGAGGCCCAACCCCAAGTGCCTCAGAGGACCTCATCTATCCGCACTGCTT 2023  
QY 1985 ACAACAGTGGGCGCGAGGGTCCCGGACGCCCAAGCACTCGTGCAGACTCCGAGCA 2044  
DB 2024 ACACCAAGTGGGCGCGAGGGTCCCGGACGCCCAAGCACTCGTGCAGACTCCGAGCA 2083  
QY 2045 ACTCGGCTGGAATCTATCTGCAAGGGGGGCAAGAGGGGCAACCCCAAGCTCCAG 2104  
DB 2084 ACTCGGCTGGAATCTATCTGCAAGGGGGGCAAGAGGGGCAACCCCAAGCTCCAG 2143  
QY 2105 GGGCCCTGCTAGCCCTGCGCCGCGCAAGCCTCTAGTAACCCCAAGCTCAGAGAGA 2164  
DB 2144 GGGCCCTGCTAGCCCTGCGCCGCGCAAGCCTCTAGTAACCCCAAGCTCAGAGAGA 2203  
QY 2165 GCGACCTGCTGAGGAAACCTGAGACGCTCTTCAAGCTCTCAAGGGCACTTCCCG 2224  
DB 2204 GCGACCTGCTGAGGAAACCTGAGACGCTCTTCAAGCTCTCAAGGGCACTTCCCG 2263  
QY 2225 AGGCTGCTCACTGGAGGGAAACCGCTGAGGACCTCTCAAGCTGAGCACTCCG 2284  
DB 2264 AGGCTGCTCACTGGAGGGAAACCGCTGAGGACCTCTCAAGCTGAGCACTCCG 2323  
QY 2285 TGCCTCCCTGGGAATAAAGCCCAAGCCGAGCAACCGCTCAAGGCGGCGCGCG 2344  
DB 2324 TGCCTCCCTGGGAATAAAGCCCAAGCCGAGCAACCGCTCAAGGCGGCGCGCG 2383  
QY 2345 CAGACTTGTGTGCTGAAAGAGCGGACTCTGAGCAAGGCCCTTGGGCTCCCAAGAG 2404  
DB 2384 CAGACTTGTGTGCTGAAAGAGCGGACTCTGAGCAAGGCCCTTGGGCTCCCAAGAG 2443  
QY 2405 CCATGGACTACTGCTGCTCAGGAGGAGGTGGAAGCAGTGAAGGAGCGAGAGAG 2464  
DB 2444 CCATGGACTACTGCTGCTCAGGAGGAGGTGGAAGCAGTGAAGGAGCGAGAGAG 2503  
QY 2465 GCGAAGGCGGCGCAGAGAGGAGGAGAGATACCCCTGGGGCGCGACGATGGGGATA 2524  
DB 2504 GCGAAGGCGGCGCAGAGAGGAGGAGAGATACCCCTGGGGCGCGACGATGGGGATA 2560  
QY 2525 CAGACAGCTCAGACCATGCTGCTCAGAGCTGAGAGAGATCAACCGGAGCCGAGCCC 2584  
DB 2561 CAGACAGCTCAGACCATGCTGCTCAGAGCTGAGAGAGATCAACCGGAGCCGAGCCC 2620  
QY 2585 CATTAAGGGGGCGGACCATGCTGCTCAGAGCCCTGGAAGGAGGGGAACTGCTGCG 2644  
DB 2621 CATTAAGGGGGCGGACCATGCTGCTCAGAGCCCTGGAAGGAGGGGAACTGCTGCG 2680  
QY 2645 ATGCTGACAGCAATGGGTACAAACCTGCTGACGCTGCTCAGCCCACTCAACCA 2704  
DB 2681 ATGCTGACAGCAATGGGTACAAACCTGCTGACGCTGCTCAGCCCACTCAACCA 2740  
QY 2705 CCGAAGACGAAAGGCCCAAGGCCCACTTCAAGAGATGGAGTGGTGACTACAGTCTC 2764  
DB 2741 CCGAAGACGAAAGGCCCAAGGCCCACTTCAAGAGATGGAGTGGTGACTACAGTCTC 2800

QY 2765 GTGGCTGTAAAGGCCCTGCGCAAGACTGTTCAAGATGTTGTGATCTAGGATCT 2824  
DB 2801 GTGGCTGTAAAGGCCCTGCGCAAGACTGTTCAAGATGTTGTGATCTAGGATCT 2860  
QY 2825 ACCAGCTGAGAGGAGTGGGAGCAGCATCCCATCAAGCCCTTGTGGTGGAGAGGCA 2884  
DB 2861 ACCAGCTGAGAGGAGTGGGAGCAGCATCCCATCAAGCCCTTGTGGTGGAGAGGCA 2920  
QY 2885 CTGGCTGACCAAGTGAAGTACGACGTGAAGAGGTTCTGTGGTCAACGTGAATCCCA 2944  
DB 2921 CTGGCTGACCAAGTGAAGTACGACGTGAAGAGGTTCTGTGGTCAACGTGAATCCCA 2980  
QY 2945 CCAACACCCGGGCGCCAGAGTGAAGACCCCTGAGATCCGGAAGTACAAAGAGGATTC 3004  
DB 2981 CCAACACCCGGGCGCCAGAGTGAAGACCCCTGAGATCCGGAAGTACAAAGAGGATTC 3040  
QY 3005 CCGAGATCTCTGTGCAAGCCCTTTGGGGGTTCAACTGCTGTGGGCAACGAGACG 3064  
DB 3041 CCGAGATCTCTGTGCAAGCCCTTTGGGGGTTCAACTGCTGTGGGCAACGAGACG 3100  
QY 3065 TGAATGCTGGAACGAAAGTGGGCAAGGATGATGACTCAATTGGGCGGACGCT 3124  
DB 3101 TGAATGCTGGAACGAAAGTGGGCAAGGATGATGACTCAATTGGGCGGACGCT 3160  
QY 3125 TCAGCAGATGATGTGCTGAGGGGCTCAACTGCTCATCAACATCTCAGGAAAGAGA 3184  
DB 3161 TCAGCAGATGATGTGCTGAGGGGCTCAACTGCTCATCAACATCTCAGGAAAGAGA 3220  
QY 3185 ACAAACTCGGGGTGATTAACCTGTCTGTGCTCCGAAACAAGATTGCAACAATGCCAG 3244  
DB 3221 ACAAACTCGGGGTGATTAACCTGTCTGTGCTCCGAAACAAGATTGCAACAATGCCAG 3280  
QY 3245 AAGTGAAGAAAGAGGGGCTGAGACCAAGTGGGGGACATGAGGGGCTGCGGGCACTAC 3304  
DB 3281 AAGTGAAGAAAGAGGGGCTGAGACCAAGTGGGGGACATGAGGGGCTGCGGGCACTAC 3340  
QY 3305 GTGTTGTAAATACAGCGGATTAAGTTCTGTGATGCGCTCAAGAGCTTCCGTGAGG 3364  
DB 3341 GTGTTGTAAATACAGCGGATTAAGTTCTGTGATGCGCTCAAGAGCTTCCGTGAGG 3400  
QY 3365 TGTATGCTGGGCGCCCAACCTCAACCAATTAAGCTTCAAGTCTTTGCCGAC 3424  
DB 3401 TGTATGCTGGGCGCCCAACCTCAACCAATTAAGCTTCAAGTCTTTGCCGAC 3460  
QY 3425 TCCCCCACGGCCCTGCTGAGGTCAGCAGAGTGAAGAGAGGAGCGGCTCAAGTCA 3484  
DB 3461 TCCCCCACGGCCCTGCTGAGGTCAGCAGAGTGAAGAGAGGAGCGGCTCAAGTCA 3520  
QY 3485 TCTATGCTCCAGTGTGCTTCCATGCTGTGATGTGACTCGGGGAAACAGCTATGCA 3544  
DB 3521 TCTATGCTCCAGTGTGCTTCCATGCTGTGATGTGACTCGGGGAAACAGCTATGCA 3580  
QY 3545 TCTATCTCTGTGCACTCCAGAGCCAGATCAAGCCCTTATGATCTTTCTCCCA 3604  
DB 3581 TCTATCTCTGTGCACTCCAGAGCCAGATCAAGCCCTTATGATCTTTCTCCCA 3640  
QY 3605 ACACGAGGAGATGAGATGCTGCTGCTACGAGAGAGAGGATGCTACGTAACAGT 3664  
DB 3641 ACACGAGGAGATGAGATGCTGCTGCTACGAGAGAGAGGATGCTACGTAACAGT 3700  
QY 3665 ACGGCGCATCTTAAGAGTGTGCTGCAAGTGGGGGAGATGCTACTTGTGGCT 3724  
DB 3701 ACGGCGCATCTTAAGAGTGTGCTGCAAGTGGGGGAGATGCTACTTGTGGCT 3760  
QY 3725 ACATCTGCTCCAAACGAATATGGGCTGGGGTGAAGAACCTTAAGATCCGCTCTGG 3784  
DB 3761 ACATCTGCTCCAAACGAATATGGGCTGGGGTGAAGAACCTTAAGATCCGCTCTGG 3820  
QY 3785 AGACGGGCACTTGAAGGGGCTTCAAGCAACAGAGCTCAGAGGCTC 3834  
DB 3821 AGACGGGCACTTGAAGGGGCTTCAAGCAACAGAGCTCAGAGGCTC 3870







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Db 665 CTGACAGAGAAATGCTGAGGTCTGAGTGAATTTTGGGGTGTAGTCTCAGCTGAGACCGC 724
Qy 547 ACCGTGGCAGACGGAAACATTTTCATTTGGAGTCTCTTAAGAGTGTCTCAGAGGTATC 606
Db 725 ACCGTGGCAGACGGAAACATTTTCATTTGGAGTCTCTTAAGAGTGTCTCAGAGGTATC 784
Qy 607 GCGCTGTATGAAACCTTGATGCCCTTATGATTAAGAGAGTGAATTTTGGTCTCTTAGA 666
Db 785 GCGCTGTATGAAACCTTGATGCCCTTATGATTAAGAGAGTGAATTTTGGTCTCTTAGA 844
Qy 667 ATCACAGCATGAGATGGCAGAGGAGCCCCCTGTGTGATGATGACCCCATGCGA 726
Db 845 ATCACAGCATGAGATGGCAGAGGAGCCCCCTGTGTGATGATGACCCCATGCGA 904
Qy 727 GCGCTGTATGAAACCTTGATGCCCTTATGATTAAGAGAGTGTCTTAG 786
Db 905 GCGCTGTATGAAACCTTGATGCCCTTATGATTAAGAGAGTGTCTTAG 964
Qy 787 AAGTTTCATGATCTTATGACATGATCTCATGAGATTTAAGTGAAGAGTGTCTTAG 846
Db 965 AAGTTTCATGATCTTATGACATGATCTCATGAGATTTAAGTGAAGAGTGTCTTAG 1024
Qy 847 GAGAGCTACTGAAAGTTTCCCTTCATCCGGGACAGCCACGAGCGGAGGTCGATC 906
Db 1025 GAGAGCTACTGAAAGTTTCCCTTCATCCGGGACAGCCACGAGCGGAGGTCGATC 1084
Qy 907 CAGCTTAAAGACCAATTGACCGATCCGGAAGAGCGGGGTGAGAAAGAGAGACAGAA 966
Db 1085 CAGCTTAAAGACCAATTGACCGATCCGGAAGAGCGGGGTGAGAAAGAGAGACAGAA 1144
Qy 967 TATGAGTACAGCGGACGAGAGAGAGAGATGACAGCTTGAAGAGAGAGAGAGAGAG 1026
Db 1145 TATGAGTACAGCGGACGAGAGAGAGAGATGACAGCTTGAAGAGAGAGAGAGAGAG 1204
Qy 1027 TCCATCATGAACTGCTGAGAGAGTGAATCTGACCGCGGAGTTTCTCCGGCTCAGAG 1086
Db 1205 TCCATCATGAACTGCTGAGAGAGTGAATCTGACCGCGGAGTTTCTCCGGCTCAGAG 1264
Qy 1087 GAAATATAGAGCAATCTGAGAGCTTTTAAACAGCAGCAGCAGCTGACAGCAGCAG 1146
Db 1265 GAAATATAGAGCAATCTGAGAGCTTTTAAACAGCAGCAGCAGCTGACAGCAGCAG 1324
Qy 1147 CGAAGCCCGAGGACACATCAAACTGCTGACCGCGGACGCGGCGCATGAGAGAG 1206
Db 1325 CGAAGCCCGAGGACACATCAAACTGCTGACCGCGGACGCGGCGCATGAGAGAG 1384
Qy 1207 CAGAAGGAGAGCGGCGCGGCTGAGAGACCAAGCGGCGGAGCGGAGCAGCGAG 1266
Db 1385 CAGAAGGAGAGCGGCGCGGCTGAGAGACCAAGCGGCGGAGCGGAGCAGCGAG 1444
Qy 1267 CTGACAGAGAGAGCAGCAGCGCGCTGAGAGCATGACAGCTTTCGCGCGGAGAGAG 1326
Db 1445 CTGACAGAGAGAGCAGCAGCGCGCTGAGAGCATGACAGCTTTCGCGCGGAGAGAG 1504
Qy 1327 GAGCGCGGCGGAGCGGAGCTGAGAGAGATCAAGCGGAGCAGCTGAGAGAGAGAG 1386
Db 1505 GAGCGCGGCGGAGCGGAGCTGAGAGAGATCAAGCGGAGCAGCTGAGAGAGAGAG 1564
Qy 1387 CAGTCAGAAAGTCTCAGAGGAGCTGACAGAGAGAGTGTCTTACCTTCAAGTCTCTGAG 1446
Db 1565 CAGTCAGAAAGTCTCAGAGGAGCTGACAGAGAGAGTGTCTTACCTTCAAGTCTCTGAG 1624
Qy 1447 CAGCAGCAACAGCAGCAGCTTCAAGAAAGCAGCAGCAGCAGCTTCTGCGGAGAC 1506
Db 1625 CAGCAGCAACAGCAGCAGCTTCAAGAAAGCAGCAGCAGCAGCTTCTGCGGAGAC 1684
Qy 1507 AGGAAAGCCCTGTATCATTTATGTTGCGGCGCATGAAATCCCGCTGACAAACAGCCTGAGGCC 1566
Db 1685 AGGAAAGCCCTGTATCATTTATGTTGCGGCGCATGAAATCCCGCTGACAAACAGCCTGAGGCC 1744
Qy 1567 CGAGAGGTGAAAGAGAGAAAGAGATGAACAAGCAGAGAGAGAGCTCTCCCTTGGCCAGAGC 1626
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Db 1745 CGAGAGGTGAGAGAGAGAACAGAGATGAACAAGCAGACAGAACTCTCTTGGCCAAAGAC 1804
Qy 1627 AAGCAGCAGCAGCAGCGGCGCTGAGACCCCTTATCCCTTCAAGGCTTCCCAAGGCGCCCAAGGA 1686
Db 1805 AAGCAGCAGCAGCAGCGGCGCTGAGACCCCTTATCCCTTCAAGGCTTCCCAAGGCGCCCAAGGA 1864
Qy 1687 CCCCTTCCAGACTCTCTTATGAGAGCGGCTGAGAGCCCGGAGAGAGAGAGAGAGAGAGAGAG 1746
Db 1865 CCCCTTCCAGACTCTCTTATGAGAGCGGCTGAGAGCCCGGAGAGAGAGAGAGAGAGAGAGAG 1924

RESULT 7
ID AAL61132 standard; DNA; 4863 BP.
XX
AC AAL61132;
XX
DT 22-SEP-2003 (first entry)
XX
DE Human MINK2 antisense transcript DNA.
XX
KW Transcript; therapy; systemic lupus erythematosus; inflammatory disease;
KW cardiovascular; gastrointestinal disease; atherosclerosis; skin disease;
KW rheumatoid disorder; autoimmune disease; diabetes; multiple sclerosis;
KW cancer; neuroprotective; human; MINK2; antisense; gene; ds.
XX
OS Homo sapiens.
XX
MO MO2003046220-A1.
XX
PD 05-JUN-2003.
XX
PF 11-NOV-2002; 2002MO-IL000904.
XX
PR 26-NOV-2001; 2001US-0093398.
XX
PR 24-JUL-2002; 2002US-00201605.
XX
PA (COMP-) COMPUGEN LTD.
XX
PI Levanon E, Pollock S, Nemzer S, Shoshan A, Khosravi R, Walach S;
PI Levine Z, Bernstein J, Dahari D, Wasserman A, Rotman G;
DR WPI: 2003-505211/47.
XX
PT Identifying putative naturally occurring antisense transcripts, useful
PT for quantifying gene expression levels, and detecting and/or treating
PT inflammatory, autoimmune or cardiovascular diseases, diabetes, arthritis
PT and cancer.
XX
PS Example; Page 214-216; 230pp; English.
XX
CC The invention relates to methods and systems for identifying naturally
CC occurring antisense transcripts. The method is useful for quantifying
CC gene expression levels and for detecting, quantifying or specifically
CC regulating antisense and respective sense transcripts thereby enabling
CC detection and treatment of a wide range of disorders, such as systemic
CC lupus erythematosus, inflammatory diseases, rheumatoid disorders,
CC autoimmune diseases, diabetes, multiple sclerosis, cardiovascular and
CC gastrointestinal diseases, atherosclerosis, skin diseases and cancer. The
CC present sequence is human MINK2 transcript DNA used to illustrate the
CC method of the invention
XX
SQ Sequence 4863 BP; 1072 A; 1509 C; 1447 G; 835 T; 0 U; 0 Other;

Query Match 42.7%; Score 1689; DB 8; Length 4863;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1739; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ATGGGCGACCCAGCCCGCGCGGAGCTTGAAGAGATGACCTGTCTGCGGCGGAGC 66
Db 185 ATGGGCGACCCAGCCCGCGCGGAGCTTGAAGAGATGACCTGTCTGCGGCGGAGC 244
Qy 67 CTTGCTGGATCTTTAGCTTTGAGAGTGTGGCAATGAACTTACGAGCAGGTGTAC 126
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Db      245 CCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCCGGAATGAACCTACGGA CAGGGTATC 304
Qy      127 AAGGCTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATTAAGTCAATGATCAACGAG 186
Db      305 AAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATTAAGTCAATGATCAACGAG 364
Qy      187 GACGAGGAGGAGAGATCAACAGGAGATCAATGCTGAAAAAAGTCACTCCACACCGC 246
Db      365 GACGAGGAGGAGAGATCAACAGGAGATCAATGCTGAAAAAAGTCACTCCACACCGC 424
Qy      247 AACATGCCCACTTACTACGAGCCTTCAACAGAGAGCCCCCGGAAAAAGATGACGAG 306
Db      425 AACATGCCCACTTACTACGAGCCTTCAACAGAGAGCCCCCGGAAAAAGATGACGAG 484
Qy      307 CTCTGGCTGGTATGAGAGTTCTGTGGTGTGGTCAATGATCACTGCTGTAAGAACCA 366
Db      485 CTCTGGCTGGTATGAGAGTTCTGTGGTGTGGTCAATGATCACTGCTGTAAGAACCA 544
Qy      367 AAAGGCAACGCCCTGAGAGGAGCTGATCGCTATATCTGACGAGGAGATCTCAGGGGT 426
Db      545 AAAGGCAACGCCCTGAGAGGAGCTGATCGCTATATCTGACGAGGAGATCTCAGGGGT 604
Qy      427 CTGGCCCATCTCCATGCCCCAAGGTGATCAACGAGATCAACAGGGGAGAGATGTCTG 486
Db      605 CTGGCCCATCTCCATGCCCCAAGGTGATCAACGAGATCAACAGGGGAGAGATGTCTG 664
Qy      487 CTGACAGAGATGCTGAGGTCAAGCTAGTGAATTTGGGGTGAAGTCACTGACGACCGC 546
Db      665 CTGACAGAGATGCTGAGGTCAAGCTAGTGAATTTGGGGTGAAGTCACTGACGACCGC 724
Qy      547 ACCGTGGGAGACGGAAACATTTGAGGACCTCCCTACTGATGGCTCCAGAGGTCAATC 606
Db      725 ACCGTGGGAGACGGAAACATTTGAGGACCTCCCTACTGATGGCTCCAGAGGTCAATC 784
Qy      607 GCCTGTGATGAGAACCTCTGATGCACTTATGATTAAGAGAGTATTTGTTCTTAA 666
Db      785 GCCTGTGATGAGAACCTCTGATGCACTTATGATTAAGAGAGTATTTGTTCTTAA 844
Qy      667 ATCAACGCCATGAGATGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 726
Db      845 ATCAACGCCATGAGATGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 904
Qy      727 GCCCTCTTCTCTATCTCTGGAACCTCCGCGCAGGCTGAAGTCAAGAGTGTCTAAG 786
Db      905 GCCCTCTTCTCTATCTCTGGAACCTCCGCGCAGGCTGAAGTCAAGAGTGTCTAAG 964
Qy      787 AAGTTCATTGACTTCAATTGACATGTCTCATCAAGACTTAACCTGAGCGGCCACCGCAG 846
Db      965 AAGTTCATTGACTTCAATTGACATGTCTCATCAAGACTTAACCTGAGCGGCCACCGCAG 1024
Qy      847 GAGCAGCTACTGAAGTTTCCCTTCAATCGGGAGCAAGCCCAAGAGGGAGAGTCCGCAATC 906
Db      1025 GAGCAGCTACTGAAGTTTCCCTTCAATCGGGAGCAAGCCCAAGAGGGAGAGTCCGCAATC 1084
Qy      907 CAGCTTAAGACCACTGACCGATCCCGGAAGAGCGGGGTGAGAAAGAGAGACAGAA 966
Db      1085 CAGCTTAAGACCACTGACCGATCCCGGAAGAGCGGGGTGAGAAAGAGAGACAGAA 1144
Qy      967 TATGATACAGCGGAGCAGAGAGAGAGATGACAGCCATGAGAGAGAGAGAGAGCCAGC 1026
Db      1145 TATGATACAGCGGAGCAGAGAGAGAGATGACAGCCATGAGAGAGAGAGAGAGCCAGC 1204
Qy      1027 TCCATCATTAAGAGTGTGCTGAGAGTGAATCTTACCGCGGAGAGTTTCTCCGCTCCAGCAG 1086
Db      1205 TCCATCATTAAGAGTGTGCTGAGAGTGAATCTTACCGCGGAGAGTTTCTCCGCTCCAGCAG 1264
Qy      1087 GAAATTAAGAGAACTCAGAGCTTAAAGACAGACAGACAGCTGACAGAGAGAGAGAGCAGCAG 1146
Db      1265 GAAATTAAGAGAACTCAGAGCTTAAAGACAGACAGACAGCTGACAGAGAGAGAGAGCAGCAG 1324
Qy      1147 CGAGACCCCGAGGACACATCAACCACTGCTGACACAGCGGAGCGGCGCATAGAGAG 1206

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Db      1325 CGAGACCCCGAGGACACATCAAA CACTGCTGACACAGCGGAGCGGCGCATAGAGAG 1384
Qy      1207 CAGAAAGAGAGCGGCGCGCGGTGAGAGAGCAACAGCGCGGAGCGGAGCAGCGAG 1266
Db      1385 CAGAGAGAGAGCGGCGCGCGGTGAGAGAGCAACAGCGCGGAGCGGAGCAGCGAG 1444
Qy      1267 CTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1326
Db      1445 CTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1504
Qy      1327 GAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1386
Db      1505 GAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1564
Qy      1387 CAGTCAAGAGCTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1446
Db      1565 CAGTCAAGAGCTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1624
Qy      1447 CAGCAGCAACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1506
Db      1625 CAGCAGCAACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1684
Qy      1507 AGAAGCCCTCTGACATTAATGCTCGGGGAGATGAATCCCGCTGACAAACAGAGCTGAGG 1566
Db      1685 AGAAGCCCTCTGACATTAATGCTCGGGGAGATGAATCCCGCTGACAAACAGAGCTGAGG 1744
Qy      1567 CGAGAGGTAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1626
Db      1745 CGAGAGGTAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1804
Qy      1627 AAGCCAGGACACCGGGCTGAGGCCCCCATATCCCCAGGCTTCCAGGGCCCCCAGAG 1686
Db      1805 AAGCCAGGACACCGGGCTGAGGCCCCCATATCCCCAGGCTTCCAGGGCCCCCAGAG 1864
Qy      1687 CCCCTTCCAGACTCTCTCATGAGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1746
Db      1865 CCCCTTCCAGACTCTCTCATGAGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1924

RESULT 8
ADE34153
ID ADE34153 standard; DNA; 4414 BP.
XX
XX
AC ADE34153;
XX
XX
DT 29-JAN-2004 (first entry)
XX
XX
DE Human DNA encoding misshapen/NIKs-related kinase, Mink3b.
XX
XX
KW Human; misshapen/NIKs-related kinase; Mink3b; de; antiinflammatory;
KW immunosuppressive; cytostatic; germinal centre kinase;
KW c-JUN N-terminal kinase; JNK; extracellular signal response kinase; ERK;
KW growth factor induced-ERK activation; proliferation;
KW cell proliferation disorder; cell survival;
KW intracellular signal transduction; apoptosis; morphological change;
KW cell migration; gene therapy; inflammatory disease; autoimmune disease;
KW immunodeficiency; cancer.
XX
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 209..2587
FT FT /*tag= a
FT FT /product= "Mink3b"
XX
XX
PN US2003077597-A1.
XX
XX
PD 24-APR-2003.
XX
XX
PF 19-OCT-2001; 2001US-00029115.
XX
XX
PR 19-OCT-2001; 2001US-00029115.
XX
XX

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PA (LINOY/) LINO Y.  
PA (FUCA/) FU C A.  
PA (SHEN/) SHEN M.  
PI Luo Y, Fu CA, Shen M;  
DR WPI: 2003-635076/60.  
DR P-PSDB: ADEB34152.  
XX  
XX New misshapen/NIKs-related kinase nucleic acids and proteins useful in  
PT gene therapy and for treating disorders, e.g. acute and chronic  
PT inflammatory diseases.  
XX  
XX Claim 3; SEQ ID NO 3; 53bp; English.  
XX  
XX The invention relates to a recombinant nucleic acid capable of  
CC hybridising to a Human DNA encoding misshapen/NIKs-related kinase  
CC (Mink3a, 3b and 3c, geminal centre kinase proteins) appearing as  
CC ADEB34151, ADEB34153 and ADEB34155, or at least 90% identity to them, or  
CC their complements. Also included are a recombinant polypeptide at least  
CC 95 % sequence identity to Mink3a, 3b or 3c (appearing as ADEB34150,  
CC ADEB34152 and ADEB34154), screening for a candidate bioactive agent capable  
CC of modulating c-JUN N-terminal kinase (JNK) or extracellular signal  
CC response kinase (ERK) phosphorylation or activity, screening for a  
CC candidate bioactive agent capable of modulating growth factor induced-ERK  
CC activation in a mammalian cell, screening for a candidate bioactive agent  
CC capable of modulating proliferation in a mammalian cell, diagnosing a  
CC mammalian cell proliferation disorder, a medicament for treating a  
CC mammalian cell proliferation disorder and screening for a candidate agent  
CC capable of modulating cell survival. The MINK3 (misshapen/NIKs-related  
CC kinase) nucleic acids are useful in the modulation of intracellular  
CC signal transduction, cell proliferation, apoptosis, morphological change  
CC and migration of mammalian cells. MINK3 nucleic acids and proteins are  
CC specifically useful in gene therapy, and for treating, preventing or  
CC diagnosing acute and chronic inflammatory diseases, autoimmune diseases  
CC and diseases characterised by immunodeficiency. The compositions may also  
CC be used to treat MINK3 dysfunction related disorders, e.g. cancer. The  
CC nucleotide sequences may also be used as hybridisation probes, in  
CC chromosome and gene mapping, and in generating antisense RNA and DNA. The  
CC present sequence encodes Mink3p.  
XX  
SQ Sequence 4414 BP; 1010 A; 1339 C; 1317 G; 748 T; 0 U; 0 Other;  
Query Match 42.6%; Score 1683; DB 9; Length 4414;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1683; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 64 GACCTGCTGGGATCTTGAAGCTTGTGAGGTGTCGGCAATGGAACCTAGGACAGGTG 123  
Db 101 GACCTGCTGGGATCTTGAAGCTTGTGAGGTGTCGGCAATGGAACCTAGGACAGGTG 160  
QY 124 TACAAGGGTCCGCATGTCAAGACGGGCGAGCTGTCGCCATCAAGTCAATGTCACG 183  
Db 161 TACAAGGGTCCGCATGTCAAGACGGGCGAGCTGTCGCCATCAAGTCAATGTCACG 220  
QY 184 GAGGACGAGGAGAGAGATCAACAGAGATCAACATGCTGAAAAAGTACTCTACAC 243  
Db 221 GAGGACGAGGAGAGAGATCAACAGAGATCAACATGCTGAAAAAGTACTCTACAC 280  
QY 244 CGCAACATTCGCACCTACTAGGAGCCTTCATCAAGAGAGACCCCGGGAAGAGTAC 303  
Db 281 CGCAACATTCGCACCTACTAGGAGCCTTCATCAAGAGAGACCCCGGGAAGAGTAC 340  
QY 304 CAGCTGTGGCTGTGATGAGATTCTGTGTCGTGCTGATCACTGATCTGTAAGAAC 363  
Db 341 CAGCTGTGGCTGTGATGAGATTCTGTGTCGTGCTGATCACTGATCTGTAAGAAC 400  
QY 364 ACAAAGGCAACGCCCTGAAGAGAGCTGTATCGCTTATCTGTGAGAGATCTCTCAG 423  
Db 401 ACAAAGGCAACGCCCTGAAGAGAGCTGTATCGCTTATCTGTGAGAGATCTCTCAG 460  
QY 424 GGTGCGGCATCTTCATATGCCCAAGAGGTGATTCATGAGATCAAGGGGAGAGTGTG 483

Db 461 GGTGCGGCATCTTCATATGCCCAAGAGGTGATTCATGAGATCAAGGGGAGAGTGTG 520  
QY 484 CTGCTGACAGGAATGCTGAGGTCAAGCTAGTGAATTTTGGGGTGAAGTCTCAGCTGAC 543  
Db 521 CTGCTGACAGGAATGCTGAGGTCAAGCTAGTGAATTTTGGGGTGAAGTCTCAGCTGAC 580  
QY 544 CGACCGTGGGCAACGGGAACATTTTATGGGAGCTCCCTACTGATGGCTCCAGAGGTG 603  
Db 581 CGACCGTGGGCAACGGGAACATTTTATGGGAGCTCCCTACTGATGGCTCCAGAGGTG 640  
QY 604 ATCCCTGTGATGAGAACCTGTATGCCACTATGATTTACAGAGTGAATTTTGTCTCTA 663  
Db 641 ATCCCTGTGATGAGAACCTGTATGCCACTATGATTTACAGAGTGAATTTTGTCTCTA 700  
QY 664 GGAATCAAGCATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 723  
Db 701 GGAATCAAGCATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 760  
QY 724 CGAGCCCTTCCCTCATTTCCCTCGGAGCCCTCCGCGGAGGCTCAAGTCCAGAGAGTGTCT 783  
Db 761 CGAGCCCTTCCCTCATTTCCCTCGGAGCCCTCCGCGGAGGCTCAAGTCCAGAGAGTGTCT 820  
QY 784 AAGAAGTTCAATGACTTCAATGACATGTCATCAAGACTTACTGAGCCGCCCAACC 843  
Db 821 AAGAAGTTCAATGACTTCAATGACATGTCATCAAGACTTACTGAGCCGCCCAACC 880  
QY 844 ACGGAGAGCTACTGAAGTTTCCCTTCATCCGAGCAAGCCCAAGCCGAGAGTCTCC 903  
Db 881 ACGGAGAGCTACTGAAGTTTCCCTTCATCCGAGCAAGCCCAAGCCGAGAGTCTCC 940  
QY 904 ATCCAGCTTAAAGACCAATTTGACCCGAGAGAGAGAGAGAGAGAGAGAGAGAG 963  
Db 941 ATCCAGCTTAAAGACCAATTTGACCCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1000  
QY 964 GAATATGATGACAGCGGCAAGAGAGAGAGATGACAGCATGAGAGAGAGAGAGAGCA 1023  
Db 1001 GAATATGATGACAGCGGCAAGAGAGAGAGATGACAGCATGAGAGAGAGAGAGAGCA 1060  
QY 1024 AGCTTCATCATGAACGTGCTGAGAGTCACTTACCGCGGAGTTTCTCCGCTCCAG 1083  
Db 1061 AGCTTCATCATGAACGTGCTGAGAGTCACTTACCGCGGAGTTTCTCCGCTCCAG 1120  
QY 1084 CAGGAAATTAAGCACTGAGAGGCTTTAAACAGAGAGAGAGAGAGAGAGAGAGAG 1143  
Db 1121 CAGGAAATTAAGCACTGAGAGGCTTTAAACAGAGAGAGAGAGAGAGAGAGAGAG 1180  
QY 1144 CAGGAGAGCCCGAGGACACATCAACCTGCTGACAGCGGAGCGGCGCATAGAG 1203  
Db 1181 CAGGAGAGCCCGAGGACACATCAACCTGCTGACAGCGGAGCGGCGCATAGAG 1240  
QY 1204 GAGCAGAGAGAGAGAGCGGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1263  
Db 1241 GAGCAGAGAGAGAGAGCGGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1300  
QY 1264 AAGCTGAG 1323  
Db 1301 AAGCTGAG 1360  
QY 1324 GAGGAGCGGCGGAG 1383  
Db 1361 GAGGAGCGGCGGAG 1420  
QY 1384 CGGAGTCAGAAAGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1443  
Db 1421 CGGAGTCAGAAAGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1480  
QY 1444 CAGCAG 1503  
Db 1481 CAGCAG 1540  
QY 1504 GACAG 1563  
Db 1541 GACAG 1600

Oy	1554	GCCCCGAGGCTTGAAGAGAGAAACAAGATGAAACAAGACAGCAAGAACTCTCCCTTGGCCAAAG	1623
Dd	1601	GCCCCGAGGCTTGAAGAGAGAAACAAGATGAAACAAGACAGCAAGAACTCTCTCTTGGCCAAAG	1666
Oy	1624	AGCAGACCCAGGAGCAGCAGCGGCGCTTGAAGCCCTCCCATCCCAAGGCTCTCCCAAGGCCCCCA	1683
Dd	1661	AGCAAGCCAGGAGCAGCAGCGGCGCTTGAAGCCCTCCCATCCCAAGGCTCTCCCAAGGCCCCCA	1720
Oy	1664	GGACCCCTTTTCCCAAGACTCTCTCTATGCAAGAGCCCGGTGAGAGCCCCAGAGAGAACCCGAC	1743
Dd	1721	GGACCCCTTTTCCCAAGACTCTCTCTATGCAAGAGCCCGGTGAGAGCCCCAGAGAGAACCCGAC	1780
Oy	1744	AAAG 1746	
Dd	1781	AAAG 1783	
RESULT 9			
ID	AAAD17762	standard; DNA; 3735 BP.	
XX	AAAD17762;		
XX	10-DEC-2001	(first entry)	
DE	Human novel STE20-like protein, NOV-3d encoding DNA.		
XX	Human; NOV-X protein; KIAA1233-like protein; STE20-like protein; tumour;		
KW	trypsin inhibitor-like protein; gene therapy; haematopoietic; illness;		
KW	immunological disorder; neurodegenerative disorder; Alzheimer's disease;		
KW	Parkinson's disease; immunomodulatory; pharmacogenomic; haemostatic;		
KW	human immunodeficiency virus; HIV; fertility disorder; neuroprotective;		
KW	cytostatic; neotrophic; anti-interfility; cancer; chromosome 17;		
XX	NOV-3d protein; ds.		
XX	Homo sapiens.		
XX	Key	Location/Qualifiers	
PH	CDS	1..3735	
FT		/tag= a	
FT		/product= "Human novel STE20-like protein, NOV-3d"	
PN	WO200162928-A2.		
XX	30-AUG-2001.		
XX	26-FEB-2001; 2001WO-US006151.		
XX	25-FEB-2000; 2000US-0184951P.		
PR	28-FEB-2000; 2000US-0185548P.		
PR	01-MAR-2000; 2000US-0185967P.		
PR	18-APR-2000; 2000US-0197723P.		
PR	27-APR-2000; 2000US-019957P.		
XX	23-FEB-2001; 2001US-00789390.		
PA	(CURA-) CURAGEN CORP.		
PI	Vernet CAM, Fernandes E, Shinkets RA, Macdougall J, Spaderma SK;		
XX	WPI; 2001-582051/65.		
DR	P-PSDB; AAE10614.		
PT	New isolated KIAA1233-like, STE20-like, or trypsin inhibitor-like		
PT	polypeptide for diagnosing and treating pathological disorders, such as		
PT	Parkinson's disease and for use in pharmacogenomics.		
PS	Claim 9; Page 67-68; 189pp; English.		
CC	The invention relates to novel human polypeptides referred as NOV-X and		
CC	their corresponding nucleic acid sequences NOV-X collectively include		
CC	NOV-1, NOV-2a and NOV-2b which are novel KIAA1233-like polypeptides, NOV-		
CC	3a, NOV-3b, NOV-3c and NOV-3d which are novel STE20-like polypeptides and		

Query Match	40.5%	Score 1599	DB 5	Length 3735	
Best Local Similarity	100.0%	Pred. No. 0			
Matches 1599	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
NOV-4a, NOV-4b, NOV-4c, NOV-4d and NOV-4e which are novel trypsin inhibitor-like polypeptides. NOV-X is used to identify a potential therapeutic agent that can modulate its activity and can be used for treating a pathology related to aberrant expression or aberrant physiological interactions of NOV-X. NOV-X or its DNA is used to determine the presence or prediposition to a disease associated with altered levels of NOV-X. NOV-X, its DNA and its antibody are used to treat or prevent a pathology associated with NOV-X. The pathological states that can be treated or prevented are haematopoietic, cancer, immunological, tumour, neurodegenerative (e.g. Alzheimer's and Parkinson's disease), human immunodeficiency virus (HIV) illness and fertility disorders. NOV-X and its DNA are used in pharmacogenomics for predictive medicine. NOV-X DNA is used in gene therapy. The present sequence is a DNA encoding human novel STR20-like protein, NOV-3d gene is located at chromosome 17					
Sequence 3735 BP; 880 A; 1105 C; 1137 G; 613 T; 0 U; 0 Other;					
2347 GACTTTGTGTGCTGAAAGAGCGGACTCTGAGCGAGGCCCCCTCGGCTCCCAAGAGGCC					2406
2137 GACTTTGTGTGCTGAAAGAGCGGACTCTGAGCGAGGCCCCCTCGGCTCCCAAGAGGCC					2196
2407 ATGAGCTACTGTGTCTCCAGCAGAGAGTGTGAAAGCATGTAGACCAACGAGAGGAAAGGC					2466
2197 ATGAGCTACTGTGTCTCCAGCAGAGAGTGTGAAAGCATGTAGACCAACGAGAGGAAAGGC					2256
2467 GAAGCGGGGCGCAGAGAGGGGAGCAGAGATACCCCTTGSGGGCGCAGCGATGGGGATACA					2526
2257 GAAGCGGGGCGCAGAGAGGGGAGCAGAGATACCCCTTGSGGGCGCAGCGATGGGGATACA					2316
2527 GACAGCGTCAGCACCATGTGTGTCTCAGCAGCTGTGAGGAGATCAACCGGACCCACGCCCA					2586
2317 GACAGCGTCAGCACCATGTGTGTCTCAGCAGCTGTGAGGAGATCAACCGGACCCACGCCCA					2376
2587 TACGGGGGGCGCACCATGTGTGTCTCAGCGCACCCCTTAAGAAGAGCGGAACCTGTGTCAT					2646
2377 TACGGGGGGCGCACCATGTGTGTCTCAGCGCACCCCTTAAGAAGAGCGGAACCTGTGTCAT					2436
2647 GCTGACAGCAATGGGTACACAAACCTGCTGACGTGTCTCAGCGCACCCACTGACCCACC					2706
2437 GCTGACAGCAATGGGTACACAAACCTGCTGACGTGTCTCAGCGCACCCACTGACCCACC					2496
2707 GAGAACAGCAAAAGGCCAAAGCCCACTCGAAGGATGGAGTGTGATCTACCAAGTCTGCT					2766
2497 GAGAACAGCAAAAGGCCAAAGCCCACTCGAAGGATGGAGTGTGATCTACCAAGTCTGCT					2556
2767 GGGCTGTAAAGGCCCTCTGGCAGAGAGCTCGTTCAACATGTTTGTGATCTTAGGATCTTAC					2826
2557 GGGCTGTGTAAAGGCCCTCTGGCAGAGAGCTCGTTCAACATGTTTGTGATCTTAGGATCTTAC					2616
2827 CAGCTGTGAGGCAATGGGGGAGCAGATCCCATCTCAGCCCTAGTGGGTGAGAGGGCACT					2886
2617 CAGCTGTGAGGCAATGGGGGAGCAGATCCCATCTCAGCCCTAGTGGGTGAGAGGGCACT					2676
2887 CGGCTCGACCAAGCTGCACTAGTGAAGAGAGGTTCTGTGTCAACGTGAATCCACCC					2946
2677 CGGCTCGACCAAGCTGCACTAGTGAAGAGAGGTTCTGTGTCAACGTGAATCCACCC					2736
2947 AACACCCGGGGCCCAAGTGAAGACCCCTGAGATCCGGAAGATACAAGAAAGCAATTCACCTCC					3006
2737 AACACCCGGGGCCCAAGTGAAGACCCCTGAGATCCGGAAGATACAAGAAAGCAATTCACCTCC					2796
3007 GAGATCCTCTGTGACAGCCCTTTGGGGGGGTCAACCTGCTGGTGGGCAAGGAGAACGGGCTG					3066
2797 GAGATCCTCTGTGACAGCCCTTTGGGGGGGTCAACCTGCTGGTGGGCAAGGAGAACGGGCTG					2856
3067 ATGTGTCTGGAACCAAGTGGGCAAGGCTGTATGACTCATTTGGGCGGCGACGCTTC					3126
2857 ATGTGTCTGGAACCAAGTGGGCAAGGCTGTATGACTCATTTGGGCGGCGACGCTTC					2916





QY 2527 GACAGGTCAGACCATGTTGTCACGACGTGAGAGATCACCAGGAGCCAGCCGCCA 2586  
 DB 2404 GACAGGTCAGACCATGTTGTCACGACGTGAGAGATCACCAGGAGCCAGCCGCCA 2463  
 QY 2587 TACGGGGGGGCGGACCATGTTGTCACGACGTGAGAGATCACCAGGAGCCAGCCGCCA 2646  
 DB 2464 TACGGGGGGGCGGACCATGTTGTCACGACGTGAGAGATCACCAGGAGCCAGCCGCCA 2523  
 QY 2647 GCTGACAGATGAGGTCACAACTGCTGACGTGAGAGATCACCAGGAGCCAGCCGCCA 2706  
 DB 2524 GCTGACAGATGAGGTCACAACTGCTGACGTGAGAGATCACCAGGAGCCAGCCGCCA 2583  
 QY 2707 GAGAACAGAAAGGCGCAAGCCGCTGAGAGATGAGAGATCACCAGGAGCCAGCCGCCA 2766  
 DB 2584 GAGAACAGAAAGGCGCAAGCCGCTGAGAGATGAGAGATCACCAGGAGCCAGCCGCCA 2643  
 QY 2767 GGGGCTGTAAGGCGGCGCAAGGCTGTTCAAGATGTTGAGATCTAGGAGATCTAC 2826  
 DB 2644 GGGGCTGTAAGGCGGCGCAAGGCTGTTCAAGATGTTGAGATCTAGGAGATCTAC 2703  
 QY 2827 GAGGCTGAGAGGCGAGTGGGAGACGATCCTCCATCAGAGCCCTGAGTGGTGGAGAGGCACT 2886  
 DB 2704 GAGGCTGAGAGGCGAGTGGGAGACGATCCTCCATCAGAGCCCTGAGTGGTGGAGAGGCACT 2763  
 QY 2887 GGGGCTGAGAGGCGAGTGGGAGACGATCCTCCATCAGAGCCCTGAGTGGTGGAGAGGCACT 2946  
 DB 2764 GGGGCTGAGAGGCGAGTGGGAGACGATCCTCCATCAGAGCCCTGAGTGGTGGAGAGGCACT 2823  
 QY 2947 AACACCCGGGCGGACGATGAGACCCCTGAGATCCGGAGTACAGAGGCGATTCATCTCC 3006  
 DB 2824 AACACCCGGGCGGACGATGAGACCCCTGAGATCCGGAGTACAGAGGCGATTCATCTCC 2883  
 QY 3007 GAGATCTCTGTCGACGCTTTTGGGGGTCACCTGCTGTTGGGAGCGAGAGACGGGCTG 3066  
 DB 2884 GAGATCTCTGTCGACGCTTTTGGGGGTCACCTGCTGTTGGGAGCGAGAGACGGGCTG 2943  
 QY 3067 ATGTTGCTGGAACGAGTGGGAGCGGAGAGTATGATCTCATTTGGGCGGAGACGCTTC 3126  
 DB 2944 ATGTTGCTGGAACGAGTGGGAGCGGAGAGTATGATCTCATTTGGGCGGAGACGCTTC 3003  
 QY 3127 GAGCAGATGATGTCGTCGAGGAGGCTCAACTGCTCATCACTCAGGAGAGAGAGAC 3186  
 DB 3004 GAGCAGATGATGTCGTCGAGGAGGCTCAACTGCTCATCACTCAGGAGAGAGAGAC 3063  
 QY 3187 AACATGCGGGGTGATTAATCTGTCCTGCTCCGGAACAATCTGTCATGACATGACCCAGAA 3246  
 DB 3064 AACATGCGGGGTGATTAATCTGTCCTGCTCCGGAACAATCTGTCATGACATGACCCAGAA 3123  
 QY 3247 GTGAGAGAAAGAGGCGGCTGACCACTGTCGAGGAGATGAGAGGCGCTGCGGAGCTACCGT 3306  
 DB 3124 GTGAGAGAAAGAGGCGGCTGACCACTGTCGAGGAGATGAGAGGCGCTGCGGAGCTACCGT 3183  
 QY 3307 GTTGTGAATAACGAGCGGATTAAGTTCTGTCATGCTCCCTCAAGAGCTCTGTCGAGGTTG 3366  
 DB 3184 GTTGTGAATAACGAGCGGATTAAGTTCTGTCATGCTCCCTCAAGAGCTCTGTCGAGGTTG 3243  
 QY 3367 TATGCTGAGGCGGCGGAGAGCCCTTCAACAATTCATGAGCTTCAAGCTCTTTCGCGGAGCTC 3426  
 DB 3244 TATGCTGAGGCGGCGGAGAGCCCTTCAACAATTCATGAGCTTCAAGCTCTTTCGCGGAGCTC 3303  
 QY 3427 CCCCAACGCGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 3486  
 DB 3304 CCCCAACGCGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 3363  
 QY 3487 TATGCTGTCAGTGTGCTGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 3546  
 DB 3364 TATGCTGTCAGTGTGCTGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 3423  
 QY 3547 TATGCTGTCAGTGTGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 3606  
 DB 3424 TATGCTGTCAGTGTGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 3483

QY 3607 ACCGACGATGAGATGCTGCTGTCATGACGAGACGAGGCTGTCATGACATGACCTAC 3666  
 DB 3484 ACCGACGATGAGATGCTGCTGTCATGACGAGACGAGGCTGTCATGACATGACCTAC 3543  
 QY 3667 GGGGCGATTAATGAGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 3726  
 DB 3544 GGGGCGATTAATGAGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 3603  
 QY 3727 ATGCTCTCAACAGATTAATGAGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 3786  
 DB 3604 ATGCTCTCAACAGATTAATGAGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 3663  
 QY 3787 ACGGCGCATCTGACGCGGCTCTTATGACCAAGAGCTCAGAGCTCAAGTCTGTCGT 3846  
 DB 3664 ACGGCGCATCTGACGCGGCTCTTATGACCAAGAGCTCAGAGCTCAAGTCTGTCGT 3723  
 QY 3847 GAGGCGAATGACCAAGGCTTTTGGCCCTGAGTCCGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCG 3906  
 DB 3724 GAGGCGAATGACCAAGGCTTTTGGCCCTGAGTCCGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCG 3783  
 QY 3907 TTCACTGCTGAAACGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 3945  
 DB 3784 TTCACTGCTGAAACGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 3822

RESULT 11  
 AAD17760  
 ID AAD17760 standard; DNA; 3912 BP.  
 XX  
 AC AAD17760;  
 XX  
 DT 10-DEC-2001 (first entry)  
 XX  
 DE Human novel STE20-like protein, NOV-3b encoding DNA.  
 KW Human; NOV-X protein; KIAA1233-like protein; STE20-like protein; tumour;  
 KW trypsin inhibitor-like protein; gene therapy; haematopoietic; illness;  
 KW immunological disorder; neurodegenerative disorder; Alzheimer's disease;  
 KW Parkinson's disease; immunomodulatory; pharmacogenomic; haemostatic;  
 KW human immunodeficiency virus; HIV; fertility disorder; neuroprotective;  
 KW cytoskeletal; neotropic; anti-fertility; cancer; chromosome 17;  
 KW NOV-3b protein; ds.  
 KM  
 OS  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..3912  
 FT /\*tag=a  
 FT /Product="Human novel STE20-like protein, NOV-3b"  
 FT  
 PN MO200162928-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 26-FEB-2001; 2001WO-US006151.  
 XX  
 PR 25-FEB-2000; 2000US-0184951P.  
 PR 28-FEB-2000; 2000US-0185548P.  
 PR 01-MAR-2000; 2000US-0185967P.  
 PR 18-APR-2000; 2000US-0197723P.  
 PR 27-APR-2000; 2000US-0199957P.  
 PR 23-FEB-2001; 2001US-00789390.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Vernet CM, Fernandes E, Shinkens RA, Macdougall J, Spaderna SK,  
 DR WPI; 2001-582051/65.  
 DR P-PSDB; AAE10612.  
 XX  
 PT New isolated KIAA1233-like, STE20-like, or trypsin inhibitor-like  
 PT polypeptide for diagnosing and treating pathological disorders, such as  
 PT Parkinson's disease and for use in pharmacogenomics.

XX Claim 9; Page 51-52; 189pp; English.

CC The invention relates to novel human polypeptides referred to as NOV-X and  
 CC their corresponding nucleic acid sequences. NOV-X collectively include  
 CC NOV-1, NOV-2a and NOV-2b which are novel KIAA1233-like polypeptides, NOV-  
 CC 3a, NOV-3b, NOV-3c and NOV-3d which are novel STE20-like polypeptides and  
 CC NOV-4a, NOV-4b, NOV-4c, NOV-4d and NOV-4e which are novel tyrosin  
 CC inhibitor-like polypeptides. NOV-X is used to identify a potential  
 CC therapeutic agent that can modulate its activity and can be used for  
 CC treating a pathology related to aberrant expression or aberrant  
 CC physiological interactions of NOV-X. NOV-X or its DNA is used to  
 CC determine the presence or predisposition to a disease associated with  
 CC altered levels of NOV-X. NOV-X, its DNA and its antibody are used to  
 CC treat or prevent a pathology associated with NOV-X. The pathological  
 CC states that can be treated or prevented are haematopoietic, cancer,  
 CC immunological, tumour, neurodegenerative (e.g. Alzheimer's and  
 CC Parkinson's disease), human immunodeficiency virus (HIV) illness and  
 CC fertility disorders. NOV-X and its DNA are used in pharmacogenomics for  
 CC predictive medicine. NOV-X DNA is used in gene therapy. The present  
 CC sequence is a DNA encoding human novel STE20-like protein, NOV-3b. NOV-3b  
 CC gene is located at chromosome 17

SQ Sequence 3912 BP; 924 A; 1171 C; 1187 G; 630 T; 0 U; 0 Other;

Query Match 40.5%; Score 1599; DB 5; Length 3912;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2247 GACTTTGTGTTGTAAGACGCACTGTGACGAGGCGCTCGGAGCTCCCAAGAGGCC 2406  
 DB 2214 GACTTTGTGTTGTAAGACGCACTGTGACGAGGCGCTCGGAGCTCCCAAGAGGCC 2373  
 QY 2407 ATGAGCTACTGTCGTCTCAGAGAGAGGTGAAAACGATGAGACGACGAGAGAGAGGC 2466  
 DB 2274 ATGAGCTACTGTCGTCTCAGAGAGAGGTGAAAACGATGAGACGACGAGAGAGAGGC 2433  
 QY 2467 GAAGCGGCGCCAGACGAGAGAGAGAGATACCCCTGGGGGCGCCGACGATGGGGATACA 2536  
 DB 2434 GAAGCGGCGCCAGACGAGAGAGAGAGATACCCCTGGGGGCGCCGACGATGGGGATACA 2493  
 QY 2527 GACAGCGTCAGACCAATGCTGTGTCAAGAGATCAACGAGACCCAGAGCCCA 2586  
 DB 2494 GACAGCGTCAGACCAATGCTGTGTCAAGAGATCAACGAGACCCAGAGCCCA 2553  
 QY 2587 TACGGGGCGGCGACCATGCTGTGTCAAGGCAACCCCTGAAGAGAGCGGAACCTGCTGAT 2646  
 DB 2554 TACGGGGCGGCGACCATGCTGTGTCAAGGCAACCCCTGAAGAGAGCGGAACCTGCTGAT 2613  
 QY 2647 GCTGACACGCAATGGGTACCAAACTGCTGACGTCGTCCAGCCCACTCAACCCACC 2706  
 DB 2614 GCTGACACGCAATGGGTACCAAACTGCTGACGTCGTCCAGCCCACTCAACCCACC 2673  
 QY 2707 GAGAACGCAAAAGGCGCAAGGCGCAACCCCTGAAGAGAGTGGGATCTACCACTGCTGAT 2766  
 DB 2674 GAGAACGCAAAAGGCGCAAGGCGCAACCCCTGAAGAGAGTGGGATCTACCACTGCTGAT 2733  
 QY 2767 GGGGTGTAAAGGCGCCCTGCGCAAGAGCTGTTCAAGATGTTTGTGATCTAAGGATCTAC 2826  
 DB 2734 GGGGTGTAAAGGCGCCCTGCGCAAGAGCTGTTCAAGATGTTTGTGATCTAAGGATCTAC 2793  
 QY 2827 CAGGCTGAGAGCACTGGGAGACGACATCCCATCAACGCTTCAAGTGGGTGAGAGGCGCT 2886  
 DB 2794 CAGGCTGAGAGCACTGGGAGACGACATCCCATCAACGCTTCAAGTGGGTGAGAGGCGCT 2853  
 QY 2887 CGGCTGACACGACGTCAGTACGAGTGAAGAGGTTCTGTGCTCAAGTGAATCCACACC 2946  
 DB 2854 CGGCTGACACGACGTCAGTACGAGTGAAGAGGTTCTGTGCTCAAGTGAATCCACACC 2913  
 QY 2947 AACACCCGGGCGCCACGATGAGACCCCTGAGATCCGGAAGTCAAGAACGATTCACCTCC 3006  
 DB 2914 AACACCCGGGCGCCACGATGAGACCCCTGAGATCCGGAAGTCAAGAACGATTCACCTCC 2973

QY 3007 GAGATCCTGTGTGACGCCCTTTGGGGGTCAACCTGTGTGGGACGAGAACGGGCTG 3066  
 DB 2974 GAGATCCTGTGTGACGCCCTTTGGGGGTCAACCTGTGTGGGACGAGAACGGGCTG 3033  
 QY 3067 ATGTGTGTGACCGAAGTGGGACAGGCGCAAGGTGTATGACTCATATTGGGCGGACGCTTC 3126  
 DB 3034 ATGTGTGTGACCGAAGTGGGACAGGCGCAAGGTGTATGACTCATATTGGGCGGACGCTTC 3093  
 QY 3127 CAGCAATGATGTGTGTGAGAGGCGCTCACTGCTCATACCATCTCAAGGAAAAAGAAC 3186  
 DB 3094 CAGCAATGATGTGTGTGAGAGGCGCTCACTGCTCATACCATCTCAAGGAAAAAGAAC 3153  
 QY 3187 AAATCGGGGGGTATTAATCTGCTGCTCGGAGCAAGATTTGTGCACAATGACCCAGAA 3246  
 DB 3154 AAATCGGGGGGTATTAATCTGCTGCTCGGAGCAAGATTTGTGCACAATGACCCAGAA 3213  
 QY 3247 GTGAGAAAGAACGAGGCTGACACACCGTGGGGACATGAGGCGTCCGCGCACTACCGT 3306  
 DB 3214 GTGAGAAAGAACGAGGCTGACACACCGTGGGGACATGAGGCGTCCGCGCACTACCGT 3273  
 QY 3307 GTTGTGAATATACGAGCGGATTAATGTTCTGTGCTATGCGCCCTCAAGAGCTCCGTGAGGTG 3366  
 DB 3274 GTTGTGAATATACGAGCGGATTAATGTTCTGTGCTATGCGCCCTCAAGAGCTCCGTGAGGTG 3333  
 QY 3367 TATGCTGGGGCGCCCAACCTTACACAAATTCATGGGCTTCAAGTCCCTTGCCGACCTC 3426  
 DB 3334 TATGCTGGGGCGCCCAACCTTACACAAATTCATGGGCTTCAAGTCCCTTGCCGACCTC 3393  
 QY 3427 CCCACCGCCCTCTGCTGTGTGACAGTACAGTAAAGAGGGGCGAGCGGCTCAAGGTCATC 3486  
 DB 3394 CCCACCGCCCTCTGCTGTGTGACAGTACAGTAAAGAGGGGCGAGCGGCTCAAGGTCATC 3453  
 QY 3487 TATGCTTCAGTGTGCTCTTCATGCTGTGATGTGCACTCTGGGAAACAGCTATGACATC 3546  
 DB 3454 TATGCTTCAGTGTGCTCTTCATGCTGTGATGTGCACTCTGGGAAACAGCTATGACATC 3513  
 QY 3547 TACATCCCTGTGACATCCAGAGCAATACAGCCCATGCGCATCTTCTCCCAAC 3606  
 DB 3514 TACATCCCTGTGACATCCAGAGCAATACAGCCCATGCGCATCTTCTCCCAAC 3573  
 QY 3607 ACCGACGGCATGAGATGCTGTGTGCTACAGAGACGAGGGTGTCTACGTCAACACGTAC 3666  
 DB 3574 ACCGACGGCATGAGATGCTGTGTGCTACAGAGACGAGGGTGTCTACGTCAACACGTAC 3633  
 QY 3667 GGGCGCATCTTAAGATGTGTGCTGCAAGTGGGGGAGATGCTTCTGTGGCTTAC 3726  
 DB 3634 GGGCGCATCTTAAGATGTGTGCTGCAAGTGGGGGAGATGCTTCTGTGGCTTAC 3693  
 QY 3727 ATTCGCTCCAAACGATTAATGGGCTGGGGTGAAGAACCAATTGATCCGCTGTGGAG 3786  
 DB 3694 ATTCGCTCCAAACGATTAATGGGCTGGGGTGAAGAACCAATTGATCCGCTGTGGAG 3753  
 QY 3787 ACCGGCCACCTCGACGCGGGTCTTCATGACCAAAAGAGCTGAGAGGCTCAAGTTCGTGT 3846  
 DB 3754 ACCGGCCACCTCGACGCGGGTCTTCATGACCAAAAGAGGCTCAAGTTCGTGTGT 3813  
 QY 3847 GAGCGAATGACAAAGGTGTTTTCCTCACTGCTGCTGTGGGGACGACGCAAGTTTAC 3906  
 DB 3814 GAGCGAATGACAAAGGTGTTTTCCTCACTGCTGCTGTGGGGACGACGCAAGTTTAC 3873  
 QY 3907 TTGATGACTGTGAACCGTAACTGATCATGAACCTGGA 3945  
 DB 3874 TTGATGACTGTGAACCGTAACTGATCATGAACCTGGA 3912

RESULT 12

AAD17759 standard; DNA; 3999 BP.

AAD17759;

10-DEC-2001 (first entry)

DE Human novel STE20-like protein, NOV-3a encoding DNA.

XX Human; NOV-X protein; KIAA1233-like protein; STE20-like protein; tumour;  
XX trypsin inhibitor-like protein; gene therapy; haematopoietic illness;  
XX immunological disorder; neurodegenerative disorder; Alzheimer's disease;  
XX Parkinson's disease; immunomodulatory; pharmacogenomic; haemostatic;  
XX human immunodeficiency virus; HIV; fertility disorder; neuroprotective;  
XX cytoskeletal; noctropic; anti-fertility; cancer; chromosome 17;  
XX NOV-3a protein; ds.

OS Homo sapiens.

XX Key Location/Qualifiers  
FH 1..3999  
FT CDS /tag= a  
FT /product= "Human novel STE20-like protein, NOV-3a"

XX MO200162928-A2.

XX 30-AUG-2001.

XX 26-FEB-2001; 2001WO-US006151.

XX 25-FEB-2000; 2000US-0184951P.  
XX 28-FEB-2000; 2000US-0185548P.  
XX 01-MAR-2000; 2000US-0185967P.  
XX 18-APR-2000; 2000US-0197723Z.  
XX 27-APR-2000; 2000US-0199957Z.  
XX 23-FEB-2001; 2001US-00789390.

XX (CURA-) CURAGEN CORP.

XX Vernet CAM, Fernandes E, Shinkens RA, Macdougall J, Spaderna SK;  
XX WPI; 2001-582051/65.  
XX P-PsDB; AAE10611.

XX New isolated KIAA1233-like, STE20-like, or trypsin inhibitor-like  
XX polypeptide for diagnosing and treating pathological disorders, such as  
XX Parkinson's disease and for use in pharmacogenomics.

XX Claim 9; Page 44-45; 189pp; English.

XX The invention relates to novel human polypeptides referred as NOV-X and  
XX their corresponding nucleic acid sequences. NOV-X collectively include  
XX NOV-1, NOV-2a and NOV-2b which are novel KIAA1233-like polypeptides, NOV-  
XX 3a, NOV-3b, NOV-3c and NOV-3d which are novel STE20-like polypeptides and  
XX NOV-4a, NOV-4b, NOV-4c, NOV-4d and NOV-4e which are novel trypsin  
XX inhibitor-like polypeptides. NOV-X is used to identify a potential  
XX therapeutic agent that can modulate its activity and can be used for  
XX treating a pathology related to aberrant expression or aberrant  
XX physiological interactions of NOV-X. NOV-X or its DNA is used to  
XX determine the presence or predisposition to a disease associated with  
XX altered levels of NOV-X. NOV-X, its DNA and its antibody are used to  
XX treat or prevent a pathology associated with NOV-X. The pathological  
XX states that can be treated or prevented are haematopoietic, cancer,  
XX immunological, tumour, neurodegenerative (e.g. Alzheimer's and  
XX Parkinson's disease), human immunodeficiency virus (HIV) illness and  
XX fertility disorders. NOV-X and its DNA are used in pharmacogenomics for  
XX predictive medicine. NOV-X DNA is used in gene therapy. The present  
XX sequence is a DNA encoding human novel STE20-like protein, NOV-3a  
XX gene is located at chromosome 17

XX Sequence 3999 BP; 948 A; 1195 C; 1215 G; 641 T; 0 U; 0 Other;

XX SQ

Query Match 40.5%; Score 1599; DB 5; Length 3999;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2347 GACTTGTGTGCTGAAGAAGCGACTGTGACGAGGCCCTCGGCTCCAGAAAGGCC 2406  
DB 2401 GACTTGTGTGCTGAAGAAGCGACTGTGACGAGGCCCTCGGCTCCAGAAAGGCC 2460

QY 2407 ATGAGTACTCTGCTGCTCCAGCGAGAGGTGAAAAGCATGAGACGACGAGAGAAAGGC 2466  
DB 2461 ATGAGTACTCTGCTGCTCCAGCGAGAGGTGAAAAGCATGAGACGACGAGAGAAAGGC 2520  
QY 2467 GAAGCGGGCCACGACGAGAGGGAGAGATACCCCTGGGGGGCCGACGATGAGGATACA 2526  
DB 2521 GAAGCGGGCCACGACGAGAGGGAGAGATACCCCTGGGGGGCCGACGATGAGGATACA 2580  
QY 2527 GACAGCGTCAGACCAATGATGATGTCACGACGTCGAGAGATACCGGGACCACGCCCA 2586  
DB 2581 GACAGCGTCAGACCAATGATGATGTCACGACGTCGAGAGATACCGGGACCACGCCCA 2640  
QY 2587 TACGGGGGGCCGACCATGATGATGTCACGACGACCCCTGAAGAGAGCGGAACCTGTGAT 2646  
DB 2641 TACGGGGGGCCGACCATGATGATGTCACGACGACCCCTGAAGAGAGCGGAACCTGTGAT 2700  
QY 2647 GCTGACGACATATGGGTATACAAACCTGCTGACGATGTCAGCCGACGACCTCACCCAC 2706  
DB 2701 GCTGACGACATATGGGTATACAAACCTGCTGACGATGTCAGCCGACGACCTCACCCAC 2760  
QY 2707 GAGAAACAGCAAAAGGCCAAAGCCCACTCGAAGAGATGAGATGATACCAAGTCTGCT 2766  
DB 2761 GAGAAACAGCAAAAGGCCAAAGCCCACTCGAAGAGATGAGATGATACCAAGTCTGCT 2820  
QY 2767 GGGCTGTAAAGGCCCTTGCGAAGACTGTTTCAAGATGTTTGTGATCTAGGATCTAC 2826  
DB 2821 GGGCTGTAAAGGCCCTTGCGAAGACTGTTTCAAGATGTTTGTGATCTAGGATCTAC 2880  
QY 2827 CAGCTTGAGGACATGAGGGGACAGCATCCCAATCAGCCCTAGTGGGGTGAAGGGGCACT 2886  
DB 2881 CAGCTTGAGGACATGAGGGGACAGCATCCCAATCAGCCCTAGTGGGGTGAAGGGGCACT 2940  
QY 2887 CGGCTGACCAAGCTCAGTACGACGTCGAGAAAGGTTCTGTGTCACGTGAATCCAC 2946  
DB 2941 CGGCTGACCAAGCTCAGTACGACGTCGAGAAAGGTTCTGTGTCACGTGAATCCAC 3000  
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DB 3001 AACACCCGGGCCCAAGTGAAGACCCCTGAATCCGGAAGTACAGAGCATTTCACTCC 3060  
QY 3007 GAGATCTCTGTGACGACCCCTTGGGGGGTCAACCTGCTGAGGGGACGAGAAACGGGCTG 3066  
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QY 3067 ATGTTGCTGACCAAGTGGGACGAGGCAAGGTGTATGATCTCATTTGGGCGGACGCTTC 3126  
DB 3121 ATGTTGCTGACCAAGTGGGACGAGGCAAGGTGTATGATCTCATTTGGGCGGACGCTTC 3180  
QY 3127 CAGCAGATGATGTCGTGAGGGGCTCAACCTGCTCATTCACATCTCAGGAAAAAGAAC 3186  
DB 3181 CAGCAGATGATGTCGTGAGGGGCTCAACCTGCTCATTCACATCTCAGGAAAAAGAAC 3240  
QY 3187 AACCTGGGGTATATTAACCTGCTGCTCGGCTCGGAAACAAGATCTGTCACAAATGACCA 3246  
DB 3241 AACCTGGGGTATATTAACCTGCTGCTCGGCTCGGAAACAAGATCTGTCACAAATGACCA 3300  
QY 3247 GTTGAAGAAATACGAGCGATTAAGTTCTGTGATGCGCTTCAAGAGCTCGTGAAGTGC 3306  
DB 3301 GTTGAAGAAATACGAGCGATTAAGTTCTGTGATGCGCTTCAAGAGCTCGTGAAGTGC 3360  
QY 3307 GTTGAAGAAATACGAGCGATTAAGTTCTGTGATGCGCTTCAAGAGCTCGTGAAGTGC 3366  
DB 3361 GTTGAAGAAATACGAGCGATTAAGTTCTGTGATGCGCTTCAAGAGCTCGTGAAGTGC 3420  
QY 3367 TATGCTGGGCCCCCAAAACCTTACCAAAATTCATGAGCTTGAAGCTTGGCCGACCTC 3426  
DB 3421 TATGCTGGGCCCCCAAAACCTTACCAAAATTCATGAGCTTGAAGCTTGGCCGACCTC 3480  
QY 3427 CCCACCGGCTCTGCTGTGTCAGCTGACATGAGAGAGGGGACGCGCTCAAGGTCAATC 3486  
DB 3481 CCCACCGGCTCTGCTGTGTCAGCTGACATGAGAGAGGGGACGCGCTCAAGGTCAATC 3540  
QY 3487 TATGCTCCAGTGTGGCTTTCATGCTGTGATGTCAGCTCGGGGAAACGATATGACATC 3546

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Db 3541 TATGCTCAGTGGCTGCTTCATCTGTGATGTGCACTGGGGAACAGCATATACATC 3600
Qy 3547 TACATCCTGTGACATCCAGACCAATACAGCCCAATCCATATCTTCTCCCAAC 3606
Db 3601 TACATCCTGTGACATCCAGACCAATACAGCCCAATCCATATCTTCTCCCAAC 3660
Qy 3607 ACCGACCGCATGAGATCTGCTGTGCTACAGAGAGAGGCTGTAGTCAACAGCTAC 3666
Db 3661 ACCGACCGCATGAGATCTGCTGTGCTACAGAGAGAGGCTGTAGTCAACAGCTAC 3720
Qy 3667 GGGCGCATCATTAAGATGTGTGTGTGCAAGTGGGGAGATGCTACTTCTGTGGCTAC 3726
Db 3721 GGGCGCATCATTAAGATGTGTGTGTGCAAGTGGGGAGATGCTACTTCTGTGGCTAC 3780
Qy 3727 ATCTGCTCCAACCAAGATATGAGGCTGTGGGCTGAGAAAGCCATTGAGATCCGCTGTGGAG 3786
Db 3781 ATCTGCTCCAACCAAGATATGAGGCTGTGGGCTGAGAAAGCCATTGAGATCCGCTGTGGAG 3840
Qy 3787 ACGGCGCATCTGCAAGGCTGTTCATGTGCAACCAAGCTCAGAGCTCAAGTCTGTGT 3846
Db 3841 ACGGCGCATCTGCAAGGCTGTTCATGTGCAACCAAGCTCAGAGCTCAAGTCTGTGT 3900
Qy 3847 GAGCGGAATGACAAGGTGTTTTTCTCAGTCCGCTGTGGGGGAGAGCCAAAGTTAC 3906
Db 3901 GAGCGGAATGACAAGGTGTTTTTCTCAGTCCGCTGTGGGGGAGAGCCAAAGTTAC 3960
Qy 3907 TTCATGACTGTGAACCGTACTGATCATGATGAATGCTGTGA 3945
Db 3961 TTCATGACTGTGAACCGTACTGATCATGATGAATGCTGTGA 3999

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## RESULT 13

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AAS88207
ID AAS88207 standard; cDNA: 7132 BP.
XX AAS88207;
AC AAS88207;
XX 13-FEB-2002 (first entry)
XX DNA encoding novel human diagnostic protein #24011.
XX Human: chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
XX OS
XX PN WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX P-PSDB; ABG24020.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX Claim 1; SEQ ID NO 24011; 103bp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

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CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC electronic format directly from WIPO at  
 CC ftp://wipo.int/pub/published\_pct\_sequences

XX Sequence 7132 BP; 1569 A; 2123 C; 2159 G; 1280 T; 0 U; 1 Other;

Query Match 33.9%; Score 1340; DB 5; Length 7132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 7 ATGGGCGACCCAGCCCGCCCGCAGCTGAGACGACATCGACTGTCCGCCCTCGGGAC 66
Db 158 ATGGGCGACCCAGCCCGCCCGCAGCTGAGACGACATCGACTGTCCGCCCTCGGGAC 217
Qy 67 CCTGCTGGGATCTTTGAGCTGTGTGAGGTGTGTGGCAATGGAACCTACGAGAGTGTAC 126
Db 218 CCTGCTGGGATCTTTGAGCTGTGTGAGGTGTGTGGCAATGGAACCTACGAGAGTGTAC 277
Qy 127 AAGGCTGGCATGTCAAGACGGGAGCTGTGCTCCATCAAGTCAATGATGTACAGGAG 186
Db 278 AAGGCTGGCATGTCAAGACGGGAGCTGTGCTCCATCAAGTCAATGATGTACAGGAG 337
Qy 187 GACGAGAGAGAGATCAACAGAGATCAACATGCTGTGAAAAAGTACTCTCACACCGC 246
Db 338 GACGAGAGAGAGATCAACAGAGATCAACATGCTGTGAAAAAGTACTCTCACACCGC 397
Qy 247 AACATGCGACCTTACTACGAGCCTTATCATCAAGAGAGCCCGGGGAAAGATGACCGAG 306
Db 398 AACATGCGACCTTACTACGAGCCTTATCATCAAGAGAGCCCGGGGAAAGATGACCGAG 457
Qy 307 CTTGCTGTGTGATGAGATTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 366
Db 458 CTTGCTGTGTGATGAGATTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 517
Qy 367 AAGGCAACGCGCTGAAAGAGAGCTGTATGTGCTGTATCTGACGAGAGATCTCAGGGGT 426
Db 518 AAGGCAACGCGCTGAAAGAGAGCTGTATGTGCTGTATCTGACGAGAGATCTCAGGGGT 577
Qy 427 CTGGCCCATCTCCATGTGCCCAAGAGTATCCATGAGACATCAAGGGGAGAGATGTGCTG 486
Db 578 CTGGCCCATCTCCATGTGCCCAAGAGTATCCATGAGACATCAAGGGGAGAGATGTGCTG 637
Qy 487 CTGACAGAGATGCTGAGGTCAAGCTAGTGAATTTGGGGTGTGTGTGTGTGTGTGTGTGT 546
Db 638 CTGACAGAGATGCTGAGGTCAAGCTAGTGAATTTGGGGTGTGTGTGTGTGTGTGTGTGT 697
Qy 547 ACCGTGGGAGAGCGGAACCTTTCATTGGGACTCTCTTATCTGATGTGCTCAGAGTATC 606
Db 698 ACCGTGGGAGAGCGGAACCTTTCATTGGGACTCTCTTATCTGATGTGCTCAGAGTATC 757
Qy 607 GCGTGTATAGAAACCTGTATGCACTTATGATTAACAGAGTATTTGGTCTCTAGGA 666
Db 758 GCGTGTATAGAAACCTGTATGCACTTATGATTAACAGAGTATTTGGTCTCTAGGA 817
Qy 667 ATCACAGCATTCGATGAGAGAGAGAGCCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 726
Db 818 ATCACAGCATTCGATGAGAGAGAGAGCCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 877

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QY 727 GCCCTCTTCTCTATTCCTCGAACCCTCCGCCAGGCTCAAGTCCAGAAAGTGTCTAG 786  
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 QY 787 AAGTTCATTGACTTCAATGACACATGTCTCATCAAGATTCTTACCTGAGCCGCCACCCACG 846  
 DB 938 AAGTTCATTGACTTCAATGACACATGTCTCATCAAGATTCTTACCTGAGCCGCCACCCACG 997  
 QY 847 GAGCAGCTCTGAAGTTCCCTTCATCCGGGACCCAGCCACGAGGCGGAGGCTCCGCATC 906  
 DB 998 GAGCAGCTCTGAAGTTCCCTTCATCCGGGACCCAGCCACGAGGCGGAGGCTCCGCATC 1057  
 QY 907 CAGCTTAAAGACCACTTGAACCATCCCGAAGAGCGGGGTGAGAAAGAGAGACAGAA 966  
 DB 1058 CAGCTTAAAGACCACTTGAACCATCCCGAAGAGCGGGGTGAGAAAGAGAGACAGAA 1117  
 QY 967 TATGAGTACAGCGGACGAGAGAGAGAAATGACAGCCATGAGAGAGAGAGAGCCACG 1026  
 DB 1118 TATGAGTACAGCGGACGAGAGAGAGAAATGACAGCCATGAGAGAGAGAGAGCCACG 1177  
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 QY 1087 GAAATTAAGACCACTCAGAGGCTTTAAACAGACAGCAGCTGACAGCAGCAGCAG 1146  
 DB 1238 GAAATTAAGACCACTCAGAGGCTTTAAACAGCAGCAGCAGCTGACAGCAGCAGCAG 1297  
 QY 1147 CGAGACCCGAGGACACATCAAAACCTGTCTGACACAGCGGCGCATAGAGAG 1206  
 DB 1298 CGAGACCCGAGGACACATCAAAACCTGTCTGACACAGCGGCGCATAGAGAG 1357  
 QY 1207 CAGAAGAGAGACCGCGCGCGCTGAGAGAGCAACAGCGCGGAGGAGAGAGAGAG 1266  
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 QY 1267 CTGCAAGAGAGAGAGAGAGCGCGCTGAGAGAGCATGCAAGCTTCTGCGCGGAGAGAG 1326  
 DB 1418 CTGCAAGAGAGAGAGAGAGCGCGCTGAGAGAGCATGCAAGCTTCTGCGCGGAGAGAG 1477  
 QY 1327 GAGCGGCGGACGCGGAGCG 1346  
 DB 1478 GAGCGGCGGACGCGGAGCG 1497  
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 AAC98909  
 ID AAC98909 standard; cDNA; 2345 BP.  
 AC AAC98909;  
 DT 09-MAR-2001 (first entry)  
 DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:137.  
 XX Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection;  
 KW diagnosis; identification; cytostatic; neuroprotective; nootropic;  
 KW immunomodulatory; relaxant; contraceptive; gynaecological;  
 KW antiinflammatory; cardiant; gene therapy; chromosome mapping;  
 KW linkage analysis; tissue identification; tissue typing; forensic; neural;  
 KW immune system; muscular; reproductive; gastrointestinal; pulmonary;  
 KW cardiovascular; renal; proliferative; ss.  
 OS Homo sapiens.  
 PN WO200055320-A1.  
 PD 21-SEP-2000.  
 PF 08-MAR-2000; 2000MO-US005989.  
 PR 12-MAR-1999; 99US-0124270P.  
 XX

PA (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Ruben SM;  
 PI WPI, 2000-579444/54.  
 DR F-PSDB; AAB54144.  
 PT New nucleic acid that is a pancreatic cancer antigen for preventing,  
 PT treating, or ameliorating a medical condition, particular pancreatic  
 PT cancer, or for use in assays for diagnosing a pathological condition.  
 XX  
 PS Claim 1; Page 596-597; 1379pp; English.  
 CC AAC98773 to AAC99231 encode the human pancreatic cancer associated  
 CC proteins, called pancreatic cancer antigens, given in AAB54008 to  
 CC AAB54466. The human pancreatic cancer antigens have cytostatic,  
 CC neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,  
 CC gynaecological, cardiant and antiinflammatory activities, and can be used  
 CC in gene therapy. The polynucleotide and proteins can be used for  
 CC preventing, treating, or ameliorating a medical condition or in assays  
 CC for diagnosing a pathological condition or a susceptibility to one in a  
 CC subject. Binding partners to the proteins and the activity of the  
 CC proteins can be identified. The pancreatic cancer antigens can be used to  
 CC detect, treat or prevent pancreatic disorders, especially cancer.  
 CC Agonists and antagonists to the antigens can be screened for. The  
 CC pancreatic cancer antigen polynucleotides can be used to design nucleic  
 CC acid hybridisation probes that can be used in chromosome mapping, linkage  
 CC analysis, tissue identification and/or typing and a variety of forensic  
 CC and diagnostic methods. The proteins can be used to generate antibodies  
 CC which are used to purify, detect and target the polypeptides, including  
 CC both in vivo and in vitro diagnostic and therapeutic methods. The  
 CC proteins can be used to treat or prevent neural, immune system, muscular,  
 CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or  
 CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent  
 CC sequences used in the exemplification of the present invention  
 XX  
 SQ Sequence 2345 BP; 499 A; 693 C; 671 G; 467 T; 0 U; 15 Other;  
 Query Match 26.1%; Score 1030; DB 3; Length 2345;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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 DB 351 TCGTGGGCTGTGTAAGGCCCTTGGCAAGAGCTGTTACGATGTTGTGATCTAGGAT 410  
 QY 2823 CTACCAAGCTTGAGGACATGTTGGGAGACAGATCCCATCAACAGCCCTTATGAGGAGG 2882  
 DB 411 TTACCAAGCTTGAGGACATGTTGGGAGACAGATCCCATCAACAGCCCTTATGAGGAGG 470  
 QY 2883 CACTCGGCTCGACAGCTGCACTGACAGCTGAGAGAGGTTCTGTGTCAACGTGAATCC 2942  
 DB 471 CACTCGGCTCGACAGCTGCACTGACAGCTGAGAGAGGTTCTGTGTCAACGTGAATCC 530  
 QY 2943 CACCAACACCCGGGCGCCACAGTGAAGACCCCTGAGATCCGAGATCAAGAACGATTCAA 3002  
 DB 531 CACCAACACCCGGGCGCCACAGTGAAGACCCCTGAGATCCGAGATCAAGAACGATTCAA 590  
 QY 3003 CTCCGAGATCTCTGTGACAGCCCTTTGGGGGGTCAACTGTGTGTGGGACCGGAGAACG 3062  
 DB 591 CTCCGAGATCTCTGTGACAGCCCTTTGGGGGGTCAACTGTGTGTGGGACCGGAGAACG 650  
 QY 3063 GCTGATGTTGTGACCGGAGTGGGAGGGGCAAGGTGTATGAGCTCATTTGGGCGCGACG 3122  
 DB 651 GCTGATGTTGTGACCGGAGTGGGAGGGGCAAGGTGTATGAGCTCATTTGGGCGCGACG 710  
 QY 3123 CTTCCAGCAGATGATGATGCTGAGAGGGGCTCAACTGCTCATACATCTCAGGAGAAAG 3182  
 DB 711 CTTCCAGCAGATGATGATGCTGAGAGGGGCTCAACTGCTCATACATCTCAGGAGAAAG 770  
 QY 3183 GAACAAACTGCGGGGTATTAATCTGCTGTGGCTCCGGAACAAGATTTGCAATAAGACCC 3242  
 DB 771 GAACAAACTGCGGGGTATTAATCTGCTGTGGCTCCGGAACAAGATTTGCAATAAGACCC 830



QY 3243 AGAAGTGGAGAAGAGCAGGGCTGGACCAACCGTGGGGGACATGAGGGCTGGGGCACTA 3302  
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QY 3543 CATCTATGCTGCTGAGTGTGCTTCCATGCTGTGATGTGACATCGGGGAAACAGCTATGA 3602  
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QY 3603 CAACACCGAGCGGATGAGATGCTGTGCTGACATGAGAGAGGGGTCTACGTCACAC 3662  
DB 1191 CAACACCGAGCGGATGAGATGCTGTGCTGACATGAGAGAGGGGTCTACGTCACAC 1250  
QY 3663 GTACGGGCGCATCTTAAGATGTGTGCTGACATGAGGGGGAGATGCTTCTGTGTC 3722  
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DB 1311 CTACATCTGCTCCACACGATTAATGAGGCTGGGGTGAAGAACCATTTGATCCGCTGT 1370  
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DB 1491 TTACTTCATGACTCTGAACCGGTAATGATGATGAACTGTGA 1533

RESULT 15  
AB139593  
ID ABL39593 standard; cDNA; 1964 BP.  
XX ABL39593;  
AC 09-MAY-2002 (first entry)  
XX Human cancer suppressing gene P928 encoding cDNA SEQ ID NO:30.  
DE Human cancer suppressing gene P928 encoding cDNA SEQ ID NO:30.  
XX Human cancer suppressing gene P928 encoding cDNA SEQ ID NO:30.  
KM Human cancer suppressing gene P928 encoding cDNA SEQ ID NO:30.  
XX Homo sapiens.  
OS Homo sapiens.  
XX Key  
FH 383.1261 Location/Qualifiers  
FT CDS /\*tag= a  
FT /product= "cancer suppressing protein"  
XX CNI31318-A.  
XX 19-SEP-2001.  
XX

PF 14-MAR-2000; 2000CN-00111997.  
XX 14-MAR-2000; 2000CN-00111997.  
PR 14-MAR-2000; 2000CN-00111997.  
XX (SHAN-) SHANGHAI INST ONCOLOGY.  
PA Gu J, Yang S;  
PI WPI: 2002-042196/06.  
XX P-PSDB; ABB06007.  
DR New human protein able to suppress growth of cancer cells and its  
XX encoding polynucleotide.  
PT Claim 5; Page 44-46 (Disclosure); 65pp; Chinese.  
XX The present invention describes human proteins with cancer suppressing  
XX activity. Also described are the polynucleotides encoding the proteins  
XX and a process for preparing the proteins by DNA recombination. The  
XX proteins and polynucleotides can be used in the treatment of diseases  
XX such as cancer. The present sequence encodes a human cancer suppressing  
XX protein from the present invention  
SQ Sequence 1964 BP; 450 A; 583 C; 518 G; 413 T; 0 U; 0 Other;  
Query Match 24.6%; Score 970; DB 6; Length 1964;  
Best Local Similarity 99.8%; Pred. No. 0; Mismatches 1; Indels 2; Gaps 2;  
Matches 1260; Conservative 0; Mismatches 1; Indels 2; Gaps 2;  
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QY 2743 GGGAGTGTGACTACAGTCTCGTGGGCTGTAAAGGCTTGGCAAGAGCTCTTACG 2802  
DB 61 GGGAGTGTGACTACAGTCTCGTGGGCTGTAAAGGCTTGGCAAGAGCTCTTACG 120  
QY 2803 ATGTTTGTGATCTAAGGATCTACAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2862  
DB 121 ATGTTTGTGATCTAAGGATCTACAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 180  
QY 2863 GCCCTAATGAGTGTGAT 2922  
DB 181 GCCCTAATGAGTGTGAT 240  
QY 2923 TCTGTGTCAAGTGAATCCACCAACACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2982  
DB 241 TCTGTGTCAAGTGAATCCACCAACACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 299  
QY 2983 AAGTAAAGAGAGAGATCTACAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 3042  
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QY 3043 CTGGTGGGACAGAT 3102  
DB 360 CTGGTGGGACAGAT 418  
QY 3103 GAACTATTGAGGCGGAT 3162  
DB 419 GAACTATTGAGGCGGAT 478  
QY 3163 ATCACCATCTCAGGAT 3222  
DB 479 ATCACCATCTCAGGAT 538  
QY 3223 AAGATTCTGACATGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 3282  
DB 539 AAGATTCTGACATGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 598  
QY 3283 ATGAGAGGCTGCGGAT 3342  
DB 599 ATGAGAGGCTGCGGAT 658

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QY 3403 GCTTCAAGTCTTTGCGAGCTTCCCAACGCGCTTGTGTGACCTTGACATGAG 3462
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Db 719 GCTTCAAGTCTTTGCGAGCTTCCCAACGCGCTTGTGTGACCTTGACATGAG 778
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QY 3463 GAGGGGCAAGCGGCTCAAGGTCTATGAGCTCCAGTGGCTTCATGCTGTGATGTC 3522
    |||||
Db 779 GAGGGGCAAGCGGCTCAAGGTCTATGAGCTCCAGTGGCTTCATGCTGTGATGTC 838
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QY 3523 GACTCGGGGAAACAGCTATGACAATCTACATCCCTGTGCAATCAGAGCCAGATCAAGCCC 3582
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Db 839 GACTCGGGGAAACAGCTATGACAATCTACATCCCTGTGCAATCAGAGCCAGATCAAGCCC 898
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QY 3763 GCCATTGAGATCCGCTGTGTGAGACGGGCCACTTCGACGGGCTTTCATGCAAAACGA 3822
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QY 3943 TGA 3945
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Db 1259 TGA 1261
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 17:16:23 ; Search time 190 Seconds  
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Title: US-10-029-115-1

Perfect score: 3951

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Word size : 0

Total number of hits satisfying chosen parameters: 1365418

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1787	45.2	4133	4 US-09-688-188B-11	Sequence 11, Appl
2	1787	45.2	4133	4 US-09-291-417D-11	Sequence 11, Appl
3	47	1.2	896	4 US-09-579-664B-1	Sequence 1, Appl
4	31	0.8	2913	4 US-09-976-594-368	Sequence 368, App
5	29	0.7	2214	3 US-08-864-038A-1	Sequence 1, Appl
6	29	0.7	3331	3 US-08-864-038A-2	Sequence 2, Appl
7	29	0.7	3331	4 US-08-864-038A-4	Sequence 4, Appl
8	27	0.7	8411	3 US-09-976-594-560	Sequence 560, App
9	26	0.7	57	3 US-09-043-303-14	Sequence 14, Appl
10	26	0.7	69	3 US-09-043-303-13	Sequence 13, Appl
11	26	0.7	75	3 US-09-043-303-10	Sequence 10, Appl
12	26	0.7	78	3 US-09-043-303-11	Sequence 11, Appl
13	26	0.7	78	3 US-09-043-303-12	Sequence 12, Appl
14	26	0.7	107	4 US-09-205-995-75	Sequence 75, Appl
15	26	0.7	169	4 US-09-205-995-72	Sequence 72, Appl
16	26	0.7	183	4 US-09-707-919A-16	Sequence 16, Appl
17	26	0.7	190	4 US-09-205-995-77	Sequence 77, Appl
18	26	0.7	459	4 US-09-707-919A-13	Sequence 13, Appl
19	26	0.7	516	4 US-09-083-268-1	Sequence 1, Appl
20	26	0.7	623	3 US-09-043-303-5	Sequence 5, Appl
21	26	0.7	800	1 US-08-468-853-7	Sequence 7, Appl
22	26	0.7	800	1 US-08-468-853-7	Sequence 7, Appl
23	26	0.7	800	1 US-08-310-357-7	Sequence 7, Appl
24	26	0.7	800	1 US-08-468-853-7	Sequence 7, Appl
25	26	0.7	800	2 US-08-468-857-7	Sequence 78, Appl
26	26	0.7	2156	4 US-09-086-663A-78	Sequence 2, Appl
27	26	0.7	2201	3 US-09-330-970-2	Sequence 2, Appl

28	26	0.7	2294	4 US-09-086-663A-70	Sequence 70, Appl
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37	26	0.7	3798	4 US-09-688-188B-9	Sequence 9, Appl
38	26	0.7	3798	4 US-09-291-417D-9	Sequence 9, Appl
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44	26	0.7	4481	4 US-09-707-919A-20	Sequence 20, Appl
45	26	0.7	4481	4 US-09-083-268-2	Sequence 2, Appl
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51	26	0.7	7344	3 US-08-961-739-1	Sequence 1, Appl
52	26	0.7	161652	4 US-09-497-855A-40	Sequence 40, Appl
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54	25	0.6	379	1 US-09-591-383-5	Sequence 5, Appl
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57	25	0.6	1396	3 US-09-370-102-2	Sequence 2, Appl
58	25	0.6	2056	3 US-09-334-601-12	Sequence 12, Appl
59	25	0.6	2623	3 US-09-234-332-6	Sequence 6, Appl
60	25	0.6	4621	4 US-09-125-635-9	Sequence 9, Appl
61	25	0.6	5125	1 US-08-094-948A-4	Sequence 4, Appl
62	25	0.6	5125	5 PCT-US96-09319-4	Sequence 4, Appl
63	25	0.6	5175	2 US-08-843-530B-3	Sequence 3, Appl
64	25	0.6	5697	2 US-08-843-530B-5	Sequence 5, Appl
65	25	0.6	6545	2 US-08-843-530B-1	Sequence 1, Appl
66	24	0.6	1578	4 US-09-130-491-10	Sequence 10, Appl
67	24	0.6	4835	1 US-08-386-495-9	Sequence 9, Appl
68	24	0.6	4835	1 PCT-US96-02331-9	Sequence 9, Appl
69	24	0.6	8147	4 US-09-514-247A-9	Sequence 9, Appl
70	23	0.6	23	4 US-09-688-188B-60	Sequence 60, Appl
71	23	0.6	23	4 US-09-688-188B-61	Sequence 61, Appl
72	23	0.6	23	4 US-09-291-417D-60	Sequence 60, Appl
73	23	0.6	23	4 US-09-669-751-15	Sequence 15, Appl
74	23	0.6	562	4 US-09-588-256-1	Sequence 1, Appl
75	23	0.6	2160	3 US-09-365-842-7	Sequence 7, Appl
76	23	0.6	3462	4 US-09-442-100-1	Sequence 1, Appl
77	23	0.6	5720	4 US-08-935-106-1	Sequence 1, Appl
78	23	0.6	5720	4 US-09-442-102-1	Sequence 1, Appl
79	23	0.6	5720	4 US-09-442-102-1	Sequence 1, Appl
80	22	0.6	196	3 US-09-158-863C-63	Sequence 63, Appl
81	22	0.6	267	4 US-09-059-625-5	Sequence 5, Appl
82	22	0.6	267	4 US-09-059-625-8	Sequence 8, Appl
83	22	0.6	508	4 US-09-059-625-60	Sequence 60, Appl
84	22	0.6	533	6 5482709-5	Patent No. 5482709
85	22	0.6	539	2 US-08-709-924-1	Sequence 1, Appl
86	22	0.6	539	2 US-08-709-925-1	Sequence 1, Appl
87	22	0.6	539	4 US-08-709-948-1	Sequence 1, Appl
88	22	0.6	539	4 US-09-220-415-1	Sequence 1, Appl
89	22	0.6	539	4 US-09-675-776-1	Sequence 1, Appl
90	22	0.6	539	4 US-09-676-739-1	Sequence 1, Appl
91	22	0.6	543	6 5273901-6	Patent No. 5273901
92	22	0.6	549	3 US-08-918-288-37	Sequence 37, Appl
93	22	0.6	549	3 US-09-282-357-37	Sequence 37, Appl
94	22	0.6	575	3 US-08-918-288-35	Sequence 35, Appl
95	22	0.6	575	3 US-09-282-357-35	Sequence 35, Appl
96	22	0.6	587	4 US-09-035-625-2	Sequence 2, Appl
97	22	0.6	717	3 US-08-918-288-7	Sequence 7, Appl
98	22	0.6	717	3 US-08-918-288-22	Sequence 22, Appl
99	22	0.6	717	3 US-08-918-288-25	Sequence 25, Appl
100	22	0.6	717	3 US-09-282-357-7	Sequence 7, Appl

101	22	0.6	717	3	US-09-282-357-22	Sequence 22, Appl	c 174	21	0.5	390	1	US-08-661-168-7	Sequence 7, Appl
102	22	0.6	717	3	US-09-282-357-25	Sequence 25, Appl	175	21	0.5	397	1	US-09-253-691-3	Sequence 3, Appl
103	22	0.6	718	3	US-08-918-288-10	Sequence 10, Appl	c 176	21	0.5	639	4	US-09-336-536-57	Sequence 57, Appl
104	22	0.6	718	3	US-09-282-357-10	Sequence 10, Appl	177	21	0.5	1080	2	US-08-918-727-2	Sequence 2, Appl
c 105	22	0.6	725	4	US-09-059-625-36	Sequence 36, Appl	178	21	0.5	1080	2	US-09-205-680A-2	Sequence 2, Appl
c 106	22	0.6	725	4	US-09-059-625-50	Sequence 50, Appl	179	21	0.5	1093	4	US-09-010-147B-1	Sequence 1, Appl
c 107	22	0.6	725	4	US-09-059-625-55	Sequence 55, Appl	180	21	0.5	1144	1	US-08-014-943A-1	Sequence 1, Appl
c 108	22	0.6	726	3	US-08-918-288-16	Sequence 16, Appl	181	21	0.5	1144	1	US-08-486-421-2	Sequence 2, Appl
109	22	0.6	726	3	US-08-918-288-19	Sequence 19, Appl	182	21	0.5	1144	1	US-08-470-911-2	Sequence 2, Appl
110	22	0.6	726	3	US-09-282-357-16	Sequence 16, Appl	183	21	0.5	1144	2	US-08-486-809-2	Sequence 2, Appl
111	22	0.6	726	3	US-09-282-357-19	Sequence 19, Appl	c 184	21	0.5	1686	4	US-09-833-381-2019	Sequence 2019, Ap
c 112	22	0.6	729	4	US-09-059-625-33	Sequence 33, Appl	185	21	0.5	1776	2	US-08-531-927B-1	Sequence 1, Appl
c 113	22	0.6	729	4	US-09-059-625-44	Sequence 44, Appl	186	21	0.5	1776	2	US-09-041-886-12	Sequence 12, Appl
c 114	22	0.6	729	4	US-09-059-625-47	Sequence 47, Appl	c 187	21	0.5	1858	4	US-09-336-536-56	Sequence 56, Appl
c 115	22	0.6	743	3	US-08-918-288-5	Sequence 5, Appl	188	21	0.5	1884	3	US-08-753-007A-5	Sequence 5, Appl
c 116	22	0.6	743	3	US-08-918-288-20	Sequence 20, Appl	189	21	0.5	1884	3	US-09-398-496-5	Sequence 5, Appl
c 117	22	0.6	743	3	US-08-918-288-23	Sequence 23, Appl	c 190	21	0.5	2104	1	US-07-984-044A-4	Sequence 4, Appl
c 118	22	0.6	743	3	US-09-282-357-5	Sequence 5, Appl	c 191	21	0.5	2104	1	US-08-458-393-4	Sequence 4, Appl
c 119	22	0.6	743	3	US-09-282-357-20	Sequence 20, Appl	c 192	21	0.5	2568	4	US-09-489-039A-5258	Sequence 5258, Ap
c 120	22	0.6	743	3	US-09-282-357-23	Sequence 23, Appl	c 193	21	0.5	3736	4	US-09-489-039A-5366	Sequence 6366, Ap
c 121	22	0.6	744	3	US-08-918-288-8	Sequence 8, Appl	194	21	0.5	3609	4	US-09-799-875-6	Sequence 6, Appl
c 122	22	0.6	744	3	US-09-282-357-8	Sequence 8, Appl	195	21	0.5	5983	4	US-09-799-875-4	Sequence 4, Appl
c 123	22	0.6	752	3	US-08-918-288-14	Sequence 14, Appl	196	21	0.5	6794	4	US-09-491-356C-2	Sequence 2, Appl
c 124	22	0.6	752	3	US-08-918-288-17	Sequence 17, Appl	197	21	0.5	6794	4	US-09-491-356C-1	Sequence 1, Appl
c 125	22	0.6	752	3	US-09-282-357-14	Sequence 14, Appl	198	20	0.5	55298	4	US-09-688-188B-59	Sequence 59, Appl
c 126	22	0.6	752	3	US-09-282-357-17	Sequence 17, Appl	c 199	20	0.5	20	4	US-09-291-417D-59	Sequence 59, Appl
c 127	22	0.6	834	3	US-08-918-288-4	Sequence 4, Appl	c 200	20	0.5	252	2	US-08-623-906A-1	Sequence 1, Appl
128	22	0.6	834	3	US-09-282-357-4	Sequence 4, Appl	c 201	20	0.5	314	3	US-09-060-410-6	Sequence 6, Appl
c 129	22	0.6	835	3	US-08-918-288-40	Sequence 40, Appl	c 202	20	0.5	314	4	US-09-723-458-6	Sequence 86, Appl
c 130	22	0.6	835	3	US-09-282-357-40	Sequence 40, Appl	203	20	0.5	328	4	US-09-016-434-966	Sequence 966, Appl
c 131	22	0.6	836	3	US-08-918-288-2	Sequence 2, Appl	204	20	0.5	448	4	US-09-669-751-88	Sequence 88, Appl
c 132	22	0.6	836	3	US-09-282-357-2	Sequence 2, Appl	c 205	20	0.5	822	4	US-09-228-986-38	Sequence 38, Appl
c 133	22	0.6	837	3	US-08-918-288-38	Sequence 38, Appl	c 206	20	0.5	879	1	US-08-243-545-1	Sequence 1, Appl
c 134	22	0.6	837	3	US-09-282-357-38	Sequence 38, Appl	c 207	20	0.5	879	2	US-08-993-96C-1	Sequence 1, Appl
c 135	22	0.6	893	3	US-09-142-320-3	Sequence 3, Appl	c 208	20	0.5	879	2	US-09-160-841-1	Sequence 1, Appl
c 136	22	0.6	893	3	US-09-142-320-5	Sequence 5, Appl	c 209	20	0.5	879	4	US-08-669-692-1	Sequence 1, Appl
c 137	22	0.6	893	3	US-09-142-320-8	Sequence 8, Appl	c 210	20	0.5	879	4	US-08-444-626-1	Sequence 1, Appl
c 138	22	0.6	893	3	US-09-142-320-7	Sequence 7, Appl	c 211	20	0.5	879	5	PCR-US94-05365-1	Sequence 1, Appl
c 139	22	0.6	893	3	US-09-142-320-8	Sequence 8, Appl	c 212	20	0.5	1017	5	PCR-US94-05365-21	Sequence 21, Appl
c 140	22	0.6	893	3	US-09-142-320-9	Sequence 9, Appl	c 213	20	0.5	1383	3	US-09-400-742-7	Sequence 7, Appl
c 141	22	0.6	893	3	US-09-142-320-10	Sequence 10, Appl	c 214	20	0.5	1383	3	US-08-618-651A-7	Sequence 7, Appl
c 142	22	0.6	893	3	US-09-760-294-3	Sequence 3, Appl	c 215	20	0.5	1383	4	US-09-215-252-6	Sequence 6, Appl
c 143	22	0.6	893	4	US-09-760-294-5	Sequence 5, Appl	c 216	20	0.5	1383	4	US-09-970-988A-6	Sequence 6, Appl
c 144	22	0.6	893	4	US-09-760-294-6	Sequence 6, Appl	217	20	0.5	1866	3	US-08-909-742-1	Sequence 1, Appl
c 145	22	0.6	893	4	US-09-760-294-7	Sequence 7, Appl	218	20	0.5	1866	3	US-09-412-289-1	Sequence 1, Appl
c 146	22	0.6	893	4	US-09-760-294-8	Sequence 8, Appl	c 219	20	0.5	1909	4	US-09-461-657B-16	Sequence 16, Appl
c 147	22	0.6	893	4	US-09-760-294-9	Sequence 9, Appl	c 220	20	0.5	2097	4	US-09-461-657B-14	Sequence 14, Appl
c 148	22	0.6	893	4	US-09-760-294-10	Sequence 10, Appl	221	20	0.5	2450	4	US-09-620-312D-336	Sequence 336, Appl
c 149	22	0.6	1345	3	US-08-592-214A-7	Sequence 7, Appl	222	20	0.5	2513	4	US-09-620-312D-337	Sequence 337, Appl
c 150	22	0.6	1345	3	US-08-659-188-7	Sequence 7, Appl	c 223	20	0.5	2787	4	US-09-254-594-2	Sequence 2, Appl
c 151	22	0.6	1345	3	US-08-655-227-7	Sequence 7, Appl	c 224	20	0.5	2799	4	US-09-461-657B-11	Sequence 11, Appl
c 152	22	0.6	1345	3	US-08-655-241-7	Sequence 7, Appl	225	20	0.5	2900	4	US-09-620-312D-673	Sequence 673, Appl
c 153	22	0.6	1345	3	US-09-149-976-7	Sequence 7, Appl	c 226	20	0.5	2987	4	US-07-757-347D-1	Sequence 1, Appl
c 154	22	0.6	1345	4	US-09-398-326-7	Sequence 7, Appl	c 227	20	0.5	2987	4	US-09-461-657B-10	Sequence 1, Appl
c 155	22	0.6	1408	2	US-08-222-124-10	Sequence 10, Appl	228	20	0.5	3110	4	US-09-023-655-1072	Sequence 1072, Ap
c 156	22	0.6	1408	2	US-08-842-657A-10	Sequence 10, Appl	229	20	0.5	3116	4	US-09-976-594-283	Sequence 283, Appl
c 157	22	0.6	1414	1	US-08-222-124-9	Sequence 9, Appl	230	20	0.5	3132	2	US-08-224-482-3	Sequence 3, Appl
c 158	22	0.6	1414	1	US-08-842-657A-9	Sequence 9, Appl	231	20	0.5	3132	3	US-09-205-921-1	Sequence 1, Appl
c 159	22	0.6	1578	4	US-09-016-434-1377	Sequence 1377, Ap	232	20	0.5	3132	4	US-09-300-958A-32	Sequence 32, Appl
c 160	22	0.6	1665	3	US-08-766-354A-29	Sequence 29, Appl	233	20	0.5	3132	4	US-09-702-705-330	Sequence 320, Appl
c 161	22	0.6	1809	1	US-08-453-956-24	Sequence 24, Appl	234	20	0.5	3132	4	US-09-736-457-330	Sequence 320, Appl
c 162	22	0.6	1809	1	US-08-086-631-24	Sequence 24, Appl	235	20	0.5	3132	4	US-09-614-124B-320	Sequence 320, Appl
c 163	22	0.6	1809	2	US-08-452-930-24	Sequence 24, Appl	236	20	0.5	3132	4	US-09-671-325-330	Sequence 320, Appl
c 164	22	0.6	1809	5	PCR-US93-08174-24	Sequence 24, Appl	237	20	0.5	3132	4	US-09-589-184-320	Sequence 320, Appl
c 165	22	0.6	3501	1	US-08-524-757-5	Sequence 5, Appl	238	20	0.5	3137	4	US-09-620-311D-714	Sequence 714, Appl
c 166	22	0.6	3502	4	US-09-976-594-659	Sequence 659, Appl	c 239	20	0.5	3195	4	US-09-254-594-1	Sequence 1, Appl
c 167	22	0.6	3909	4	US-09-016-434-1119	Sequence 1119, Ap	240	20	0.5	3223	2	US-08-620-694A-9	Sequence 9, Appl
c 168	22	0.6	4262	4	US-09-521-511C-10	Sequence 10, Appl	241	20	0.5	3223	3	US-09-022-255-9	Sequence 9, Appl
c 169	22	0.6	9997	1	US-08-246-982A-15	Sequence 15, Appl	242	20	0.5	3223	3	US-09-022-666-9	Sequence 9, Appl
c 170	22	0.6	9997	1	US-08-453-265-15	Sequence 15, Appl	243	20	0.5	3223	3	US-08-978-773-3	Sequence 3, Appl
c 171	22	0.6	10103	2	US-08-457-273B-7	Sequence 7, Appl	244	20	0.5	3223	3	US-09-022-253-9	Sequence 9, Appl
c 172	21	0.5	21	4	US-09-688-188B-58	Sequence 58, Appl	245	20	0.5	3223	3	US-09-022-260-9	Sequence 9, Appl
c 173	21	0.5	21	4	US-09-291-417D-58	Sequence 58, Appl	246	20	0.5	3223	3	US-09-022-259-9	Sequence 9, Appl

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248	20	0.5	3223	4	US-09-549-679-9	Sequence 9, Appli	c 321	19	0.5	2103	3	US-09-190-476B-5	Sequence 5, Appli
249	20	0.5	3715	3	US-09-041-886-10	Sequence 10, Appli	c 322	19	0.5	2103	3	US-09-190-476B-7	Sequence 7, Appli
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251	20	0.5	3985	4	US-10-164-595-3	Sequence 3, Appli	c 324	19	0.5	2103	3	US-09-190-889A-7	Sequence 7, Appli
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256	20	0.5	4262	4	US-09-521-511C-10	Sequence 10, Appli	c 329	19	0.5	2289	2	US-08-461-379A-30	Sequence 30, Appli
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258	20	0.5	4296	4	US-09-723-458-3	Sequence 3, Appli	c 331	19	0.5	2289	3	US-08-463-074B-30	Sequence 30, Appli
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270	19	0.5	250	3	US-08-929-208-16	Sequence 16, Appli	c 343	19	0.5	2946	3	US-08-463-074B-7	Sequence 7, Appli
271	19	0.5	250	4	US-09-568-315-16	Sequence 16, Appli	c 344	19	0.5	2946	3	US-08-465-585C-7	Sequence 7, Appli
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273	19	0.5	265	4	US-09-491-356C-14	Sequence 14, Appli	c 346	19	0.5	2946	4	US-08-481-659C-1	Sequence 1, Appli
274	19	0.5	265	4	US-09-491-356C-16	Sequence 16, Appli	c 347	19	0.5	2984	5	PCT-US93-00893-2	Sequence 1, Appli
275	19	0.5	265	4	US-09-491-356C-17	Sequence 17, Appli	c 348	19	0.5	2984	5	PCT-US93-00893-2	Sequence 2, Appli
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279	19	0.5	301	3	US-08-905-223-267	Sequence 267, App	c 352	19	0.5	3302	4	US-09-620-312D-475	Sequence 475, Appli
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282	19	0.5	504	3	US-09-328-111-123	Sequence 123, App	c 355	19	0.5	3879	3	US-08-916-352-1	Sequence 1, Appli
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285	19	0.5	590	4	US-09-118-627-67	Sequence 67, Appli	c 358	19	0.5	4250	4	US-09-706-594-6	Sequence 6, Appli
286	19	0.5	590	4	US-09-602-877A-67	Sequence 67, Appli	c 359	19	0.5	4279	3	US-09-041-886-6	Sequence 6, Appli
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292	19	0.5	795	4	US-09-404-879A-86	Sequence 86, Appli	c 365	19	0.5	5630	2	US-08-937-931-1	Sequence 1, Appli
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294	19	0.5	795	4	US-09-215-681-86	Sequence 86, Appli	c 367	19	0.5	5630	4	US-09-709-126-1	Sequence 1, Appli
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688	18	0.5	7498	2	US-08-816-693A-1	Sequence 1, Appl	17	0.4	68	1	US-08-704-744-23	Sequence 23, Appl
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691	18	0.5	8252	1	US-08-046-585-15	Sequence 15, Appl	17	0.4	69	1	US-08-374-641-2	Sequence 2, Appl
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## ALIGNMENTS

## RESULT 1

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US-09-688-188B-11
; Sequence 11, Application US/09688188B
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; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
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; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 4133
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-688-188B-11
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Query Match 45.2%; Score 1787; DB 4; Length 4133;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2177; Conservative 0; Mismatches 3; Indels 3; Gaps 1;
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Qy 3245 AAGTGAAGAAAGAGAGGCTGACCAACGCTGGGGGACATGAGGGCTTCGGGCACTAC 3304  
Db 3281 AAGTGAAGAAAGAGAGGCTGACCAACGCTGGGGGACATGAGGGCTTCGGGCACTAC 3340  
Qy 3305 GTGTGTGAAATACAGCGGATTTAAGTTCTGTGTATGCGCTTCAAGAGCTTCGTGAGG 3364  
Db 3341 GTGTGTGAAATACAGCGGATTTAAGTTCTGTGTATGCGCTTCAAGAGCTTCGTGAGG 3400  
Qy 3365 TGTATGCTGGGGCCCCCAACCTTACCAAAATTCAATGCTTCAAGTCTTTGCGGAC 3424  
Db 3401 TGTATGCTGGGGCCCCCAACCTTACCAAAATTCAATGCTTCAAGTCTTTGCGGAC 3460  
Qy 3425 TCCCCACCGGCTCTGTGTGTGACCTGACATGACAGAGGGGAGCGGCTCAAGTCA 3484  
Db 3461 TCCCCACCGGCTCTGTGTGTGACCTGACATGACAGAGGGGAGCGGCTCAAGTCA 3520  
Qy 3485 TCTATGCTCCAGTCTGTGTGTGACCTGACATGACAGAGGGGAGCGGCTCAAGTCA 3544  
Db 3521 TCTATGCTCCAGTCTGTGTGTGACCTGACATGACAGAGGGGAGCGGCTCAAGTCA 3580  
Qy 3545 TCTATGCTCCAGTCTGTGTGTGACCTGACATGACAGAGGGGAGCGGCTCAAGTCA 3604  
Db 3581 TCTATGCTCCAGTCTGTGTGTGACCTGACATGACAGAGGGGAGCGGCTCAAGTCA 3640  
Qy 3605 AACACGAGGAGATGAGTGTGTGTGACAGAGGAGTGTCAACGCAACAGT 3664  
Db 3641 AACACGAGGAGATGAGTGTGTGTGACAGAGGAGTGTCAACGCAACAGT 3700  
Qy 3665 ACGGCGCATCATTAAGATGTGTGTGTGACAGTGGGGGAGATGCTTCTGTGGCT 3724  
Db 3701 ACGGCGCATCATTAAGATGTGTGTGTGACAGTGGGGGAGATGCTTCTGTGGCT 3760  
Qy 3725 ACATGTCTCCAAACAGATTAATGGGCTGGGGTGAAGAACATTGAGATCCGCTTGTGG 3784  
Db 3761 ACATGTCTCCAAACAGATTAATGGGCTGGGGTGAAGAACATTGAGATCCGCTTGTGG 3820  
Qy 3785 AGACGGGCGACCTGACAGGGGCTTCATGCAAAAGAGCTCAGAGGCTCAAGTTCCGT 3844  
Db 3821 AGACGGGCGACCTGACAGGGGCTTCATGCAAAAGAGCTCAGAGGCTCAAGTTCCGT 3880  
Qy 3845 GTGAGCGGAATGACAAAGGTGTTTTTGTGCTCAGTCCGCTTGGGGGAGAGCCAAAGTT 3904  
Db 3881 GTGAGCGGAATGACAAAGGTGTTTTTGTGCTCAGTCCGCTTGGGGGAGAGCCAAAGTT 3940  
Qy 3905 ACTTCATGACTCTGAACCGTAAAC 3927  
Db 3941 ACTTCATGACTCTGAACCGTAAAC 3963

RESULT 2  
US-09-291-417D-11

; Sequence 11, Application US/09291417D  
; Patent No. 6680170  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHITE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 038602/0329  
; CURRENT APPLICATION NUMBER: US/09/291,417D  
; CURRENT FILING DATE: 1999-04-13  
; PRIOR APPLICATION NUMBER: 60/081,784

; PRIOR FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 4133  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-291-417D-11

Query Match 45.2%; Score 1787; DB 4; Length 4133;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2177; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

Qy 1745 AGTCCCTGACAGACCAAGCCCAACCCGAAACCTGTGCTTCCGACCTCCCATACCCG 1804  
Db 1784 AGTCCCTGACAGACCAAGCCCAACCCGAAACCTGTGCTTCCGACCTCCCATACCCG 1843  
Qy 1805 ACCCTGACATCCCGGACACCACTGACAGGCCAGTGCAGAGAGCTGTCAATCCGACGA 1864  
Db 1844 ACCCTGACATCCCGGACACCACTGACAGGCCAGTGCAGAGAGCTGTCAATCCGACGA 1903  
Qy 1865 ATTCAAGACCCGACCTTGAAGAGACTGTGACAGGCCGAAATCCCGACCTGGGTCCGC 1924  
Db 1904 ATTCAAGACCCGACCTTGAAGAGACTGTGACAGGCCGAAATCCCGACCTGGGTCCGC 1963  
Qy 1925 CAGATTAAGAGAGCCCAACCCGAAAGTGCCTGACAGAGACTCAATCTATGCGCACTGCCCTTA 1984  
Db 1964 CAGATTAAGAGAGCCCAACCCGAAAGTGCCTGACAGAGACTCAATCTATGCGCACTGCCCTTA 2023  
Qy 1985 AACACAGTGGGGGAGAGGTCCTGCGCAAGCCGACAGAGTCCGTGCGCAGACTCGACGA 2044  
Db 2024 AACACAGTGGGGGAGAGGTCCTGCGCAAGCCGACAGAGTCCGTGCGCAGACTCGACGA 2083  
Qy 2045 ACTCCGCTGGCAATCTATCTGCAAAAGCGGGGAGAGCGGGCAACCCCAAGCTTCAG 2104  
Db 2084 ACTCCGCTGGCAATCTATCTGCAAAAGCGGGGAGAGCGGGCAACCCCAAGCTTCAG 2143  
Qy 2105 GGGCCCCCTGCTACAGCCCCCTGTGGCCCCGCAACGCTTCTAGTAACCCCGACCTCAGAGGA 2164  
Db 2144 GGGCCCCCTGCTACAGCCCCCTGTGGCCCCGCAACGCTTCTAGTAACCCCGACCTCAGAGGA 2203  
Qy 2165 GCGACCTGGGTGGGAAACGCTCGGACAGAGCTCTTCCAGCTCTCAAGGCACTCCCTG 2224  
Db 2204 GCGACCTGGGTGGGAAACGCTCGGACAGAGCTCTTCCAGCTCTCAAGGCACTCCCTG 2263  
Qy 2225 AGGCTGCTCACTGAGAGCGAACCAGTGGAGCTCTCCAACTGACAGCTCCCTG 2284  
Db 2264 AGGCTGCTCACTGAGAGCGAACCAGTGGAGCTCTCCAACTGACAGCTCCCTG 2323  
Qy 2285 TGTCTCTCCCTGGGAAATTAAGCCCAAGCCGACACACGCTCAAGGCTCAGGCGGCTCG 2344  
Db 2324 TGTCTCTCCCTGGGAAATTAAGCCCAAGCCGACACACGCTCAAGGCTCAGGCGGCTCG 2383  
Qy 2345 CAGACTTGTGTGCTGTAAGAGCGGACTGTGACAGAGGCCCTTCGGCTTCCAAAGAG 2404  
Db 2384 CAGACTTGTGTGCTGTAAGAGCGGACTGTGACAGAGGCCCTTCGGCTTCCAAAGAG 2443  
Qy 2405 CCATGACTACTGCTGTCTGACAGAGAGTGAAGCAGTGAAGACGACGAGAGAG 2464  
Db 2444 CCATGACTACTGCTGTCTGACAGAGAGTGAAGCAGTGAAGACGACGAGAGAG 2503  
Qy 2465 GCGAAGGCGGGCGACGAGAGGAGACAGATACCTCTGGGGGCGGACGATGAGGATA 2524  
Db 2504 GCGAAGGCGGGCGACGAGAGGAGACAGATACCTCTGGGGGCGGACGATGAGGATA 2560  
Qy 2525 CAGACAGGTCAGACCAATGATGTGTCCAGAGCGTCCAGAGATCACCGGAGACCCAGGCC 2584  
Db 2561 CAGACAGGTCAGACCAATGATGTGTCCAGAGCGTCCAGAGATCACCGGAGACCCAGGCC 2620  
Qy 2585 CATACGGGGGCGGACCAATGATGTGTCCAGAGCGCACCCTGAAGAGAGCGAACTGTGTC 2644  
Db 2621 CATACGGGGGCGGACCAATGATGTGTCCAGAGCGCACCCTGAAGAGAGCGAACTGTGTC 2680

QY 2645 ATGCTAGCAGCAATGGGTACACAACTGCTGAGTGTCTCCAGCCCACTGACCA 2704  
DB 2661 ATGCTAGCAGCAATGGGTACACAACTGCTGAGTGTCTCCAGCCCACTGACCA 2740  
QY 2705 CCGAGAACGCAAGGCGCAAGCCCACTCGAAGATGGAGTGTGACTACAGTCTC 2764  
DB 2741 CCGAAGACGCAAGGCGCAAGCCCACTCGAAGATGGAGTGTGACTACAGTCTC 2800  
QY 2765 GTGGGCTGGTAAGGCGCCCTGGCAAGAGCTGTTCAACGATGTTGATCTAGGAGATCT 2824  
DB 2801 GTGGGCTGGTAAGGCGCCCTGGCAAGAGCTGTTCAACGATGTTGATCTAGGAGATCT 2860  
QY 2825 ACCAGCTGAGAGCAGTGGGGAAGAGTCCCATCAACAGCCCTAGTGGTGAAGAGGA 2884  
DB 2861 ACCAGCTGAGAGCAGTGGGGAAGAGTCCCATCAACAGCCCTAGTGGTGAAGAGGA 2920  
QY 2885 CTGGGCTGACCAAGCTGCAATACAGCTGAGAGAGGTTCTGTGTTCAACGTTGATCCCA 2944  
DB 2921 CTGGGCTGACCAAGCTGCAATACAGCTGAGAGAGGTTCTGTGTTCAACGTTGATCCCA 2980  
QY 2945 CCAAGACCCGGGCGCAAGTGAAGCCCTGAGATCCGGAAGTCAAGAGAGGATTCACACT 3004  
DB 2981 CCAAGACCCGGGCGCAAGTGAAGCCCTGAGATCCGGAAGTCAAGAGAGGATTCACACT 3040  
QY 3005 CCGAGATCCTCTGTGAGAGCCTTTGGGGGGTCAACCTGTGTGGGCAAGAGAGCGGAC 3064  
DB 3041 CCGAGATCCTCTGTGAGAGCCTTTGGGGGGTCAACCTGTGTGGGCAAGAGAGCGGAC 3100  
QY 3065 TGATGTTGCTGAGACCGAAGTGGGCAAGGTTGATGAGACTCATTTGGGCGGACGCT 3124  
DB 3101 TGATGTTGCTGAGACCGAAGTGGGCAAGGTTGATGAGACTCATTTGGGCGGACGCT 3160  
QY 3125 TCCAGAGATGAGATGCTGAGAGGGGCTCAACCTGTCTCATCAATCTGAGGAAAGGA 3184  
DB 3161 TCCAGAGATGAGATGCTGAGAGGGGCTCAACCTGTCTCATCAATCTGAGGAAAGGA 3220  
QY 3185 ACAAACTGCGGGTGTATTAATCTGCTGCTCGGCAAGATTTGCAAAATGACCCAG 3244  
DB 3221 ACAAACTGCGGGTGTATTAATCTGCTGCTCGGCAAGATTTGCAAAATGACCCAG 3280  
QY 3245 AAGTGAGAGAGAGCAGGGCTGAGCAACGTTGGGGGACATGAGGGGCTCGGGCACTTACC 3304  
DB 3281 AAGTGAGAGAGAGCAGGGCTGAGCAACGTTGGGGGACATGAGGGGCTCGGGCACTTACC 3340  
QY 3305 GTGTTGTAATACAGCGGATTAAGTCTGCTGATCGCCCTCAAGAGCTCGTGGAGAG 3364  
DB 3341 GTGTTGTAATACAGCGGATTAAGTCTGCTGATCGCCCTCAAGAGCTCGTGGAGAG 3400  
QY 3365 TGTATGCTGGGCGCCCAACCTTACCAAAATTCATGAGCTTTCAGTCCGAGC 3424  
DB 3401 TGTATGCTGGGCGCCCAACCTTACCAAAATTCATGAGCTTTCAGTCCGAGC 3460  
QY 3425 TCCGCCAGCGGCTCTGTGCTGCTGAGACTGACAGTGAAGAGGGGCGCTCAAGGTCA 3484  
DB 3461 TCCGCCAGCGGCTCTGTGCTGCTGAGACTGACAGTGAAGAGGGGCGCTCAAGGTCA 3520  
QY 3485 TCTATGAGCTCAGTGTGCTTCAAGCTGAGATGCTGAGCTCGGGGAGCAGCTATGACA 3544  
DB 3521 TCTATGAGCTCAGTGTGCTTCAAGCTGAGATGCTGAGCTCGGGGAGCAGCTATGACA 3580  
QY 3545 TCTATGAGCTCAGTGTGCTTCAAGAGCCAGATCAAGCCCATGATCTTCTCCCA 3604  
DB 3581 TCTATGAGCTCAGTGTGCTTCAAGAGCCAGATCAAGCCCATGATCTTCTCCCA 3640  
QY 3605 ACAACGAGCGGATGAGATGCTGTGCTGCTACAGAGAGAGGAGTCTTCAAGTCAACGCT 3664  
DB 3641 ACAACGAGCGGATGAGATGCTGTGCTGCTACAGAGAGAGGAGTCTTCAAGTCAACGCT 3700  
QY 3665 AGGGGCGCATTAAGATGAGTGTGCTGAGTGGGGGAGATGCTTACTTCTGTGGCCT 3724  
DB 3701 AGGGGCGCATTAAGATGAGTGTGCTGAGTGGGGGAGATGCTTACTTCTGTGGCCT 3760  
QY 3725 ACATCTGCTCAACAGATTAATGGGCTGGGGTGAAGAACCATTTGAGATCCGCTGTGCTG 3784

DB 3761 ACATCTGCTCAACAGATTAATGGGCTGGGGTGAAGAGCATTTGAGATCCGCTGTGCTG 3820  
QY 3785 AGAGGCGCACCTGACAGGGGCTTTATGATGACCAACAGAGCTCAAGGCTCAAGTTCCTGT 3844  
DB 3821 AGAGGCGCACCTGACAGGGGCTTTATGATGACCAACAGAGCTCAAGGCTCAAGTTCCTGT 3880  
QY 3845 GTGAGCGGATGACAGGTTGTTTGGCTGAGTCCGCTGTGGGGCAGAGCCAAATTT 3904  
DB 3881 GTGAGCGGATGACAGGTTGTTTGGCTGAGTCCGCTGTGGGGCAGAGCCAAATTT 3940  
QY 3905 ACTTATGATCTGTAACCGTTAAC 3927  
DB 3941 ACTTATGATCTGTAACCGTTAAC 3963

## RESULT 3

US-09-579-664B-1  
; Sequence 1, Application US/09579664B  
; Patent No. 6514719  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Vitica, G. Duke  
; APPLICANT: Martin, Unja  
; APPLICANT: Anderson, Dirk M.  
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES  
; FILE REFERENCE: 2923-A  
; CURRENT APPLICATION NUMBER: US/09/579,664B  
; CURRENT FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 896  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-579-664B-1

## Query Match

Best Local Similarity 1.2%; Score 47; DB 4; Length 896;  
Pred. No. 3.8e-11;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ATGGGCGACCCAGCCCGCGAGCTGAGCAGATGACCTGTC 53  
DB 71 ATGGGCGACCCAGCCCGCGAGCTGAGCAGATGACCTGTC 117

## RESULT 4

US-09-976-594-368  
; Sequence 368, Application US/09976594  
; Patent No. 6673549  
; GENERAL INFORMATION:  
; APPLICANT: Burness, Michael  
; APPLICANT: Buchinder, Jemmy  
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
; FILE REFERENCE: PA-0041 US  
; CURRENT APPLICATION NUMBER: US/09/976,594  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/240,409  
; NUMBER OF SEQ ID NOS: 1143  
; SOFTWARE: PERL Program  
; SEQ ID NO 368  
; LENGTH: 2913  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6673549 2125081CB1  
US-09-976-594-368

## Query Match

Best Local Similarity 0.8%; Score 31; DB 4; Length 2913;  
Pred. No. 0.00043;



Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 566 CTTTCATTGGAGCTCCCTACTGATGCTCC 596  
Db 545 CTTTCATTGGAGCTCCCTACTGATGCTCC 575

## RESULT 5

US-08-864-038A-1/c  
Sequence 1, Application US/08864038A  
Patent No. 6001592

GENERAL INFORMATION:

APPLICANT: Kunio NAKASHIMA et al.

TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID

TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING

TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY

TITLE OF INVENTION: TO SAID POLYPEPTIDE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: 812-5 Hirano

STREET: Ieshinden

CITY: Tsu-city

STATE: Mie-prefecture

COUNTRY: JAPAN

ZIP: 514-01

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: Microsoft Windows 95

SOFTWARE: Word Perfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/864, 038A

FILING DATE: May 28, 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 8-184459

FILING DATE: 15-July-1996

ATTORNEY/AGENT INFORMATION:

NAME: C. Bruce Hamburg

REGISTRATION NUMBER: 22,389

REFERENCE/DOCKET NUMBER: F-5610

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)986-2340

TELEFAX: (212)953-7733

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2214

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

ORGANISM: Pinctada fucata

CELL TYPE: mantle epithelial cell

US-08-864-038A-1

Query Match 0.7%; Score 29; DB 3; Length 2214;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 6

US-08-864-038A-2/c  
Sequence 2, Application US/08864038A  
Patent No. 6001592

GENERAL INFORMATION:

APPLICANT: Kunio NAKASHIMA et al.

TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID

TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING

TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY

TITLE OF INVENTION: TO SAID POLYPEPTIDE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: 812-5 Hirano

STREET: Ieshinden

CITY: Tsu-city

STATE: Mie-prefecture

COUNTRY: JAPAN

ZIP: 514-01

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: Microsoft Windows 95

SOFTWARE: Word Perfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/864, 038A

FILING DATE: May 28, 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 8-184459

FILING DATE: 15-July-1996

ATTORNEY/AGENT INFORMATION:

NAME: C. Bruce Hamburg

REGISTRATION NUMBER: 22,389

REFERENCE/DOCKET NUMBER: F-5610

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)986-2340

TELEFAX: (212)953-7733

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 3331

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA to mRNA

ORIGINAL SOURCE:

ORGANISM: Pinctada fucata

CELL TYPE: mantle epithelial cell

FEATURE: mRNA

LOCATION: from 1 to 3331

IDENTIFICATION METHOD: E (by experiment)

US-08-864-038A-2

Query Match 0.7%; Score 29; DB 3; Length 3331;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 7

US-08-864-038A-4/c  
Sequence 4, Application US/08864038A  
Patent No. 6001592

GENERAL INFORMATION:

APPLICANT: Kunio NAKASHIMA et al.

TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID

TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING

TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: 812-5 Hirano

STREET: Ieshinden

CITY: Tsu-city

STATE: Mie-prefecture

COUNTRY: JAPAN

ZIP: 514-01

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage

COMPUTER: IBM Compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Word Perfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/864,038A  
FILING DATE: May 28, 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-184459  
FILING DATE: 15-July-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: C. Bruce Hamburg  
REGISTRATION NUMBER: 22,389  
REFERENCE/DOCKET NUMBER: F-5610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 986-2340  
TELEFAX: (212) 953-7733  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3331  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: Pinctada fucata  
CELL TYPE: mantle epithelial cell  
FEATURE:  
NAME/KEY: CDS  
LOCATION: from 50 to 2263  
IDENTIFICATION METHOD: P (by similarity to some other pattern)  
US-08-864-038A-4

Query Match 0.7%; Score 29; DB 3; Length 3331;  
Best Local Similarity 100.0%; Pred. No. 0.0033;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1120 CAGCAGCAGCTGCAGCAGCAGCAGCAGCG 1148  
DB 1706 CAGCAGCAGCTGCAGCAGCAGCAGCAGCG 1678

RESULT 8  
US-09-976-594-560  
Sequence 560, Application US/09976594  
Patent No. 6673549  
GENERAL INFORMATION:  
APPLICANT: Furness, Michael  
APPLICANT: Buchbinder, Jenny  
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
FILE REFERENCE: PA-0041 US  
CURRENT APPLICATION NUMBER: US/09/976,594  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 60/240,409  
PRIOR FILING DATE: 2000-10-12  
NUMBER OF SEQ ID NOS: 1143  
SOFTWARE: PERL Program  
SEQ ID NO 560  
LENGTH: 8411  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. 6673549 1327024.5  
NAME/KEY: unsure  
LOCATION: 8361, 8372, 8381, 8388, 8398, 8405-8406  
OTHER INFORMATION: a, t, c, g, or other  
US-09-976-594-560

Query Match 0.7%; Score 27; DB 4; Length 8411;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1118 AGCAGCAGCAGCTGCAGCAGCAGCAGCAGC 1144

DB 4073 AGCAGCAGCAGCTGCAGCAGCAGCAGCAGC 4099

RESULT 9  
US-09-043-303-14  
Sequence 14, Application US/09043303  
Patent No. 6251589  
GENERAL INFORMATION:  
APPLICANT: TSUI, Shoji  
APPLICANT: SANPEI, Kazujiro  
TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Ataxia Type 2 and  
TITLE OF INVENTION: Primers Therefor  
FILE REFERENCE: 0760-0241P  
CURRENT APPLICATION NUMBER: US/09/043,303  
CURRENT FILING DATE: 1998-05-18  
EARLIER APPLICATION NUMBER: PCT/JP96/01999  
EARLIER FILING DATE: 1996-07-18  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 57  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-043-303-14

Query Match 0.7%; Score 26; DB 3; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.084;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1443 GCAGCAGCAGCAACAGCAGCAGCAGCAGC 1468  
DB 9 GCAGCAGCAGCAACAGCAGCAGCAGCAGC 34

RESULT 10  
US-09-043-303-13  
Sequence 13, Application US/09043303  
Patent No. 6251589  
GENERAL INFORMATION:  
APPLICANT: TSUI, Shoji  
APPLICANT: SANPEI, Kazujiro  
TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Ataxia Type 2 and  
TITLE OF INVENTION: Primers Therefor  
FILE REFERENCE: 0760-0241P  
CURRENT APPLICATION NUMBER: US/09/043,303  
CURRENT FILING DATE: 1998-05-18  
EARLIER APPLICATION NUMBER: PCT/JP96/01999  
EARLIER FILING DATE: 1996-07-18  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13  
LENGTH: 69  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-043-303-13

Query Match 0.7%; Score 26; DB 3; Length 69;  
Best Local Similarity 100.0%; Pred. No. 0.083;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1443 GCAGCAGCAGCAACAGCAGCAGCAGCAGC 1468  
DB 30 GCAGCAGCAGCAACAGCAGCAGCAGCAGC 55

RESULT 11  
US-09-043-303-10  
Sequence 10, Application US/09043303  
Patent No. 6251589  
GENERAL INFORMATION:  
APPLICANT: TSUI, Shoji  
APPLICANT: SANPEI, Kazujiro

```

; TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Ataxia Type 2 and
; TITLE OF INVENTION: Primers Therefor
; FILE REFERENCE: 0760-0241P
; CURRENT APPLICATION NUMBER: US/09/043,303
; EARLIER FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: PCT/JP96/01999
; EARLIER FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 75
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-043-303-10

Query Match          0.7%; Score 26; DB 3; Length 75;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1443 GCAGCAGCAGCAACAGCAGCAGCAGC 1468
Db      15   GCAGCAGCAGCAACAGCAGCAGCAGC 40

RESULT 12
US-09-043-303-11
; Sequence 11, Application US/09043303
; Patent No. 6251589
; GENERAL INFORMATION:
; APPLICANT: TSUJI, Shoji
; APPLICANT: SANPEI, Kazuhiro
; TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Ataxia Type 2 and
; TITLE OF INVENTION: Primers Therefor
; FILE REFERENCE: 0760-0241P
; CURRENT APPLICATION NUMBER: US/09/043,303
; CURRENT FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: PCT/JP96/01999
; EARLIER FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 17
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US-09-043-303-11

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; Sequence 12, Application US/09043303
; Patent No. 6251589
; GENERAL INFORMATION:
; APPLICANT: TSUJI, Shoji
; APPLICANT: SANPEI, Kazuhiro
; TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Ataxia Type 2 and
; TITLE OF INVENTION: Primers Therefor
; FILE REFERENCE: 0760-0241P
; CURRENT APPLICATION NUMBER: US/09/043,303
; CURRENT FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: PCT/JP96/01999
; EARLIER FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
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; TYPE: DNA
; ORGANISM: Homo sapiens
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Query Match          0.7%; Score 26; DB 3; Length 78;
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; Sequence 75, Application US/09205995
; Patent No. 6368855
; GENERAL INFORMATION:
; APPLICANT: Xu, Minzhen
; APPLICANT: Qiu, Gang
; APPLICANT: Humphreys, Robert
; TITLE OF INVENTION: CANCER CELL VACCINE
; FILE REFERENCE: U.S. Application 09/205,995, (CIP)
; CURRENT APPLICATION NUMBER: US/09/205,995
; CURRENT FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: 09/036,746
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: 08/661,627
; PRIOR FILING DATE: 1996-06-11
; NUMBER OF SEQ ID NOS: 79
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; OTHER INFORMATION: Description of Artificial Sequence: Reverse gene
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US-09-205-995-75

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; Sequence 72, Application US/09205995
; Patent No. 6368855
; GENERAL INFORMATION:
; APPLICANT: Xu, Minzhen
; APPLICANT: Qiu, Gang
; APPLICANT: Humphreys, Robert
; TITLE OF INVENTION: CANCER CELL VACCINE
; FILE REFERENCE: U.S. Application 09/205,995, (CIP)
; CURRENT APPLICATION NUMBER: US/09/205,995
; CURRENT FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: 09/036,746
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: 08/661,627
; PRIOR FILING DATE: 1996-06-11
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; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: Reverse gene  
; OTHER INFORMATION: construct corresponding to a specific region of  
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US-09-205-995-72

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GenCore version 5.1.6  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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588	20	0.5	3132	15	US-10-341-434-183	Sequence 183, App	661	20	19	10	US-09-291-417-62	Sequence 62, Appl
589	20	0.5	3132	15	US-10-341-434-197	Sequence 197, App	662	20	21	13	US-09-789-390-50	Sequence 50, Appl
590	20	0.5	3132	15	US-10-085-117-167	Sequence 167, App	663	20	22	13	US-10-028-415-27	Sequence 27, Appl
591	20	0.5	3137	14	US-10-037-270-714	Sequence 714, App	664	19	49	15	US-10-148-835-23	Sequence 23, Appl
592	20	0.5	3137	15	US-10-117-722-714	Sequence 714, App	665	19	58	14	US-10-215-432-36	Sequence 36, Appl
593	20	0.5	3148	14	US-10-317-835-7	Sequence 7, Appl1	666	19	65	14	US-10-032-585-2138	Sequence 2138, Ap
594	20	0.5	3148	14	US-10-317-835-15	Sequence 15, Appl	667	19	67	14	US-10-106-698-3325	Sequence 3325, Ap
595	20	0.5	3188	15	US-10-320-797-106	Sequence 106, App	668	19	97	9	US-09-864-761-22933	Sequence 22933, A
596	20	0.5	3195	14	US-10-300-834-1	Sequence 1, Appl1	669	19	102	9	US-09-864-761-22363	Sequence 22363, A
597	20	0.5	3231	15	US-10-375-592A-2	Sequence 2, Appl1	670	19	117	9	US-09-864-761-10735	Sequence 565, App
598	20	0.5	3238	10	US-09-870-133-1	Sequence 1, Appl1	671	19	174	9	US-09-878-178-565	Sequence 565, App
599	20	0.5	3238	14	US-10-160-501-4	Sequence 4, Appl1	672	19	174	13	US-10-046-935-565	Sequence 565, App





965 19 0.5 2294 14 US-10-227-884-181 Sequence 181, App  
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983 19 0.5 2294 14 US-10-180-543-283 Sequence 283, App  
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992 19 0.5 2294 14 US-10-181-012-283 Sequence 283, App  
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995 19 0.5 2294 14 US-10-184-635-283 Sequence 283, App  
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997 19 0.5 2294 14 US-10-184-646-283 Sequence 283, App  
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## ALIGNMENTS

RESULT 1  
US-10-029-115-1  
; Sequence 1, Application US/10029115  
; Publication No. US2003007597A1  
; GENERAL INFORMATION:  
; APPLICANT: Luo, Ying  
; APPLICANT: Fu, Alan C  
; APPLICANT: Shen, Mary  
; TITLE OF INVENTION: No. US2003007597A1e1 Germinal Center Kinase Cell Cycle Proteins,  
; FILE REFERENCE: A-70229/RMS/DHR  
; CURRENT APPLICATION NUMBER: US/10/029,115  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 1  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-029-115-1

Query Match 100.0%; Score 3951; DB 14; Length 3951;  
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 3951; Conservative 0;

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DB 1 GCCCTTATGGGAGCCAGCCCGCCGAGCTGAGAGATCGACCTGTCGGCCCTG 60  
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QY 361 AACCAAAAGGCAACGCTTGAAGAGAGATGATGCTGTGTGTGTGTGTGTGTGTGTGT 420  
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DB CAGCAG 1200



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RESULT 3  
US-09-291-417-11  
; Sequence 11, Application US/09291417A  
; Publication No. US20030050230A1  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY

APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: MYHE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 240/300  
; CURRENT APPLICATION NUMBER: US/09/291.417A  
; CURRENT FILING DATE: 1999-04-13  
; EARLIER APPLICATION NUMBER: US 60/081,784  
; EARLIER FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: FastSeq For Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 4133  
; TYPE: DNA  
; ORGANISM: Mammalian (Human) ZC3  
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Matches 2177; Conservative 0; Mismatches 3; Indels 3; Gaps 1;  
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Qy 2525 CAGACAGCTGCAAGCAATGTGTCTCAAGAGCTGAGAGATCAAGCGGAGCCAGGCC 2584

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Db 2561 CAGACAGGTGACGACACATGCTGCTCAAGACGTGAGAGATCAACCGGAGCCAGCCCC 2620
Oy 2565 CATACGGGCGGCGGACCATGCTGCTCAAGCCGACCCCTGAGAGAGAGCGGAACTGCTGC 2644
Db 2621 CATACGGGCGGCGGACCATGCTGCTCAAGCCGACCCCTGAGAGAGAGCGGAACTGCTGC 2680
Oy 2645 ATGCTGACAGGCAATGGGTACAAACCTGCTGAGTGTGAGCCGACGCTGACCCA 2704
Db 2681 ATGCTGACAGGCAATGGGTACAAACCTGCTGAGTGTGAGCCGACGCTGACCCA 2740
Oy 2705 CCGAGAACGCAAAAGCCCAACCCCTCGAAGATGGAGTGTGATCAACAGTCTC 2764
Db 2741 CCGAGAACGCAAAAGCCCAACCCCTCGAAGATGGAGTGTGATCAACAGTCTC 2800
Oy 2765 GTGGCTGTGTAAGGCCCCCTGCGACAGAGTCTTCAACGATGTTTGTGATCTAGGATCT 2824
Db 2801 GTGGCTGTGTAAGGCCCCCTGCGACAGAGTCTTCAACGATGTTTGTGATCTAGGATCT 2860
Oy 2825 ACCAGCTGGAGGCAAGTGGGGAAGAGTCCCATGACAGCCCTAGTGGGTGGAGAGGCA 2884
Db 2861 ACCAGCTGGAGGCAAGTGGGGAAGAGTCCCATGACAGCCCTAGTGGGTGGAGAGGCA 2920
Oy 2885 CTGGCTCGACCACTGACAGTACGAGCTGAGAGAGGTTCTGTGCTCAACGTGAATCCCA 2944
Db 2921 CTGGCTCGACCACTGACAGTACGAGCTGAGAGAGGTTCTGTGCTCAACGTGAATCCCA 2980
Oy 2945 CCAACACCCGGGCGGACCATGAGACCCCTGAGATCCGGAAGTACAAAGACGATTCACCT 3004
Db 2981 CCAACACCCGGGCGGACCATGAGACCCCTGAGATCCGGAAGTACAAAGACGATTCACCT 3040
Oy 3005 CCGACATCTCTGTGAGGCTTGTGGGGGGTCAACCTGTGTGGGCAAGGAAAGGGC 3064
Db 3041 CCGACATCTCTGTGAGGCTTGTGGGGGGTCAACCTGTGTGGGCAAGGAAAGGGC 3100
Oy 3065 TGATGTTGTCGACCGAAGTGGGCAAGGAGTGTATGATCTCATTTGGCGGCAAGCT 3124
Db 3101 TGATGTTGTCGACCGAAGTGGGCAAGGAGTGTATGATCTCATTTGGCGGCAAGCT 3160
Oy 3125 TCCAGACATGATGTGCTGAGAGGGGCTCAACCTGTCTATCAACATCTCAAGGAAAGGA 3184
Db 3161 TCCAGACATGATGTGCTGAGAGGGGCTCAACCTGTCTATCAACATCTCAAGGAAAGGA 3220
Oy 3185 ACAAACCTGGGGTGTATTAACCTGCTCGGGAACAAAGTTCTGCAACATGACCCAG 3244
Db 3221 ACAAACCTGGGGTGTATTAACCTGCTCGGGAACAAAGTTCTGCAACATGACCCAG 3280
Oy 3245 AAGTGAGAGAGAGAGGCTGAGCCACCGTGGGGGCAATGAGGGCTGCGGGCACTACC 3304
Db 3281 AAGTGAGAGAGAGAGGCTGAGCCACCGTGGGGGCAATGAGGGCTGCGGGCACTACC 3340
Oy 3305 GTGTTGTGAATAACGACCGGATTAAGTTCTGTCTATCCGCTCAAGAGCTCCGTGGAGG 3364
Db 3341 GTGTTGTGAATAACGACCGGATTAAGTTCTGTCTATCCGCTCAAGAGCTCCGTGGAGG 3400
Oy 3365 TGTATGCTGGGGCCCCCAACCTTACCAAAATTCATGAGCTTCAAGTCTTTGGCGAGC 3424
Db 3401 TGTATGCTGGGGCCCCCAACCTTACCAAAATTCATGAGCTTCAAGTCTTTGGCGAGC 3460
Oy 3425 TCCCCCAGCGGCTCTGCTGTGCTGACCTGACAGTAGAGAGGGGCGAGCGGCTCAAGGTCA 3484
Db 3461 TCCCCCAGCGGCTCTGCTGTGCTGACCTGACAGTAGAGAGGGGCGAGCGGCTCAAGGTCA 3520
Oy 3485 TCTATGCTGCAAGTGTGCTTCTCATGCTGTGATGTCATCTCGGGGAAACAGTATGACA 3544
Db 3521 TCTATGCTGCAAGTGTGCTTCTCATGCTGTGATGTCATCTCGGGGAAACAGTATGACA 3580
Oy 3545 TCTATGCTGCTGAGTGCATCCAGAGCAGATCAAGCCCATGCGCAATCTTCTCCCA 3604
Db 3581 TCTATGCTGCTGAGTGCATCCAGAGCAGATCAAGCCCATGCGCAATCTTCTCCCA 3640
Oy 3605 ACACGAGGAGATGAGATGCTGCTGTGCTACGAGAGAGGGGTGTCTACACAGCT 3664
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Db 3641 ACACGAGGAGATGAGATGCTGCTGTGCTACGAGAGCAGAGGTGTCTACACAGCT 3700
Oy 3665 ACAGGCGCATATTAAGAGATGTGAGTGTGAGTGGGGGAGATGCTACTTCTGTGGCT 3724
Db 3701 ACAGGCGCATATTAAGAGATGTGAGTGTGAGTGGGGGAGATGCTACTTCTGTGGCT 3760
Oy 3725 ACATCTGCTCCACAGATTAATGGGCTGGGGGTGAGAAAGCCATTGAGATCCGCTGTGG 3784
Db 3761 ACATCTGCTCCACAGATTAATGGGCTGGGGGTGAGAAAGCCATTGAGATCCGCTGTGG 3820
Oy 3785 AGACGGGCTACCTGACCGGGGCTTTCATGCAACAAAGCTCAGAGGCTCAAGTTCCTGT 3844
Db 3821 AGACGGGCTACCTGACCGGGGCTTTCATGCAACAAAGCTCAGAGGCTCAAGTTCCTGT 3880
Oy 3845 GTGAGCGGATGACAAAGGTGTTTGTGCTCAGTCCGCTGAGGGGAGAGCCAGTTT 3904
Db 3881 GTGAGCGGATGACAAAGGTGTTTGTGCTCAGTCCGCTGAGTCCGCTGAGGGGAGAGCCAGTTT 3940
Oy 3905 ACTTCATGACTCTGAACCGTAAC 3927
Db 3941 ACTTCATGACTCTGAACCGTAAC 3963

RESULT 4
US-10-441-281-30
; Sequence 30, Application US/10441281
; Publication No. US20030228618A1
; GENERAL INFORMATION:
; APPLICANT: Levanon Erez, et al.
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR IDENTIFYING NATURALLY OCCURRING ANTISENSE
; FILE REFERENCE: 02/26133
; CURRENT APPLICATION NUMBER: US/10/441,281
; PRIOR FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US 09/718,407
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: US 09/732,938
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/785,439
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: US 09/907,923
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 009/993,398
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 10/201,605
; PRIOR FILING DATE: 2002-07-24
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 4863
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-441-281-30

Query Match 42.7%; Score 1689; DB 15; Length 4863;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1739; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 7 ATGGCGACCCAGCCCGCCCGCCGAGCTGAGACGACATGACCTTCCGCTTGGGGAGC 66
Db 185 ATGGCGACCCAGCCCGCCCGCCGAGCTGAGACGACATGACCTTCCGCTTGGGGAGC 244
Oy 67 CCTGCTGGGATCTTGAAGTGTGAGGTTGTCGCAATGGAACCTACGAGAGGTATC 126
Db 245 CCTGCTGGGATCTTGAAGTGTGAGGTTGTCGCAATGGAACCTACGAGAGGTATC 304
Oy 127 AAGGCTCGGCAATGTCAGACGCGGCGAGCTGCTGCCATCAAGTATGATGTCTACGAG 186
Db 305 AAGGCTCGGCAATGTCAGACGCGGCGAGCTGCTGCCATCAAGTATGATGTCTACGAG 364
Oy 187 GACGAGAGAGAGATCAACAGAGATCAACATGCTGAAAAGTACTTCTACACACCGC 246
Db 365 GACGAGAGAGAGATCAACAGAGATCAACATGCTGAAAAGTACTTCTACACACCGC 424
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OY	247	AAACATGCGCACTTACTAGAGAGCCTTTCAATCAAAGAGCCCCCGGGAAACGATGACAG	306
Db	425	AAACATGCGCACTTACTAGAGAGCCTTTCAATCAAAGAGCCCCCGGGAAACGATGACAG	484
OY	307	CTCTGAGCTGAGATGAGAGTTCTGTGGTGCTGGTTCAAGATCTGACCTGGTAAAGAACCA	366
Db	485	CTCTGAGCTGAGATGAGAGTTCTGTGGTGCTGGTTCAAGATCTGACCTGGTAAAGAACCA	544
OY	367	AAAGGCAACGCCCTGAGAGAGGACTGTATCGCTATATCTGCAAGGAGATCTCCAGGGGT	426
Db	545	AAAGGCAACGCCCTGAGAGAGGACTGTATCGCTATATCTGCAAGGAGATCTCCAGGGGT	604
OY	427	CTGGGCCCATCTCCATGAGCCCAAGAGGTATCCATGCAAGCATCAAGGGGCAAGATGTGCTG	486
Db	605	CTGGGCCCATCTCCATGAGCCCAAGAGGTATCCATGCAAGCATCAAGGGGCAAGATGTGCTG	664
OY	487	CTGACAGAGAAATGCTGAGGTCAAGCTAGTGAATTTTGGGGTGATGCTCAGCTGACCGC	546
Db	665	CTGACAGAGAAATGCTGAGGTCAAGCTAGTGAATTTTGGGGTGATGCTCAGCTGACCGC	724
OY	547	ACCGTGGGCAAGCGGAACACTTTCAATTGGGACTCCCTACTGGAATGGCTCCAGAGTCAATC	606
Db	725	ACCGTGGGCAAGCGGAACACTTTCAATTGGGACTCCCTACTGGAATGGCTCCAGAGTCAATC	784
OY	607	GCCTGTGATGAGAAACCTGATAGCCACTATGATTTACAGAGATGATATTTGGTCTTAGGA	666
Db	785	GCCTGTGATGAGAAACCTGATAGCCACTATGATTTACAGAGATGATATTTGGTCTTAGGA	844
OY	667	ATCAACGCCATCGAGATGGCAGAGGGAGCCCCCCTGTGTGACATSCACCCCAATGCGA	726
Db	845	ATCAACGCCATCGAGATGGCAGAGGGAGCCCCCCTGTGTGACATSCACCCCAATGCGA	904
OY	727	GCCCTCTTCATCTTCCTCGGAACCCCTCGCCAGAGCTCAAGTCCAAAGATGGTCTAAG	786
Db	905	GCCCTCTTCATCTTCCTCGGAACCCCTCGCCAGAGCTCAAGTCCAAAGATGGTCTAAG	964
OY	787	AAGTTCAATGACTTTCATTGAGACACATGTCTCATCAAGACTTACCTGAGCCGCCACCCACG	846
Db	965	AAGTTCAATGACTTTCATTGAGACACATGTCTCATCAAGACTTACCTGAGCCGCCACCCACG	1022
OY	847	GAGCAGCTACTGAAAGTTTCCCTTCAATCGGGACCAAGCCCAAGAGCGCAGTCCGCAATC	906
Db	1025	GAGCAGCTACTGAAAGTTTCCCTTCAATCGGGACCAAGCCCAAGAGCGCAGTCCGCAATC	1084
OY	907	CAGCTTAAGGACCAATGATCCGATCCCGGAAAGACGGGGTGAAAGAGAGGACACAGA	966
Db	1085	CAGCTTAAGGACCAATGATCCGATCCCGGAAAGACGGGGTGAAAGAGAGGACACAGA	1144
OY	967	TATAGATACAGCCGAGCGAGAGGAGAGATGACAGCAATGAGAGAAAGAGAGCCAAAGC	1028
Db	1145	TATAGATACAGCCGAGCGAGAGGAGAGATGACAGCAATGAGAGAAAGAGAGCCAAAGC	1204
OY	1027	TCCATCAATGAACGTGCTGAGAGAGTGCATCTGACGCCGGAGATTCTCCGGCTCCAGAG	1088
Db	1205	TCCATCAATGAACGTGCTGAGAGAGTGCATCTGACGCCGGAGATTCTCCGGCTCCAGAG	1264
OY	1087	GAATAATAGACCACTCAGAGGCTTTAAACACGACGACAGAGCTGACAGCAGCAGCAG	1148
Db	1265	GAATAATAGACCACTCAGAGGCTTTAAACACGACGACAGAGCTGACAGCAGCAGCAG	1324
OY	1147	CGAGACCCCGAGGCAACAATCAACACTGTGCAACAGCCGACAGCGCGCATAGAGAG	1208
Db	1325	CGAGACCCCGAGGCAACAATCAACACTGTGCAACAGCCGACAGCGCGCATAGAGAG	1384
OY	1207	CAGAAAGAGAGCGGCGCGCGCTGAGAGAGCAACAGCGCGGAGCCGGAGACAGCGGAAG	1266
Db	1385	CAGAAAGAGAGCGGCGCGCGCTGAGAGAGCAACAGCGCGGAGCCGGAGACAGCGGAAG	1444
OY	1267	CTGCAGAGAAAGAGCAGACGCGCGCTGAGAGACATGCAGAGCTTCTCGCGCGGAGAG	1328
Db	1445	CTGCAGAGAAAGAGCAGACGCGCGCTGAGAGACATGCAGAGCTTCTCGCGCGGAGAG	1504

QY	1327	GAGCGCGCGG	CAGCGCGGAGCGTGTAGCGAGGAATATACAGCGGAAAGCGACTGTGAGAGACACGCGG	1386
Db	1505	GAGCGCGCGG	CAGCGCGGAGCGCGAGCGAGACAGAAATACAAAGCGGAAGCGCTGAGAGAGACACGCGG	1564
QY	1387	CAGTCAGAAAGT	CTTCCAGAGGCGAGCTGAGCAGGAGGATGGCTTACCTTCAAGTCCCTGAG	1446
Db	1565	CAGTGTAGAACT	CTTCCAGAGGCGAGCTGTGAGGAGGATGGCTTACTTCTTCAAGTCCCTGAG	1624
QY	1447	CAGCAGCAAC	CAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCTTGCTGGGAGC	1506
Db	1625	CAGCAGCAAC	CAGCAGCAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCTTGCTGGGAGC	1684
QY	1507	AGGAAGCCCT	GTACATTATGTGTGGGGCATGTAACTCCCTGTACAAACCAAGCTGGGACC	1566
Db	1685	AGGAAGCCCT	GTACATTATGTGTGGGGCATGTAACTCCCTGTACAAACCAAGCTGGGACC	1744
QY	1567	CGAGAGGTAGA	GAGAGAGAACAAAGATATGAACAAGCAGCAGAACTCTCCCTTGGCCAAAGGC	1626
Db	1745	CGAGAGGTAGA	GAGAGAGAACAAAGATATGAACAAGCAGCAGAACTTCCCTTGGCCAAAGGC	1804
QY	1627	AAGCCAGGCA	GACGCGGCGCTTGAGCCCCCATGCCAGGCGTTCCCAAGGCGCCCGCAGAA	1686
Db	1805	AAGCCAGGCA	GACGCGGCGCTTGAGCCCCCATGCCAGGCGTTCCCAAGGCGCCCGCAGAA	1864
QY	1667	CCCTTTCCAGA	CTCTCTCTATGACAGAGCGGCTGAGCCCCCAGAGAGGACCGCACAG	1746
Db	1865	CCCTTTCCAGA	CTCTCTCTATGACAGAGCGGCTGAGCCCCCAGAGAGGACCGCACAG	1924

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RESULT 5
US-10-029-115-3
; Sequence 3, Application US/10029115
; Publication No. US20030077597A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Fu, Alan C
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: No. US20030077597A1 Germinal Center Kinase Cell Cycle Proteins
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: A-70229/RMS/DHR
; CURRENT APPLICATION NUMBER: US/10/029,115
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 4414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-029-115-3

Query Match      42.6%; Score 1683; DB 14; Length 4414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1683; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      64  GACCCCTGCGGATCTTTGAGCTTGTGAGGTGCGCAATGGACCTACGACAGTG 123
DB      101 GACCCCTGCGGATCTTTGAGCTTGTGAGGTGCGCAATGGACCTACGACAGTG 160

QY      124 TACAAAGGTGCGCATGTTCACAGACGGGGCAGCTGCTCCATCAAGTCATGGATGTACG 183
DB      161 TACAAAGGTGCGCATGTTCACAGACGGGGCAGCTGCTCCATCAAGTCATGGATGTACG 220

QY      184 GAGACGAGAGAGAAAGATCAACACAGAGATCAACATGCTGAAAAAGTACTCTCACAC 243
DB      221 GAGACGAGAGAGAAAGATCAACACAGAGATCAACATGCTGAAAAAGTACTCTCACAC 280

QY      244 CGCAACATCGCCACCTACTACGAGCCTTCATCAAGAAAGACCCCGGGAAACGATGAC 303
DB      281 CGCAACATCGCCACCTACTACGAGCCTTCATCAAGAAAGACCCCGGGAAACGATGAC 340

QY      304 CAGCTCTGCGCTGTGATGAGAGTTCTGTGTGTGCTGGTCAATGACTGACCTGTAAAGAC 363
DB      341 CAGCTCTGCGCTGTGATGAGAGTTCTGTGTGTGCTGGTCAATGACTGACCTGTAAAGAC 400

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364 ACAAAGGCAAGCCCTGAGAGGAGCTGATGCTATATCTGAGAGGAGATCTCTCAGG 423  
401 ACAAAGGCAAGCCCTGAGAGGAGCTGATGCTATATCTGAGAGGAGATCTCTCAGG 460  
424 GGTCTGGCCCATCTCTCATGCCCCCAAGAGTGATCCATGAGACATCAAGGGGCAAGATGTG 483  
461 GGTCTGGCCCATCTCTCATGCCCCCAAGAGTGATCCATGAGACATCAAGGGGCAAGATGTG 520  
484 CTGCTGACAGAAATGCTGAGAGTCAAGCTAGTGAATTTTGGGGTGAAGTCTCAGCTGAGC 543  
521 CTGCTGACAGAAATGCTGAGAGTCAAGCTAGTGAATTTTGGGGTGAAGTCTCAGCTGAGC 580  
544 CGCACCTGGGAGAGAGGCACTTTTCATTTGGGAACTCCCTACTGATGCTCTCAGAGATCT 603  
581 CGCACCTGGGAGAGAGGCACTTTTCATTTGGGAACTCCCTACTGATGCTCTCAGAGATCT 640  
604 ATGCTCTGTGATGAGAACTCTGATGCACTTATGATTAAGAGATGATATTTGGTCTCTA 663  
641 ATGCTCTGTGATGAGAACTCTGATGCACTTATGATTAAGAGATGATATTTGGTCTCTA 700  
664 GGAATCAAGCCATGAGATGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 723  
701 GGAATCAAGCCATGAGATGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 760  
724 CGAGCCCTCTCTCTCATTTCTCGGAACTCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 783  
761 CGAGCCCTCTCTCTCATTTCTCGGAACTCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 820  
784 AAGAAATTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 843  
821 AAGAAATTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 880  
844 AAGAAATTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 903  
881 AAGAAATTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 940  
904 ATTCAGCTTAAAGAGACCACTTGAACGATCCCGGAGAGGAGGAGGAGGAGGAGGAGGAGG 963  
941 ATTCAGCTTAAAGAGACCACTTGAACGATCCCGGAGAGGAGGAGGAGGAGGAGGAGGAGG 1000  
964 GAATATGATGATGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1023  
1001 GAATATGATGATGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1060  
1024 AACTCCTATGATGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1083  
1061 AACTCCTATGATGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1120  
1084 CAGGAAATTAAGAGCACTCAGAGGCTTTAAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1143  
1121 CAGGAAATTAAGAGCACTCAGAGGCTTTAAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1180  
1144 CAGCGAGACCCCGAGGAGCAGATCAAAACCTGCTGACACGAGCGAGCGGCGCATAGAG 1203  
1181 CAGCGAGACCCCGAGGAGCAGATCAAAACCTGCTGACACGAGCGAGCGGCGCATAGAG 1240  
1204 GAGCAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1263  
1241 GAGCAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1300  
1264 AAGCTGTCAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1323  
1301 AAGCTGTCAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1360  
1324 GAGGAGCGGAGCAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1383  
1361 GAGGAGCGGAGCAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1420  
1384 CGGCACTGAGAAAGTCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1443  
1421 CGGCACTGAGAAAGTCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1480

1444 CAGCAGAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1503  
1481 CAGCAGAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1540  
1504 GAGCAGAGCCCTCTGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTAT 1563  
1541 GAGCAGAGCCCTCTGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTAT 1600  
1564 GCCCGAGAGTGAAG 1623  
1601 GCCCGAGAGTGAAG 1660  
1624 AGCAAGCCAGGAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1683  
1661 AGCAAGCCAGGAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1720  
1684 GAGCCCTTTCCAGAGCTCTCTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1743  
1721 GAGCCCTTTCCAGAGCTCTCTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1780  
1744 AAG 1746  
1781 AAG 1783

RESULT 6  
US-09-789-390-12  
Sequence 12, Application US/09789390  
Publication No. US20030059768A1  
GENERAL INFORMATION:  
APPLICANT: Vermet, Corine  
APPLICANT: Fernandes, Elma  
APPLICANT: MacDougall, John  
APPLICANT: Shinkets, Richard A  
APPLICANT: Spaderna, Steven K  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: 15966-692  
CURRENT APPLICATION NUMBER: US/09/789,390  
CURRENT FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 60/185,548  
PRIOR FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: 60/199,957  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: 60/184,951  
PRIOR FILING DATE: 2000-02-25  
PRIOR APPLICATION NUMBER: 60/185,967  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: 60/197,723  
PRIOR FILING DATE: 2000-04-18  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 12  
LENGTH: 3735  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1) .. (3732)  
US-09-789-390-12  
Query Match 40.5%; Score 1599; DB 10; Length 3735;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
2347 GACTTTGTTGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2406  
2137 GACTTTGTTGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2196  
2407 ATGACTACTGCTGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2466  
2197 ATGACTACTGCTGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2256  
2467 GAGGCGGAGCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2526



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Db 2257 |GAAGCGGCGCCGACGAGAGGAGGAGATACCCCTGGGGGCGGACGATGGGATAC 2316
Qy 2257 |GACACGCTCAGACCATGGTGTGTCAAGACGTGAGAGATGACCGGAGCCGACCCCA 2586
Db 2317 |GACAGCGTCAGACCATGGTGTGTCAAGACGTGAGAGATGACCGGAGCCGACCCCA 2376
Qy 2317 |TACGGGGGCGGACCATGGTGTGTCAAGGACCCCTGAAAGAGAGACCGAACTGTGCAT 2646
Db 2317 |TACGGGGGCGGACCATGGTGTGTCAAGGACCCCTGAAAGAGAGACCGAACTGTGCAT 2436
Qy 2647 |GCTGACAGCAATGGGTACCAAAACCTGCTGACGTGTGTCAGCCGACCTACCCACC 2706
Db 2437 |GCTGACAGCAATGGGTACCAAAACCTGCTGACGTGTGTCAGCCGACCTACCCACC 2496
Qy 2707 |GAGAACAGCAAAAGCCCAAGCCCACTTGAGAGATGGAGATGATACCAAGTCTGCT 2766
Db 2497 |GAGAACAGCAAAAGCCCAAGCCCACTTGAGAGATGGAGATGATACCAAGTCTGCT 2556
Qy 2767 |GGGCGGTGTAAGGCCCCCTGGCAAGCTGTTCACGATGTTTGTGATCTAGGGATCTAC 2826
Db 2557 |GGGCGGTGTAAGGCCCCCTGGCAAGCTGTTCACGATGTTTGTGATCTAGGGATCTAC 2616
Qy 2827 |CAGCGCTGAGGCGATGGGGAGACGATCCCGCATCAGGCGCTTGTGGGTGAGAGGGCACT 2886
Db 2617 |CAGCGCTGAGGCGATGGGGAGACGATCCCGCATCAGGCGCTTGTGGGTGAGAGGGCACT 2676
Qy 2887 |CGGCTGACAGCTGACAGTGCAGTGAAGAGGGTCTGTGTGTCAAGTGAATCCAC 2946
Db 2677 |CGGCTGACAGCTGACAGTGCAGTGAAGAGGGTCTGTGTGTCAAGTGAATCCAC 2736
Qy 2947 |AACACCGCGGCGCCACAGTGAAGACCCCTGAGATCCGGAAGTACAAAGCGATTCACCTCC 3006
Db 2737 |AACACCGCGGCGCCACAGTGAAGACCCCTGAGATCCGGAAGTACAAAGCGATTCACCTCC 2796
Qy 3007 |GAGATCTCTGTGTGACGCGCTTTGGGGGGGTCAACCTGTGTGTGGGACGGAAGACGCGGCTG 3066
Db 2797 |GAGATCTCTGTGTGACGCGCTTTGGGGGGGTCAACCTGTGTGTGGGACGGAAGACGCGGCTG 2856
Qy 3067 |ATGTTGCTGACCGAAGTGGGCGCAAGGTGTATGACTCATTTGGGCGGGAAGCGCTTC 3126
Db 2857 |ATGTTGCTGACCGAAGTGGGCGCAAGGTGTATGACTCATTTGGGCGGGAAGCGCTTC 2916
Qy 3127 |CAGCAGATGATGTGTGTGAGAGGGGTCAACCTGTGTGTATCAACATTCAGGGAAAAAGAAC 3186
Db 2917 |CAGCAGATGATGTGTGTGAGAGGGGTCAACCTGTGTGTATCAACATTCAGGGAAAAAGAAC 2976
Qy 3187 |AAACGCGGGGTATTAACCTGTGTGTGCGCGGGAACAAGATTCTGCAATGACCAAGAA 3246
Db 2977 |AAACGCGGGGTATTAACCTGTGTGTGCGCGGGAACAAGATTCTGCAATGACCAAGAA 3036
Qy 3247 |GTGAGAGAGAGAGAGGGGTGACCAACGTTGGGGGACATGAGAGGGCTGGCGGCACTACCGT 3306
Db 3037 |GTGAGAGAGAGAGAGGGGTGACCAACGTTGGGGGACATGAGAGGGCTGGCGGCACTACCGT 3096
Qy 3307 |GTTGTGAAATACGAGCGGATTAAGTTCTGTGTGTATGCGCTTCAAGAGCTCCGTGAGGTG 3366
Db 3097 |GTTGTGAAATACGAGCGGATTAAGTTCTGTGTGTATGCGCTTCAAGAGCTCCGTGAGGTG 3156
Qy 3367 |TATGCTGTGGGGCCCCCAAAACCCCTACCAAAATTCATAGGCGCTTCAAGCTTCGACCTC 3426
Db 3157 |TATGCTGTGGGGCCCCCAAAACCCCTACCAAAATTCATAGGCGCTTCAAGCTTCGACCTC 3216
Qy 3427 |CCCCACCGCCCTGTGCTGTGTGTGACCTGACAGTGAAGAGAGGGGACGCGCTCAAGGTGATC 3486
Db 3217 |CCCCACCGCCCTGTGCTGTGTGTGACCTGACAGTGAAGAGAGGGGACGCGCTCAAGGTGATC 3276
Qy 3487 |TATGCTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3546
Db 3277 |TATGCTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3336
Qy 3547 |TACATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3606
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Db 3337 |TACATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3396
Qy 3607 |ACCGACGGCATGAGATGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3666
Db 3397 |ACCGACGGCATGAGATGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3456
Qy 3667 |GGGGGCATATTAAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3726
Db 3457 |GGGGGCATATTAAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3516
Qy 3727 |ATTCGCTTCAACAGATTAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3786
Db 3517 |ATTCGCTTCAACAGATTAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3576
Qy 3787 |ACGGGCCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3846
Db 3577 |ACGGGCCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3636
Qy 3847 |GAGGGGAATGACAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3906
Db 3637 |GAGGGGAATGACAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3696
Qy 3907 |TTCATGACTCTGAACCGTAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3945
Db 3697 |TTCATGACTCTGAACCGTAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3735

RESULT 7
US-09-789-390-10
; Sequence 10, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
; APPLICANT: Verneet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: MacDougall, John
; APPLICANT: Shinkets, Richard A
; APPLICANT: Spaderna, Steven X
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-692
; CURRENT APPLICATION NUMBER: US/09/789,390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185,548
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/199,957
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/184,951
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/185,967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/197,723
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 3822
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (3819)
; US-09-789-390-10

Query Match 40.5%; Score 1599; DB 10; Length 3822;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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2467 GAAAGCGGGCCAGAGAGGAGAGAGATACCCCTGGGGGCGCAGCATGGGATACA 2526  
 2344 GAAAGCGGGCCAGAGAGGAGAGAGATACCCCTGGGGGCGCAGCATGGGATACA 2403  
 2527 GACAGCGTCAGAGATGGTGGTCCAGAGATGATCCGGGACCCAGCCCA 2586  
 2404 GACAGCGTCAGAGATGGTGGTCCAGAGATGATCCGGGACCCAGCCCA 2463  
 2587 TACGGGGGCGGACATGGTGGTCCAGAGATGATCCGGGACCCAGCCCA 2646  
 2464 TACGGGGGCGGACATGGTGGTCCAGAGATGATCCGGGACCCAGCCCA 2523  
 2647 GCTGACAGCATGGGATCAACAACCTGCTGAGTGGTCCAGAGATGATCCAGC 2706  
 2524 GCTGACAGCATGGGATCAACAACCTGCTGAGTGGTCCAGAGATGATCCAGC 2583  
 2707 GAGAACAGCAAGGCGCAAGGCCCTGCTGAGAGATGGAGTGGTCACTACAGTCT 2766  
 2584 GAGAACAGCAAGGCGCAAGGCCCTGCTGAGAGATGGAGTGGTCACTACAGTCT 2643  
 2767 GGGCGTGTAAAGGCGCCCTGGCAAGAGCTGTTCAAGATGTTGGATCTAGAGAT 2826  
 2644 GGGCGTGTAAAGGCGCCCTGGCAAGAGCTGTTCAAGATGTTGGATCTAGAGAT 2703  
 2827 CAGCTGAGGAGGAGTGGGAGAGATCCCATCAAGAGCTGAGTGGAGAGGAGCT 2886  
 2704 CAGCTGAGGAGGAGTGGGAGAGATCCCATCAAGAGCTGAGTGGAGAGGAGCT 2763  
 2887 CAGCTGAGGAGGAGTGGGAGAGATCCCATCAAGAGCTGAGTGGAGAGGAGCT 2946  
 2764 CAGCTGAGGAGGAGTGGGAGAGATCCCATCAAGAGCTGAGTGGAGAGGAGCT 2823  
 2947 AACACCGGGGCGCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3006  
 2824 AACACCGGGGCGCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2883  
 3007 GAGATCTCTGTGAG 3066  
 2884 GAGATCTCTGTGAG 2943  
 3067 ATGTTGCTGAG 3126  
 2944 ATGTTGCTGAG 3003  
 3127 CAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3186  
 3004 CAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3063  
 3187 AACACCGGGGCGCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3246  
 3064 AACACCGGGGCGCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3123  
 3247 GTGAG 3306  
 3124 GTGAG 3183  
 3307 GTTGTGAATTAAG 3366  
 3184 GTTGTGAATTAAG 3243  
 3367 TATGCTGGGGCGCCCAACCTTACCAATTCATGAGTCTTTTCCAGCTC 3426  
 3244 TATGCTGGGGCGCCCAACCTTACCAATTCATGAGTCTTTTCCAGCTC 3303  
 3427 CCCCAACCGGCTCTGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3486  
 3304 CCCCAACCGGCTCTGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3363  
 3487 TATGCTCTGAG 3546  
 3364 TATGCTCTGAG 3423

3547 TACATCCCTGTGACATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3606  
 3424 TACATCCCTGTGACATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3483  
 3607 ACCGAGGAG 3666  
 3484 ACCGAGGAG 3543  
 3667 GGGCGCATCTTAAG 3726  
 3544 GGGCGCATCTTAAG 3603  
 3727 ATCTGCTCAACAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3786  
 3604 ATCTGCTCAACAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3663  
 3787 AGGGCGCATCTTAAG 3846  
 3664 AGGGCGCATCTTAAG 3723  
 3847 GAGCGAGATGACAAAGTGTGTTTGTGCTGAGTGGGAGAGAGAGAGAGAGAGAGAG 3906  
 3724 GAGCGAGATGACAAAGTGTGTTTGTGCTGAGTGGGAGAGAGAGAGAGAGAGAGAG 3783  
 3907 TTGATGACTGTGACAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 3945  
 3784 TTGATGACTGTGACAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 3822

## RESULT 8

US-09-789-390-8  
 ; Sequence 8, Application US/09789390  
 ; Publication No. US20030059768A1

## GENERAL INFORMATION:

APPLICANT: Vernet, Corine  
 APPLICANT: Fernandes, Elma  
 APPLICANT: MacDougall, John  
 APPLICANT: Shinkels, Richard A  
 APPLICANT: Spaderna, Steven K  
 TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
 FILE REFERENCE: 15966-692

CURRENT APPLICATION NUMBER: US/09/789,390  
 PRIOR FILING DATE: 2001-02-23  
 PRIOR APPLICATION NUMBER: 60/185,548  
 PRIOR FILING DATE: 2000-02-28  
 PRIOR APPLICATION NUMBER: 60/199,957  
 PRIOR FILING DATE: 2000-04-27  
 PRIOR APPLICATION NUMBER: 60/184,951  
 PRIOR FILING DATE: 2000-02-25  
 PRIOR APPLICATION NUMBER: 60/185,967  
 PRIOR FILING DATE: 2000-03-01  
 PRIOR APPLICATION NUMBER: 60/197,723  
 PRIOR FILING DATE: 2000-04-18  
 NUMBER OF SEQ ID NOS: 77  
 SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 8  
 LENGTH: 3912  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)..(3909)  
 US-09-789-390-8

Query Match 40.5%; Score 1599; DB 10; Length 3912;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2347 GACTTGTGTTGCTGAAG 2406  
 2314 GACTTGTGTTGCTGAAG 2373  
 2407 ATGAGACTACTGTCGTCTCAG 2466

Db 2374 ATGSACTACTCTGTGTCCAGCGAGAGGTGAAAACAGTGAAGACGACGACGAGAGAGGAC 2433  
Qy 2467 GAAGGCGGCGCAGCAGAGAGGAGCAGAGATACCCCTGGGGGCGCAGGATGGGATACA 2526  
Db 2434 GAAGCGGGGCGCAGCAGAGAGGAGCAGAGATACCCCTGGGGGCGCAGGATGGGATACA 2493  
Qy 2527 GACAGCTCAGACACATGTGTGTCCAGAGTCCAGAGATACCGGGACCCAGCCCCCA 2586  
Db 2494 GACAGCTCAGACACATGTGTGTCCAGAGTCCAGAGATACCGGGACCCAGCCCCCA 2553  
Qy 2587 TACGGGGGCGCAGCAGAGTGTGTCCAGGCGACCCCTGAAGAGAGCGGACCTGTGCAT 2646  
Db 2554 TACGGGGGCGCAGCAGAGTGTGTCCAGGCGACCCCTGAAGAGAGCGGACCTGTGCAT 2613  
Qy 2647 GCTGACAGCAATGGGTACACAACTGTGTGTCCAGGCGACCCAGCCTCAACCCAC 2706  
Db 2614 GCTGACAGCAATGGGTACACAACTGTGTGTCCAGGCGACCCAGCCTCAACCCAC 2673  
Qy 2707 GAGAACAGCAAAAGCCCAAGCCCTTCGAAGATGGGATGGTGACTACAGTCTTGT 2766  
Db 2674 GAGAACAGCAAAAGCCCAAGCCCTTCGAAGATGGGATGGTGACTACAGTCTTGT 2733  
Qy 2767 GGGCTGGTAAAGGCGCCTGGCAAGAGCTGTTCAGATGTTTGTGATCTAGGGATCTAC 2826  
Db 2734 GGGCTGGTAAAGGCGCCTGGCAAGAGCTGTTCAGATGTTTGTGATCTAGGGATCTAC 2793  
Qy 2827 CAGCCTGAGAGCAGTGGGAGCAGCATCCCATCA CAGCCTGATGGGTGAGAGAGGCACT 2886  
Db 2794 CAGCCTGAGAGCAGTGGGAGCAGCATCCCATCA CAGCCTGATGGGTGAGAGAGGCACT 2853  
Qy 2887 CGGCTCGACCACTGCTGACGATGACGTGAGAGAGGTTTGTGTGTCAACGTGAATCCAC 2946  
Db 2854 CGGCTCGACCACTGCTGACGATGACGTGAGAGAGGTTTGTGTGTCAACGTGAATCCAC 2913  
Qy 2947 AACACCGGGGCGCAGTGAAGCCCTGAGATCCGGAAGTCAAGAAAGCATTAACCTCC 3006  
Db 2914 AACACCGGGGCGCAGTGAAGCCCTGAGATCCGGAAGTCAAGAAAGCATTAACCTCC 2973  
Qy 3007 GAGATCTCTGTGAGGCTTTTGGGGGCTCAACCTGTGTGTGGCAGCAGAGACGGGCTG 3066  
Db 2974 GAGATCTCTGTGAGGCTTTTGGGGGCTCAACCTGTGTGTGGCAGCAGAGACGGGCTG 3033  
Qy 3067 ATGTGCTGGAACCGAAGTGGGCAAGGCTGTATGATCTCATTTGGGCGGACGCTTC 3126  
Db 3034 ATGTGCTGGAACCGAAGTGGGCAAGGCTGTATGATCTCATTTGGGCGGACGCTTC 3093  
Qy 3127 CAGCAGTGGATGCTGAGAGGGCTCAACCTGTGCATCAACATCTCAGGGAAAAAGAAC 3186  
Db 3094 CAGCAGTGGATGCTGAGAGGGCTCAACCTGTGCATCAACATCTCAGGGAAAAAGAAC 3153  
Qy 3187 AAACCTGGGGGTATTACTGTCTGTGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3246  
Db 3154 AAACCTGGGGGTATTACTGTCTGTGCTCCGGAACAAGATTCTGCACAATGACCCAGAA 3213  
Qy 3247 GTGGAAGAAAGCAGGGCTGGAACAAGTGGGGGACATGAGGGCTGCGGCACTACCGT 3306  
Db 3214 GTGGAAGAAAGCAGGGCTGGAACAAGTGGGGGACATGAGGGCTGCGGCACTACCGT 3273  
Qy 3307 GTTGTGAATAACGAGCGGATTAAGTTCCTGTGCATCCGCCCTCAAGAGCTCCGTGAAGTG 3366  
Db 3274 GTTGTGAATAACGAGCGGATTAAGTTCCTGTGCATCCGCCCTCAAGAGCTCCGTGAAGTG 3333  
Qy 3367 TATGCTGGGCGCCCAACCTTACCAAAATTCAATGGCTTCAAGTCTTTGCCGACCTC 3426  
Db 3334 TATGCTGGGCGCCCAACCTTACCAAAATTCAATGGCTTCAAGTCTTTGCCGACCTC 3393  
Qy 3427 CCCCACGCGCTCTGTGTGTGACCTGACATGAGAGAGGGGCAAGCGCTCAAGGTCAATC 3486  
Db 3394 CCCCACGCGCTCTGTGTGTGACCTGACATGAGAGAGGGGCAAGCGCTCAAGGTCAATC 3453  
Qy 3487 TATGCTCAAGTGTGGCTTCAATGCTGTGATGTGCACTGGGGAAACAGTATGACATC 3546

Db 3454 TATGCTCAAGTGTGGCTTCAATGCTGTGATGTGCACTGGGGAAACAGTATGACATC 3513  
Qy 3547 TACATCCCTGTGCACTTCAGAGCGCAATCAAGCCCATATGCTATCTTCTCCCAAC 3606  
Db 3514 TACATCCCTGTGCACTTCAGAGCGCAATCAAGCCCATATGCTATCTTCTCCCAAC 3573  
Qy 3607 ACCGAGGCAATGAGATGCTGTGCTGCTAAGAGGACGAGGGGTCTAGTCAACAGTAC 3666  
Db 3574 ACCGAGGCAATGAGATGCTGTGCTGCTAAGAGGACGAGGGGTCTAGTCAACAGTAC 3633  
Qy 3667 GGGCGCATTAAGATGTGTGTCTCAGTGGGGGAGATGCTTACTGTGGCTTAC 3726  
Db 3634 GGGCGCATTAAGATGTGTGTCTCAGTGGGGGAGATGCTTACTGTGGCTTAC 3693  
Qy 3727 ATCTGCTCAACCAAGATTAAGGCTGGGTGAGAAAGCATTGAGATCCGTCTGTGAG 3786  
Db 3694 ATCTGCTCAACCAAGATTAAGGCTGGGTGAGAAAGCATTGAGATCCGTCTGTGAG 3753  
Qy 3787 ACCGGCCACCTCGACGGGGTCTTCATGACAAACAGCTCAGAGGCTCAAGTTCTGTGT 3846  
Db 3754 ACCGGCCACCTCGACGGGGTCTTCATGACAAACAGCTCAGAGGCTCAAGTTCTGTGT 3813  
Qy 3847 GAGCGAATGACAAGGTGTTTGTCTCAGTCCGCTCTGGGGCAGCAGCAAGTTTAC 3906  
Db 3814 GAGCGAATGACAAGGTGTTTGTCTCAGTCCGCTCTGGGGCAGCAGCAAGTTTAC 3873  
Qy 3907 TTCAATGCTGAAACCGTAACTGCATCATGAATCTGTGA 3945  
Db 3874 TTCAATGCTGAAACCGTAACTGCATCATGAATCTGTGA 3912

RESULT 9  
US-09-789-390-6  
Sequence 6, Application US/09789390  
Publication No. US20030059768A1  
GENERAL INFORMATION:  
APPLICANT: Vermet, Corine  
APPLICANT: Fernandez, Elma  
APPLICANT: MacDougall, John  
APPLICANT: Shinkets, Richard A  
APPLICANT: Spaderna, Steven K  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: 15966-692  
CURRENT APPLICATION NUMBER: US/09/789,390  
CURRENT FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 60/185,548  
PRIOR FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: 60/199,957  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: 60/184,951  
PRIOR FILING DATE: 2000-02-25  
PRIOR APPLICATION NUMBER: 60/185,967  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: 60/197,723  
PRIOR FILING DATE: 2000-04-18  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 3999  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(3996)  
US-09-789-390-6  
Query Match 40.5%; Score 1599; DB 10; Length 3999;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2347 GACTTGTGTTGCTGAAGAGCGGACCTGCAAGAGGCGCCCTCGGCTCCCAAGAGGCC 2406  
Db 2401 GACTTGTGTTGCTGAAGAGCGGACCTGCAAGAGGCGCCCTCGGCTCCCAAGAGGCC 2460





Db	301	TTGGCTTGTGATGAGATTCTGTGTGTGCTGGTTCAGTGACTGACCTGGTAAAGAACAAATAA	360
QY	370	GGCAACCGCCCTGAAGAGGAGCTGTATCGCCTATATATTCGACGAGGAGATTCCTCAGGGGTC	429
Db	361	GGCAACGCCCTGAAGAGGAGCTGTATCGCCTATATATTCGACGAGGAGATTCCTCAGGGGTC	420
QY	430	GCCCATCTTCATATGCCCAAAAGGTGATTCATTCGAGACATCAAGGGGGAGAAATGTGCTGCTG	489
Db	421	GGCCATCTTCATATGCCCAAAAGGTGATTCATTCGAGACATCAAGGGGGAGAAATGTGCTGCTG	480
QY	490	ACAGAGAAATGCTGAGGTCTAAGCTAATGTGATTTTGTGGGGTGAAGTCTCAGCTGACCCGACC	549
Db	481	ACAGAGAAATGCTGAGGTCTAAGCTAATGTGATTTTGTGGGGTGAAGTCTCAGCTGACCCGACC	540
QY	550	GTGGGCAGACGGAAACATTTTCATTGGGACCTCCCTACTGATGATGGCTCCAGAGTCAATCGCC	609
Db	541	GTGGGCAGACGGAAACATTTTCATTGGGACCTCCCTACTGATGATGGCTCCAGAGTCAATCGCC	600
QY	610	TGTGTATGAGAACCCCTGATATGCCACTATATGATATACAGAGTGAATATTTTGTGTCTTAAGAAATC	669
Db	601	TGTGTATGAGAACCCCTGATATGCCACTATATGATATACAGAGTGAATATTTTGTGTCTTAAGAAATC	660
QY	670	ACAGCATGATGATGTGCAGAGGAGGCCCCCTCTGTGTGACATGCAACCCCATGCGAGCC	729
Db	661	ACAGCATGATGATGTGCAGAGGAGGCCCCCTCTGTGTGACATGCAACCCCATGCGAGCC	720
QY	730	CTCTTCTTCATTTCTTGGAACCCCTCCGCCAGGCTCAAGTCCAAAGAGTGTCTTAAGAAAG	789
Db	721	CTCTTCTTCATTTCTTGGAACCCCTCCGCCAGGCTCAAGTCCAAAGAGTGTCTTAAGAAAG	780
QY	790	TTCATTTGACTTCATTGACATATCTTCATCAACAATTACCTGAGCCGCCCAACCCACGAG	849
Db	781	TTCATTTGACTTCATTGACATATCTTCATCAACAATTACCTGAGCCGCCCAACCCACGAG	840
QY	850	CAGCTACTGAAGTTTCCCTTCACTCCGAGGACCAAGCCCAAGAGCGGACGATCCGCAATCCAG	909
Db	841	CAGCTACTGAAGTTTCCCTTCACTCCGAGGACCAAGCCCAAGAGCGGACGATCCGCAATCCAG	900
QY	910	CTTAAAGGACCAACTTGAACCGATCCCGAAGAGCGGGGTGAGAAAGAGAGACAAATAT	969
Db	901	CTTAAAGGACCAACTTGAACCGATCCCGAAGAGCGGGGTGAGAAAGAGAGACAAATAT	960
QY	970	GAGTACAGGGCGGACGACGAGAGAAAGATGACAGGCATGAGAGAGAGAGAGCCAAAGTCC	1020
Db	961	GAGTACAGGGCGGACGACGAGAGAAAGATGACAGGCATGAGAGAGAGAGAGCCAAAGTCC	1020
QY	1030	ATCATGAACGTGCTGTGAGAGTGTGATCTTACCGCCGGGAGTTTCTCCGGCTCCAGCAGGAA	1089
Db	1021	ATCATGAACGTGCTGTGAGAGTGTGATCTTACCGCCGGGAGTTTCTCCGGCTCCAGCAGGAA	1080
QY	1090	AATTAAGGCACTCAGAGGCTTTAAACAGCAGACAGCACTGTGACAGCAGCAGCGA	1149
Db	1081	AATTAAGGCACTCAGAGGCTTTAAACAGCAGACAGCACTGTGACAGCAGCAGCGA	1140
QY	1150	GACCCCGAGGCAACAATCAAAACACTGTCTGACCAAGCGGAGCGGCGCATATAGAGAGCAG	1220
Db	1141	GACCCCGAGGCAACAATCAAAACACTGTCTGACCAAGCGGAGCGGCGCATATAGAGAGCAG	1220
QY	1210	AAGGAGAGACCGGCGCGCTGTGAGAGCAACAGCGCGGAGCGGAGCGGAGCAGCTG	1289
Db	1201	AAGGAGAGACCGGCGCGCTGTGAGAGCAACAGCGCGGAGCGGAGCGGAGCAGCTG	1280
QY	1270	CAGAGAGAGAGCAGACGCGCGGCTGTGAGAGCAATGCAAGGCTCTGCGGCGGAGAGAGAG	1339
Db	1261	CAGAGAGAGAGAGCAGACGCGCGGCTGTGAGAGCAATGCAAGGCTCTGCGGCGGAGAGAGAG	1330
QY	1330	CGGCGGACGAGCGGAGCGG	1346
Db	1321	CGGCGGACGAGCGGAGCGG	1337

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US-09-789-390-69
/ Sequence 69, Application US/09789390
/ Publication No. US20030059768A1
/ GENERAL INFORMATION:
/ APPLICANT: Vernet, Corine
/ APPLICANT: Fernandes, Elma
/ APPLICANT: MacDougall, John
/ APPLICANT: Shimkets, Richard A
/ APPLICANT: Spaderna, Steven K
/ TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 15966-692
/ CURRENT APPLICATION NUMBER: US/09/789,390
/ CURRENT FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: 60/185,548
/ PRIOR FILING DATE: 2000-02-28
/ PRIOR APPLICATION NUMBER: 60/199,957
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: 60/184,951
/ PRIOR FILING DATE: 2000-02-25
/ PRIOR APPLICATION NUMBER: 60/185,967
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: 60/197,723
/ PRIOR FILING DATE: 2000-04-18
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 69
/ LENGTH: 1717
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-789-390-69

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Query Match	Similarity	33.8%	Score 1337	DB 10	Length 1717
Best Local	Similarity	100.0%	Pred. No. 0		
Matches 1337	Conservative	0	Mismatches	0	Indels
					Gaps
					0
QY	10	GGCGACCCAGCCCCCGCCCGCAGCTTGACGACATCGACTCTGTCCGCTTGCGGACCTT	69		
Db	1	GGCGACCCAGCCCCCGCCCGCAGCTTGACGACATCGACTCTGTCCGCTTGCGGACCTT	60		
QY	70	GCTGGGATCTTTGACCTTGTGGAGGTGGTGGCAATGGACCTACGACAGGTGTAAAG	129		
Db	61	GCTGGGATCTTTGACCTTGTGGAGGTGGTGGCAATGGACCTACGACAGGTGTAAAG	120		
QY	130	GCTCGGCATGTCMAAGCGGGGCACTGGCTGGCATCAAGGTCATGATGTCCGAGGAC	189		
Db	121	GCTCGGCATGTCMAAGCGGGGCACTGGCTGGCATCAAGGTCATGATGTCCGAGGAC	180		
QY	190	GAGGAGGAAGAGATCAACAGAGATCAACATGCTGAAGAAAGTACTTCCACACGGCAAC	249		
Db	181	GAGGAGGAAGAGATCAACAGAGATCAACATGCTGAAGAAAGTACTTCCACACGGCAAC	240		
QY	250	ATCGCACCTTACTACGAGACCTTTCATCAAGAGACCCCCCGGAGAAAGATGACCAAGCTC	309		
Db	241	ATCGCACCTTACTACGAGACCTTTCATCAAGAGAGACCCCCCGGAGAAAGATGACCAAGCTC	300		
QY	310	TGGCTGTGTATGAGTTCTGTGTGTCTGTTTACGTACTGACTCTGTGTAAAGAACCAAAA	369		
Db	301	TGGCTGTGTATGAGTTCTGTGTGTCTGTTTACGTACTGACTCTGTGTAAAGAACCAAAA	360		
QY	370	GGCAACGCCCTGAGAGAGACTGTATGCGCTATCTCTCAGGAGGATCCTCAGGGGTCTG	429		
Db	361	GGCAACGCCCTGAGAGAGACTGTATGCGCTATCTCTCAGGAGGATCCTCAGGGGTCTG	420		
QY	430	GGCCATCTTCATGCTCCCAACAGGTGATCCATCGAGACATCAAGGGGCAAGATGTGCTGCTG	489		
Db	421	GGCCATCTTCATGCTCCCAACAGGTGATCCATCGAGACATCAAGGGGCAAGATGTGCTGCTG	480		
QY	490	AAGAGAGATGCTGAGGTGAAGTAACTATGAGTTTGTGGGGTGAAGTCTCAGGTGACCGCAAC	549		
Db	481	AAGAGAGATGCTGAGGTGAAGTAACTATGAGTTTGTGGGGTGAAGTCTCAGGTGACCGCAAC	540		
QY	550	GTGGGACAGCGAGAACCTTTCATTGGGACTCCCTTACTGAGTGGCTCAAGGTCATCGCC	609		



Db 541 GTGGGACAGCGAACAACCTTTGATTTGAGATCCCTACTGATGAGTCCAGAGGTATCC 600  
Qy 610 TGTGATGGAACCCCTGATGCCACCTATGATTAACAGAGTGAATTTGGTCTCTAGGAATC 669  
Db 601 TGTATGGAACCCCTGATGCCACCTATGATTAACAGAGTGAATTTGGTCTCTAGGAATC 660  
Qy 670 ACAGCATCGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 729  
Db 661 ACAGCATCGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
Qy 730 CTCTTCCTCATCTCTCGGAACCCCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 789  
Db 721 CTCTTCCTCATCTCTCGGAACCCCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
Qy 790 TTCAATGACTTCAATGACATGATGTCATCAAGATTTACCTGAGGAGGAGGAGGAGGAG 849  
Db 781 TTCAATGACTTCAATGACATGATGTCATCAAGATTTACCTGAGGAGGAGGAGGAGGAG 840  
Qy 850 CAGGACTGAGATTTCCCTTATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 909  
Db 841 CAGGACTGAGATTTCCCTTATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900  
Qy 910 CTTAAGGACCAATTTGACCGATCCCGGAAGAGCGGGGTGAGAAAGAGAGAGAGATAT 969  
Db 901 CTTAAGGACCAATTTGACCGATCCCGGAAGAGCGGGGTGAGAAAGAGAGAGAGATAT 960  
Qy 970 GAGTACAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1029  
Db 961 GAGTACAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020  
Qy 1030 ATCAATGAACTGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1089  
Db 1021 ATCAATGAACTGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
Qy 1090 AATAAGAGCACTGAGAGGCTTTAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1149  
Db 1081 AATAAGAGCACTGAGAGGCTTTAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140  
Qy 1150 GACCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1209  
Db 1141 GACCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200  
Qy 1210 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1269  
Db 1201 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260  
Qy 1270 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1329  
Db 1261 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320  
Qy 1330 CGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1346  
Db 1321 CGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1337

RESULT 13  
US-09-789-390-66

; Sequence 66, Application US/09789390  
; Publication No. US20030059768A1  
; GENERAL INFORMATION:  
; APPLICANT: Vernet, Corine  
; APPLICANT: Fernandez, Elma  
; APPLICANT: MacDougall, John  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Spedden, Steven K  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 15966-692  
; CURRENT APPLICATION NUMBER: US/09/789,390  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 60/185,548  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: 60/199,957  
; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/184,951  
; PRIOR FILING DATE: 2000-02-25  
; PRIOR APPLICATION NUMBER: 60/185,967  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 60/197,723  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 66  
; LENGTH: 1787  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-789-390-66

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 70 GCTGGATCTTTGAGCTTGTGAGAGTGTGCGCAATGGAACCTACGAGCAGGTGTACAG 129  
Db 61 GCTGGATCTTTGAGCTTGTGAGAGTGTGCGCAATGGAACCTACGAGCAGGTGTACAG 120  
Qy 130 GGTGGCATGTCAAGACGGGCGAGCTGGCTCCATCAAGGTCAATGATGTCAAGAGGAG 189  
Db 121 GGTGGCATGTCAAGACGGGCGAGCTGGCTCCATCAAGGTCAATGATGTCAAGAGGAG 180  
Qy 190 GAGGAGGAGGATCAACAGGAGATCAACATGCTGAAAAAGTACTCACCAACGCAAC 249  
Db 181 GAGGAGGAGGATCAACAGGAGATCAACATGCTGAAAAAGTACTCACCAACGCAAC 240  
Qy 250 ATCCGCACTACTACGAGCCTTCATCAAGAGAGCCCGCGGAGAAAGATGACCACTC 309  
Db 241 ATCCGCACTACTACGAGCCTTCATCAAGAGAGCCCGCGGAGAAAGATGACCACTC 300  
Qy 310 TGGTGATGAGTGTGATGCTGTGTGCTGCTGATGATGATGATGATGATGATGATGAT 369  
Db 301 TGGTGATGAGTGTGATGCTGTGTGCTGCTGATGATGATGATGATGATGATGATGAT 360  
Qy 370 GGGGAGCCCTGAAAGGAGGAGCTGATGAGCTATATCGAGGAGGAGATCTCAGGGGCTG 429  
Db 361 GGGGAGCCCTGAAAGGAGGAGCTGATGAGCTATATCGAGGAGGAGATCTCAGGGGCTG 420  
Qy 430 GCCCATCTCATGCCCAAGAGTATCATGAGACATCAAGGGGAGAAATGTCTGTG 489  
Db 421 GCCCATCTCATGCCCAAGAGTATCATGAGACATCAAGGGGAGAAATGTCTGTG 480  
Qy 490 ACAGAGATGCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 549  
Db 481 ACAGAGATGCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 540  
Qy 550 GTGGGAGAGGAGCACTTTTCAATGGGAGCTCCCACTGAGTGTGCTCAGAGGTGATGCC 609  
Db 541 GTGGGAGAGGAGCACTTTTCAATGGGAGCTCCCACTGAGTGTGCTCAGAGGTGATGCC 600  
Qy 610 TGTGATGAGAACCTGATGCACTATGATTAACAGAGTAAATTTGGTCTCTAGGAATC 669  
Db 601 TGTGATGAGAACCTGATGCACTATGATTAACAGAGTAAATTTGGTCTCTAGGAATC 660  
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Db 661 ACAGCATCGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
Qy 730 CTCTTCCTCATCTCTCGGAACCCCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 789  
Db 721 CTCTTCCTCATCTCTCGGAACCCCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
Qy 790 TTCAATGACTTCAATGACATGATGTCATCAAGATTTACCTGAGGAGGAGGAGGAGGAG 849  
Db 781 TTCAATGACTTCAATGACATGATGTCATCAAGATTTACCTGAGGAGGAGGAGGAGGAG 840

QY 850 CAGCTACTGAGTTTCCCTTCAATCCGGGACAGCCCAAGGAGGAGGTCGGATCCAG 909  
 DB 841 CAGCTACTGAGTTTCCCTTCAATCCGGGACAGCCCAAGGAGGAGGTCGGATCCAG 900  
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 DB 1321 CGGCGGAGGCGGAGCGG 1337  
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 US-09-925-297-137  
 / Sequence 137, Application US/09925297  
 / Patent No. US20020081659A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Rosen et al.  
 / TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 / FILE REFERENCE: PA105  
 / CURRENT APPLICATION NUMBER: US/09/925,297  
 / CURRENT FILING DATE: 2001-08-10  
 / PRIOR APPLICATION NUMBER: PCT/US00/05989  
 / PRIOR FILING DATE: 2000-03-08  
 / PRIOR APPLICATION NUMBER: 60/124,270  
 / PRIOR FILING DATE: 1999-03-12  
 / NUMBER OF SEQ ID NOS: 928  
 / SOFTWARE: Patent Ver. 2.0  
 / SEQ ID NO 137  
 / LENGTH: 2345  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / FEATURE:  
 / NAME/KEY: misc feature  
 / LOCATION: (184)  
 / OTHER INFORMATION: n equals a,t,g, or c  
 / NAME/KEY: misc feature  
 / LOCATION: (339)  
 / OTHER INFORMATION: n equals a,t,g, or c  
 / NAME/KEY: misc feature  
 / LOCATION: (1805)  
 / OTHER INFORMATION: n equals a,t,g, or c  
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 / LOCATION: (1887)  
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 / NAME/KEY: misc feature  
 / LOCATION: (2325)

/ OTHER INFORMATION: n equals a,t,g, or c  
 / NAME/KEY: misc feature  
 / LOCATION: (2339)  
 / OTHER INFORMATION: n equals a,t,g, or c  
 / US-09-925-297-137  
 Query Match 26.1%; Score 1030; DB 9; Length 2345;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2763 TCGTGGGCTGTGTAAGGCGCCCTGGCAAGAGCTGCTTCAAGATGTTGTGATCTAGGAT 2822  
 DB 351 TCGTGGGCTGTGTAAGGCGCCCTGGCAAGAGCTGCTTCAAGATGTTGTGATCTAGGAT 410  
 QY 2823 CTACAGCCTGAGAGCAGTGGGAGCAGGATCCCATCAACAGCCCTAGTGGTGGAGAGG 2882  
 DB 411 TTACAGCCTGAGAGCAGTGGGAGCAGGATCCCATCAACAGCCCTAGTGGTGGAGAGG 470  
 QY 2883 CACTCGGCTGACACAGCTGACAGTACGACGTGAGAGAGGTTCTGTGCTCAACGTGAATCC 2942  
 DB 471 CACTCGGTTGACACAGCTGACAGTACGACGTGAGAGAGGTTCTGTGCTCAACGTGAATCC 530  
 QY 2943 CACCAACACCGGCGCCACAGTGAAGCCCTGAGATCCGGAAGTACMAAGAGCCATTCAA 3002  
 DB 531 CACCAACACCGGCGCCACAGTGAAGCCCTGAGATCCGGAAGTACMAAGAGCCATTCAA 590  
 QY 3003 CTCCGAGATCCCTGTGTGAGCCCTTTGGGGGATCAAACCTGTGTGTGGGACAGAGAGCG 3062  
 DB 591 CTCCGAGATCCCTGTGTGAGCCCTTTGGGGGATCAAACCTGTGTGTGGGACAGAGAGCG 650  
 QY 3063 GCTGATGTTGTGAGCCGAGATGGGACAGGAGGATGATGATGATGATGATGATGATGAT 3122  
 DB 651 GCTGATGTTGTGAGCCGAGATGGGACAGGAGGATGATGATGATGATGATGATGATGAT 710  
 QY 3123 CTTCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3182  
 DB 711 CTTCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 770  
 QY 3183 GAACAAATCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3242  
 DB 771 GAACAAATCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 830  
 QY 3243 AGAAGTGAAGAGAGAGAGGCTGAGACCAAGTGGGGGACATGAGGCTGTGGGACCTA 3302  
 DB 831 AGAAGTGAAGAGAGAGAGGCTGAGACCAAGTGGGGGACATGAGGCTGTGGGACCTA 890  
 QY 3303 CCGTGTGTGAATACAGCGGATTAAGTCTGTGATGATGATGATGATGATGATGATGATGAT 3362  
 DB 891 CCGTGTGTGAATACAGCGGATTAAGTCTGTGATGATGATGATGATGATGATGATGATGAT 950  
 QY 3363 GGTGATGCTGTGGGCGCCCAAACTTACCAAAATTCATGAGCTTCAAGTCTTTGGCGGA 3422  
 DB 951 GGTGATGCTGTGGGCGCCCAAACTTACCAAAATTCATGAGCTTCAAGTCTTTGGCGGA 1010  
 QY 3423 CCTCCCAACCGGCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3482  
 DB 1011 CCTCCCAACCGGCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1070  
 QY 3483 CATCTATGCTTCAAGTGTGCTTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 3542  
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 QY 3543 CATCTATGCTTCAAGTGTGCTTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 3602  
 DB 1131 CATCTATGCTTCAAGTGTGCTTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1190  
 QY 3603 CAACACCAACCGGATGAGATGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 3662  
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 QY 3663 GTACGGGCGCATCTTAAGAGATGTGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 3722  
 DB 1251 GTACGGGCGCATCTTAAGAGATGTGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1310

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Qy 3723 CTACATCTGCTCCAAACCGATTAATGAGCTGGGGTGAAGAAAGCAATTGATCCGCTCTGT 3782
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Qy 3783 GGAGACGGGGCCACCTCGACGGGGTCTTTCATGCACAAAGAGCTGAGAGCTCAAGTTCTT 3842
Db 1371 GGAGACGGGGCCACCTCGACGGGGTCTTTCATGCACAAAGAGCTGAGAGCTCAAGTTCTT 1430
Qy 3843 GTGTGAGCGGAATGACAAAGGTGTTTTTTCCTCAGTCCGCTCTGAGGGGACAGCAAGT 3902
Db 1431 GTGTGAGCGGAATGACAAAGGTGTTTTTTCCTCAGTCCGCTCTGAGGGGACAGCAAGT 1490
Qy 3903 TTACTTCATGACTCTGAACCGTAACTGATCATGAACTGTGA 3945
Db 1491 TTACTTCATGACTCTGAACCGTAACTGATCATGAACTGTGA 1533
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## RESULT 15

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US-10-108-260A-1388
; Sequence 1388, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108, 260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1388
; LENGTH: 3152
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-1388
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Query Match 14.0%; Score 555; DB 15; Length 3152;

Best Local Similarity 100.0%; Pred. No. 1.3e-258; Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 3430 CACGGCCCTCTGCTGCTGCTGACCTGACATGAGAGGGGACGGCTCAAGTCACTTAT 3489
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Qy 3550 ATCCCTGTGCAATCCAGAGCCAGATCAAGCCCAATCCATCATCTTCTCCCAACAG 3609
Db 1592 ATCCCTGTGCAATCCAGAGCCAGATCAAGCCCAATCATCTTCTCCCAACAG 1651
Qy 3610 GACGGCATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3669
Db 1652 GACGGCATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1711
Qy 3670 CGCATCATTAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3729
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Qy 3730 TGCTTCAACCAAGATTAATGGGCTGGGGTGAAGAAAGCATTAAGATCCGCTCTGTGAGAG 3789
Db 1772 TGCTTCAACCAAGATTAATGGGCTGGGGTGAAGAAAGCATTAAGATCCGCTCTGTGAGAG 1831
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Qy 3850 CGAATGACAAAGTG 3864
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 17:02:58 ; Search time 6279 Seconds  
(without alignments)  
18790.488 Million cell updates/sec

Title: US-10-029-115-1

Perfect score: 3951  
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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0  
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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

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8: em\_hnc:\*  
9: gb\_est1:\*  
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25: em\_ges\_rtd:\*  
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27: em\_ges\_vrl:\*  
28: gb\_ges1:\*  
29: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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7	724	18.3	1515	11	BC028888
8	720	18.2	1026	12	BM541693
9	714	18.1	1022	13	BQ073811
10	697	17.6	936	12	BM451246
11	693	17.5	951	13	BQ706178
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13	633	16.0	727	12	BI000010
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15	616	15.6	629	12	BI916276
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17	611	15.5	999	12	BM477724
18	593	15.0	811	13	B0578825
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25	527	13.3	527	10	BF724524
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27	517	13.1	541	14	CB853199
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29	500	12.7	947	12	BG327623
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32	492	12.5	492	14	CB144863
33	492	12.0	873	13	CB145533
34	473	12.0	873	13	BQ717112
35	472	11.9	472	9	AA780425
36	468	11.8	1058	12	BM464994
37	467	11.8	1205	12	BM806025
38	466	11.8	534	12	BG419855
39	459	11.6	918	13	BQ945934
40	451	11.4	971	13	B0173419
41	439	11.1	1218	12	BM548024
42	432	10.9	881	14	CA454128
43	432	10.9	939	13	CF931753
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47	421	10.7	924	14	CA488783
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51	407	10.3	477	10	BF881056
52	406	10.3	715	12	BI195766
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55	390	9.9	658	14	CA392419
56	382	9.7	917	12	BG106177
57	381	9.6	438	14	CF142044
58	371	9.4	696	12	BM020958
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61	350	8.9	637	12	BI009982
62	337	8.5	617	10	AM973784
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83	276	7.0	352	9	AA349350	AA349350 EST55973	C 156	113	2.9	629	12	BC910247	BC910247 602805744
84	271	6.9	436	12	BI199531	BI199531 602758664	C 157	112	2.8	299	13	BQ326905	BQ326905 RC4-CN020
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92	253	6.4	286	10	BM051265	BM051265 603634236	C 165	102	2.6	363	10	BF851235	BF851235 IL5-EN008
93	252	6.4	749	12	BC957547	BC957547 602714720	C 166	101	2.6	223	10	BF851327	BF851327 IL5-EN008
94	242	6.1	327	9	AA295021	AA295021 EST100479	C 167	101	2.6	405	10	BE937980	BE937980 MR1-TN004
95	241	6.1	535	12	BM739040	BM739040 K-EST0008	C 168	98	2.5	451	13	BQ367113	BQ367113 RC1-GN019
96	239	6.0	258	14	R10658	R10658 yf31e12.r1	C 169	97	2.5	290	10	BF222406	BF222406 MR1-CT002
97	238	6.0	1114	14	CD558642	CD558642 AGENCOURT	C 170	95	2.4	490	13	BE476452	BE476452 DXF2P686D
98	236	6.0	353	10	BF091038	BF091038 MR3-SN003	C 171	94	2.4	302	12	BI051567	BI051567 RC4-CN020
99	232	5.9	725	10	BE536499	BE536499 601067444	C 172	94	2.4	303	12	BI051567	BI051567 CM4-GN036
100	227	5.7	270	10	AM885349	AM885349 QV4-OT006	C 173	94	2.4	450	13	BQ300059	BQ300059 MR3-KT005
101	224	5.7	398	12	BC984025	BC984025 IL5-CN006	C 174	93	2.4	276	10	AM368321	AM368321 CM2-HT018
102	223	5.6	491	9	AA434299	AA434299 zw30g06.x	C 175	93	2.4	281	10	AM368328	AM368328 CM3-HT018
103	221	5.6	256	12	BM823989	BM823989 K-EST0095	C 176	92	2.3	390	28	AZ301117	AZ301117 UP 305-1G
104	221	5.6	443	14	R18578	R18578 yf55f12.r1	C 177	92	2.3	934	14	CB990560	CB990560 AGENCOURT
105	221	5.6	512	13	BQ327795	BQ327795 MR4-RT003	C 178	91	2.3	170	10	BF931929	BF931929 PM1-BT023
106	221	5.6	800	12	BI754257	BI754257 603025559	C 179	88	2.2	236	10	AM298772	AM298772 UT-H-BT00
107	219	5.5	432	12	BC994275	BC994275 CM3-HT115	C 180	86	2.2	219	13	BQ327059	BQ327059 RC4-CN020
108	211	5.3	454	12	BI052005	BI052005 RC3-GN026	C 181	86	2.2	564	12	BM967105	BM967105 IL330e04.Y
109	210	5.3	360	10	BF924542	BF924542 IL5-NT022	C 182	85	2.2	657	12	BM722585	BM722585 UI-E-E00
110	207	5.2	524	14	BF920346	BF920346 QV2-NT014	C 183	85	2.2	507	10	BE485510	BE485510 PM1-KT004
111	206	5.2	550	14	CB119344	CB119344 K-EST0166	C 184	81	2.1	345	13	BQ300043	BQ300043 PM1-KT004
112	202	5.1	250	10	AM843642	AM843642 CM0-CN004	C 185	80	2.0	330	9	AI505697	AI505697 IL-BT096-
113	198	5.0	198	14	CB117740	CB117740 K-EST0163	C 186	79	2.0	297	14	R88464	R88464 Y922H01.r1
114	198	5.0	625	12	BI772266	BI772266 603055847	C 187	72	1.8	304	14	T32148	T32148 EST44087.Hu
115	193	4.9	497	10	BF858986	BF858986 MR0-FTO18	C 188	72	1.8	563	10	BE751204	BE751204 203083.MA
116	193	4.9	1036	12	BM044589	BM044589 603622248	C 189	70	1.8	453	12	BI012190	BI012190 PM1-EN006
117	185	4.7	203	10	AM366519	AM366519 CM3-HT014	C 190	67	1.7	161	10	BF880445	BF880445 QV3-ET019
118	183	4.6	390	9	AA578088	AA578088 n135f12.s	C 191	66	1.7	191	10	BF879175	BF879175 QV3-ET017
119	183	4.6	646	10	BE312586	BE312586 601151324	C 192	66	1.7	658	10	BF821438	BF821438 MR1-RT003
120	178	4.5	311	12	BM796679	BM796679 K-EST0079	C 193	64	1.6	467	10	BF603813	BF603813 269407.MA
121	178	4.5	606	12	BM047589	BM047589 603628918	C 194	64	1.6	453	12	BI012190	BI012190 PM1-EN006
122	174	4.4	289	9	AI905357	AI905357 IL-BT0086-	C 195	59	1.5	136	10	BE924940	BE924940 IL2-NT020
123	172	4.4	545	12	BI009462	BI009462 MR0-RT003	C 196	56	1.4	136	10	BF373997	BF373997 CM2-SN002
124	172	4.4	719	10	BG032073	BG032073 602300589	C 197	54	1.4	96	9	AI505698	AI505698 IL-BT096-
125	170	4.3	528	10	BF752910	BF752910 RC4-BN022	C 198	53	1.3	425	10	AM762248	AM762248 u155e07.Y
126	170	4.3	528	10	BE932268	BE932268 IL3-HT061	C 199	53	1.3	434	14	CB793477	CB793477 AMGNNUC:N
127	169	4.3	283	10	BF898826	BF898826 QV1-NT022	C 200	53	1.3	434	14	CB793477	CB793477 AMGNNUC:N
128	163	4.1	269	10	BF088961	BF088961 PM4-HT090	C 201	53	1.3	434	14	CB793477	CB793477 AMGNNUC:N
129	161	4.1	189	14	Z42685	Z42685 HSCORAL01.n	C 202	53	1.3	456	10	AM258584	AM258584 UG37A10.Y
130	160	4.0	959	13	BQ716738	BQ716738 AGENCOURT	C 203	53	1.3	567	14	CB616524	CB616524 AMGNNUC:N
131	158	4.0	508	10	BF086296	BF086296 QV1-GN006	C 204	53	1.3	595	14	CB584150	CB584150 AMGNNUC:N
132	156	3.9	473	9	AA233207	AA233207 z69b04.x	C 205	53	1.3	600	12	BI1991507	BI1991507 4101-82.M
133	155	3.9	337	10	BF868921	BF868921 IL5-ET011	C 206	53	1.3	696	12	BM932728	BM932728 UI-M-CG0P
134	154	3.9	362	13	BQ334589	BQ334589 QV1-NT023	C 207	53	1.3	696	14	CB244053	CB244053 UI-M-FX0-
135	151	3.8	399	9	AA339349	AA339349 EST55972	C 208	53	1.3	698	12	BC665574	BC665574 DRACEH03
136	151	3.8	451	13	BQ367113	BQ367113 RC1-GN019	C 209	53	1.3	709	12	BC665574	BC665574 DRACEH03
137	150	3.8	360	9	AA788891	AA788891 ae93f02.s	C 210	53	1.3	709	14	CA316178	CA316178 UI-M-FW0-
138	145	3.7	349	10	BF087135	BF087135 PM1-HT045	C 211	53	1.3	790	14	CF733432	CF733432 UI-M-HB0-
139	143	3.6	1201	9	AL575366	AL575366 AL575366	C 212	53	1.3	794	12	BI409187	BI409187 602961334
140	140	3.5	424	10	BF805131	BF805131 QV1-CT017	C 213	53	1.3	832	13	BUS58574	BUS58574 AGENCOURT
141	137	3.5	351	13	BQ346024	BQ346024 PM3-NT031	C 214	50	1.3	297	9	AI007546	AI007546 EST108048
142	135	3.4	251	14	R00019	R00019 yf69h10.r1	C 215	50	1.3	425	14	CB696067	CB696067 AMGNNUC:N
143	135	3.4	387	10	BG014371	BG014371 CM3-GN029	C 216	50	1.3	538	10	BF450846	BF450846 uz71f01.Y
144	134	3.4	303	13	BQ364055	BQ364055 MR4-ST024	C 217	50	1.3	628	10	BE5659708	BE5659708 601332311
145	131	3.3	180	10	BG011162	BG011162 IL5-GN024	C 218	50	1.3	640	9	AU2966392	AU2966392 AU2966392
146	130	3.3	387	9	AA325902	AA325902 EST28976	C 219	50	1.3	721	13	BI707794	BI707794 UI-M-FR0-
147	129	3.3	298	10	BF946362	BF946362 RC6-NN117	C 220	49	1.2	219	13	BQ368422	BQ368422 PM3-GN051
148	125	3.2	557	10	BF926778	BF926778 MR2-NT013	C 221	49	1.2	428	14	CB793968	CB793968 AMGNNUC:N
149	119	3.0	376	12	BI021730	BI021730 CM3-MT018	C 222	47	1.2	247	9	AA673268	AA673268 v136804.x
150	118	3.0	179	9	AA335971	AA335971 EST29058	C 223	47	1.2	331	9	AI641825	AI641825 vq32d10.Y



224	47	1.2	388	14	W64920	W64920 me02a11..r1	297	37	0.9	212	12	BG865361	BG865361 602783968
225	47	1.2	396	10	AM742571	AM742571 up259e05.y	298	36	0.9	136	10	BE174066	BE174066 QV1-HT057
226	47	1.2	411	10	BE226541	BE226541 ha22b12.y	299	36	0.9	480	10	BF850781	BF850781 CM3-EN011
227	47	1.2	448	14	W88105	W88105 mt70D04..r1	300	36	0.9	440	14	CE749027	CE749027 AMGNNUC:C
228	47	1.2	452	9	AA871207	AA871207 vq32d10..r	301	36	0.9	442	10	BE198798	BE198798 ug82f10.y
229	47	1.2	506	13	B0694525	B0694525 lI2i1n1065	302	36	0.9	455	14	CE741237	CE741237 AMGNNUC:N
230	47	1.2	514	10	BF233525	BF233525 602024122	303	36	0.9	501	10	BE863915	BE863915 UI-M-BHO-
231	47	1.2	635	14	CD351693	CD351693 UI-M-GIO-	304	36	0.9	582	28	AZ860896	AZ860896 2M0167C08
232	47	1.2	643	10	BF167402	BF167402 601773690	305	36	0.9	617	12	B1108465	B1108465 602902176
233	47	1.2	679	12	BM947633	BM947633 UI-M-EGOP	306	36	0.9	969	14	CEB590530	CEB590530 AGENCOURT
234	47	1.2	714	12	BG294704	BG294704 602392074	307	35	0.9	406	9	AL913187	AL913187 AL913187
235	47	1.2	771	12	B1646294	B1646294 603276438	308	35	0.9	482	10	BF230263	BF230263 251785 BA
236	47	1.2	778	14	CB246214	CB246214 UI-M-PYO-	309	35	0.9	557	29	CE066918	CE066918 l1gr-q8s-
237	47	1.2	786	12	B1737039	B1737039 603360892	310	35	0.9	584	9	AA97295	AA97295 fa03e11..r
238	47	1.2	791	12	B1852403	B1852403 603378228	311	35	0.9	628	28	AZ937732	AZ937732 2M0196H04
239	47	1.2	835	12	BI430479	BI430479 UMN41C01	312	35	0.9	646	10	BE303496	BE303496 601086375
240	47	1.2	898	13	BQ885202	BQ885202 AGENCOURT	313	35	0.9	652	12	BJ000404	BJ000404 BU000404
241	47	1.2	956	12	BG297263	BG297263 602394974	314	35	0.9	813	12	BI104219	BI104219 602889769
242	46	1.2	372	10	BF847314	BF847314 CM3-EN004	315	34	0.9	506	12	B1895322	B1895322 EREStea30
243	46	1.2	524	10	BE369969	BE369969 601221191	316	34	0.9	574	9	AI533382	AI533382 SD05170..5
244	46	1.2	652	10	BB034168	BB034168 BB034168	317	34	0.9	800	12	B1649693	B1649693 603276611
245	46	1.2	916	13	BQ922876	BQ922876 AGENCOURT	318	33	0.8	480	12	BI232278	BI232278 R28324.5
246	44	1.1	168	14	CF171538	CF171538 B0843G02-	319	33	0.8	778	12	BG766518	BG766518 602739280
247	44	1.1	341	10	AM231063	AM231063 uo70d04..y	320	33	0.8	978	13	BQ675493	BQ675493 AGENCOURT
248	44	1.1	347	13	BY151323	BY151323 BY151323	321	32	0.8	330	12	BG834273	BG834273 352430 MA
249	44	1.1	395	9	AA646811	AA646811 vn37b07..r	322	32	0.8	361	12	B1895643	B1895643 ERESteb01
250	44	1.1	455	14	CB741202	CB741202 AMGNNUC:N	323	32	0.8	362	12	B1895650	B1895650 ERESteb02
251	44	1.1	459	9	AA921243	AA921243 vy54g09..r	324	32	0.8	385	10	BF079670	BF079670 230334 MA
252	44	1.1	508	14	CB518343	CB518343 UI-M-GHO-	325	32	0.8	404	14	CB811652	CB811652 AMGNNUC:S
253	44	1.1	593	12	BI664323	BI664323 603289080	326	32	0.8	407	14	CD343746	CD343746 EREStea79
254	44	1.1	607	13	B0554558	B0554558 H40286G09-	327	32	0.8	424	12	B1895715	B1895715 ERESted27
255	44	1.1	635	10	CP171784	CP171784 B0847D08-	328	32	0.8	461	10	BE751193	BE751193 203072 MA
256	44	1.1	641	10	BB620167	BB620167 BB620167	329	32	0.8	560	14	CD344531	CD344531 EREStea80
257	44	1.1	663	14	CF533672	CF533672 UI-M-PYO-	330	32	0.8	581	14	CD344526	CD344526 EREStea80
258	44	1.1	692	13	B0611352	B0611352 UI-M-FIO-	331	32	0.8	228	12	BJ488644	BJ488644 BU488644
259	44	1.1	720	14	CB249067	CB249067 UI-M-EXO-	332	31	0.8	282	12	BI042331	BI042331 MR4-NT014
260	44	1.1	724	14	CE531764	CE531764 UI-M-PYO-	333	31	0.8	297	12	B1895975	B1895975 ERESted84
261	44	1.1	757	14	CB519879	CB519879 UI-M-GHO-	334	31	0.8	319	9	AI676744	AI676744 etRESt052
262	44	1.1	764	13	BQ180764	BQ180764 UI-M-EXO-	335	31	0.8	368	12	B1895096	B1895096 EREStea10
263	44	1.1	827	10	BE295363	BE295363 601175870	336	31	0.8	370	14	CD658393	CD658393 EREStea22
264	44	1.1	834	12	BI104781	BI104781 602891326	337	31	0.8	373	14	CD345428	CD345428 EREStea793
265	44	1.1	848	13	BQ443922	BQ443922 UI-M-EXO-	338	31	0.8	376	9	AI371500	AI371500 qY07b02..x
266	44	1.1	1490	10	BE539764	BE539764 602049976	339	31	0.8	379	12	B1896060	B1896060 EREStea02
267	44	1.1	3585	29	AY400358	AY400358 MUE muscu	340	31	0.8	390	12	B1895228	B1895228 EREStea22
268	44	1.1	593	12	BI372041	BI372041 RES7474.5	341	31	0.8	397	12	B1895395	B1895395 EREStea36
269	42	1.1	599	12	BI234317	BI234317 RE30007.5	342	31	0.8	423	12	B1895942	B1895942 ERESted77
270	42	1.1	611	12	BI232730	BI232730 RE28851.5	343	31	0.8	434	9	AV625698	AV625698 AV625698
271	42	1.1	618	12	BI235813	BI235813 RE31748.5	344	31	0.8	435	12	B1895247	B1895247 EREStea22
272	42	1.1	624	12	BI236867	BI236867 RE51260.5	345	31	0.8	443	12	B1895849	B1895849 EREStea25
273	42	1.1	637	12	BI231531	BI231531 RE22407.5	346	31	0.8	448	12	BG561507	BG561507 EREStea01
274	42	1.1	668	12	BG637447	BG637447 SD15452.5	347	31	0.8	472	12	B1895246	B1895246 EREStea22
275	42	1.1	705	13	BQ180518	BQ180518 UI-M-EXO-	348	31	0.8	489	14	CD345681	CD345681 EREStea181
276	42	1.1	710	9	AA979568	AA979568 LD31491..5	349	31	0.8	525	10	BG929650	BG929650 etREStea00
277	41	1.0	140	28	BH067865	BH067865 RPCI-24-3	350	31	0.8	547	10	BF821712	BF821712 MR1-RT007
278	41	1.0	267	9	AA930283	AA930283 vs58c07..r	351	31	0.8	550	14	CD658484	CD658484 EREStea23
279	41	1.0	393	14	CB777351	CB777351 AMGNNUC:N	352	31	0.8	552	12	BM306701	BM306701 EREStea34
280	41	1.0	405	14	CB808584	CB808584 AMGNNUC:N	353	31	0.8	561	12	BM306709	BM306709 EREStea34
281	41	1.0	479	14	CB546650	CB546650 AMGNNUC:N	354	31	0.8	576	12	BM306708	BM306708 EREStea34
282	41	1.0	624	28	BH068131	BH068131 RPCI-24-3	355	31	0.8	582	14	CD661353	CD661353 EREStea946
283	41	1.0	847	13	B0935745	B0935745 AGENCOURT	356	31	0.8	704	12	BJ015692	BJ015692 BU015692
284	41	1.0	988	12	BG679244	BG679244 602627326	357	31	0.8	808	29	CNS02NGR	AL205380 Tetraddon
285	40	1.0	316	10	BE929101	BE929101 PM3-GN001	358	31	0.8	816	14	CA326779	CA326779 UI-M-PYO-
286	39	1.0	821	12	BI217509	BI217509 602933930	359	31	0.8	857	14	BQ686424	BQ686424 AGENCOURT
287	38	1.0	272	14	Z44886	Z44886 HSC2BH081.n	360	31	0.8	881	12	B1868319	B1868319 603392278
288	38	1.0	290	10	BP947862	BP947862 CM2-NN021	361	31	0.8	905	14	CF411097	CF411097 CH3#071_E
289	38	1.0	301	10	AM480426	AM480426 31229 MAR	362	31	0.8	925	29	CNS0381E	AL123043 Tetraddon
290	38	1.0	563	10	BF385542	BF385542 602047087	363	31	0.8	1007	12	BM458161	BM458161 AGENCOURT
291	38	1.0	577	14	CD350084	CD350084 UI-M-PYO-	364	31	0.8	1201	13	EX366767	EX366767 BX366767
292	38	1.0	646	12	BI103781	BI103781 602887788	365	31	0.8	1201	13	EX378991	EX378991 BX378991
293	38	1.0	751	14	CF736764	CF736764 UI-M-HDO-	366	31	0.8	1201	13	BX420108	BX420108 BX420108
294	38	1.0	941	10	BE573180	BE573180 601332853	367	31	0.8	1383	13	BU766484	BU766484 SUBAEF09
295	38	1.0	1143	29	CNS03KMS	AL248725 Tetraddon	368	31	0.8	2309	29	AY411306	AY411306 Homo sapi
296	38	1.0	1570	13	B0865190	B0865190 AGENCOURT	369	30	0.8	125	14	CF540002	CF540002 UI-M-EXO-

370	30	0.8	297	10	AM346522	443	29	0.7	559	28	A2661862	A2661862	1M0540H08
371	30	0.8	308	12	BG516537	444	29	0.7	573	14	CD660303	CD660303	CESTef33
372	30	0.8	397	12	BI895688	445	29	0.7	574	14	CF103526	CF103526	CESTef72
373	30	0.8	401	12	BI895693	446	29	0.7	589	14	CD660432	CD660432	CESTef40
374	30	0.8	428	12	BI895672	447	29	0.7	600	9	AV616533	AV616533	AV616533
375	30	0.8	428	14	CB794209	448	29	0.7	601	28	A2357375	A2357375	1M0098A24
376	30	0.8	440	10	AM436687	449	29	0.7	604	12	BM024735	BM024735	BM024735
377	30	0.8	441	12	BI895586	450	29	0.7	614	12	BI981369	BI981369	fu72b02.x
378	30	0.8	451	12	BI895633	451	29	0.7	629	12	BM024223	BM024223	fu7909.x
379	30	0.8	501	14	CD345170	452	29	0.7	633	13	BY749990	BY749990	BY749990
380	30	0.8	508	12	BI895774	453	29	0.7	634	12	BC634231	BC634231	AT10371.5
381	30	0.8	532	12	BI895372	454	29	0.7	635	10	BB654214	BB654214	BB654214
382	30	0.8	538	14	CD665292	455	29	0.7	650	13	BY727248	BY727248	BY727248
383	30	0.8	547	14	CD665558	456	29	0.7	653	10	BB630275	BB630275	BB630275
384	30	0.8	566	14	CD665296	457	29	0.7	673	28	BH067947	BH067947	RPCT-24-3
385	30	0.8	571	14	CD345341	458	29	0.7	679	28	CC321178	CC321178	TAM32-505
386	30	0.8	571	14	CD665644	459	29	0.7	686	13	BY747575	BY747575	BY747575
387	30	0.8	577	14	CB606109	460	29	0.7	690	9	AL585202	AL585202	AL585202
388	30	0.8	583	14	CD570032	461	29	0.7	704	9	AM076957	AM076957	fj33a09.x
389	30	0.8	670	29	CD572946	462	29	0.7	720	13	BY720619	BY720619	BY720619
390	30	0.8	712	12	BI733567	463	29	0.7	724	12	BM715816	BM715816	UI-E-EJ0-
391	30	0.8	728	12	BUS36233	464	29	0.7	732	12	BG633803	BG633803	AT29732.5
392	29	0.7	160	10	BF599374	465	29	0.7	732	14	CB170818	CB170818	BK1603001
393	29	0.7	176	10	BB606636	466	29	0.7	747	10	BF506735	BF506735	AT09292.5
394	29	0.7	204	12	BC945838	467	29	0.7	775	28	BF489425	BF489425	AT25543.5
395	29	0.7	225	12	BC950812	468	29	0.7	779	28	CC320252	CC320252	TAM32-4M1
396	29	0.7	281	12	BI895553	469	29	0.7	857	14	CA321177	CA321177	UI-M-FW0-
397	29	0.7	290	13	BI356663	470	29	0.7	904	14	CA475635	CA475635	ACENICOURT
398	29	0.7	309	13	BY355786	471	29	0.7	910	29	CNS04104	CNS04104	ACENICOURT
399	29	0.7	313	10	AM417152	472	29	0.7	1243	11	BC034882	BC034882	Mus muscu
400	29	0.7	316	12	BI895455	473	29	0.7	1246	11	AK037155	AK037155	Mus muscu
401	29	0.7	322	14	CD343484	474	29	0.7	1327	11	AK083309	AK083309	Mus muscu
402	29	0.7	330	14	CD344805	475	28	0.7	168	12	BI895635	BI895635	CESTef89
403	29	0.7	340	14	CD660081	476	28	0.7	232	14	CD518840	CD518840	ACENICOURT
404	29	0.7	342	14	CD570299	477	28	0.7	234	9	AA627411	AA627411	ng49d07.8
405	29	0.7	402	12	BM305750	478	28	0.7	239	12	BI793012	BI793012	1e50f07.x
406	29	0.7	404	10	BB848390	479	28	0.7	251	10	BE504942	BE504942	h23f011.x
407	29	0.7	408	12	BI895547	480	28	0.7	259	12	BI895605	BI895605	CESTef86
408	29	0.7	411	12	BI895541	481	28	0.7	269	12	BI799314	BI799314	1e50f07.y
409	29	0.7	415	12	BM321582	482	28	0.7	274	13	BK610827	BK610827	BK610827
410	29	0.7	417	10	BB848238	483	28	0.7	336	12	BI895725	BI895725	CESTef32
411	29	0.7	417	12	BG466220	484	28	0.7	406	14	CB808295	CB808295	AMGNNUC:S
412	29	0.7	418	12	BM321570	485	28	0.7	408	14	CB771221	CB771221	AMGNNUC:S
413	29	0.7	425	12	BI895456	486	28	0.7	418	12	BI895103	BI895103	CESTef11
414	29	0.7	425	13	BY259515	487	28	0.7	434	12	BI895077	BI895077	CESTef89
415	29	0.7	426	14	CD665730	488	28	0.7	436	12	BJ271085	BJ271085	CESTef09
416	29	0.7	427	12	BI895104	489	28	0.7	443	14	CB788577	CB788577	AMGNNUC:N
417	29	0.7	429	12	BI895111	490	28	0.7	449	13	BY291744	BY291744	BY291744
418	29	0.7	437	13	BY246545	491	28	0.7	452	9	AT759506	AT759506	CESTef28
419	29	0.7	440	10	AM481298	492	28	0.7	453	14	CD659409	CD659409	CESTef41
420	29	0.7	441	14	CB546776	493	28	0.7	464	14	BM306489	BM306489	CESTef43
421	29	0.7	443	12	BI895285	494	28	0.7	472	14	CB730426	CB730426	AMGNNUC:N
422	29	0.7	445	12	CB744466	495	28	0.7	487	12	BI896074	BI896074	CESTef04
423	29	0.7	446	14	BG329838	496	28	0.7	487	12	BI895049	BI895049	CESTef06
424	29	0.7	450	10	BE851514	497	28	0.7	494	28	A2325941	A2325941	1M0048B06
425	29	0.7	450	14	CD664705	498	28	0.7	514	14	CB968416	CB968416	CESTef74
426	29	0.7	453	9	AT759230	499	28	0.7	518	14	CD661382	CD661382	CESTef46
427	29	0.7	454	12	BI342913	500	28	0.7	526	14	CB118612	CB118612	K-RST0165
428	29	0.7	454	12	BM305567	501	28	0.7	543	14	CD342339	CD342339	CESTef51
429	29	0.7	457	10	BB856190	502	28	0.7	550	14	CD661226	CD661226	CESTef50
430	29	0.7	470	12	BI895549	503	28	0.7	554	14	CD343941	CD343941	CESTef89
431	29	0.7	475	12	BM701243	504	28	0.7	563	12	BG326499	BG326499	602425344
432	29	0.7	476	12	BI896023	505	28	0.7	564	14	CD658353	CD658353	CESTef20
433	29	0.7	484	12	BI895470	506	28	0.7	575	14	CD665884	CD665884	EPSTeg38
434	29	0.7	484	14	CD661175	507	28	0.7	577	14	CD666062	CD666062	CESTeg28
435	29	0.7	485	10	BB851360	508	28	0.7	579	14	CD658994	CD658994	CESTeg15
436	29	0.7	487	12	BM258980	509	28	0.7	583	29	AL229352	AL229352	Tetradon
437	29	0.7	518	14	CD569083	510	28	0.7	586	29	CNS03JHV	CNS03JHV	1M0098A24
438	29	0.7	518	28	AZ357021	511	28	0.7	589	14	CD660432	CD660432	CESTef40
439	29	0.7	527	14	CD657839	512	28	0.7	591	14	CF103543	CF103543	EPSTeg72
440	29	0.7	541	14	CF103583	513	28	0.7	593	14	CD666237	CD666237	CESTef12
441	29	0.7	543	14	CD342339	514	28	0.7	611	14	CD658342	CD658342	CESTef20
442	29	0.7	558	9	AI878252	515	28	0.7	683	14	CA340866	CA340866	NISC_1208

516	28	0.7	709	14	CA501370	WHE4032.G	589	27	0.7	812	12	BG921179	BG921179	602823079
517	28	0.7	709	14	CP994655	AGENCOURT	590	27	0.7	815	9	AU118352	AU118352	AU118352
518	28	0.7	728	12	B0611085	UI-M-FCO-	591	27	0.7	815	9	AU137741	AU137741	AU137741
519	28	0.7	734	12	BM009770	603630414	592	27	0.7	815	14	CB909566	CB909566	tr:c088xj
520	28	0.7	736	10	BES65585	601338358	593	27	0.7	815	14	CF883425	CF883425	tr:c088xj
521	28	0.7	769	14	CB234590	AGENCOURT	594	27	0.7	817	14	CA317642	CA317642	UI-M-FW0-
522	28	0.7	800	13	BUS05482	AGENCOURT	595	27	0.7	823	9	AU205370	AU205370	AU205370
523	28	0.7	827	13	BUS376059	603813931	596	27	0.7	824	14	CK146312	CK146312	AGENCOURT
524	28	0.7	843	13	BX353115	BX353115	597	27	0.7	829	9	AU139258	AU139258	AU139258
525	28	0.7	894	14	CB849227	MRA-0921	598	27	0.7	851	14	CA789259	CA789259	AGENCOURT
526	28	0.7	908	13	BQ678480	AGENCOURT	599	27	0.7	855	9	AU130348	AU130348	AU130348
527	28	0.7	950	13	BQ641701	AGENCOURT	600	27	0.7	859	29	CC532797	CC532797	CH240_410
528	28	0.7	1047	29	CNS0157C	B0641701	601	27	0.7	877	12	B1689167	B1689167	B1689167
529	28	0.7	1091	12	BME57591	AGENCOURT	602	27	0.7	889	14	CA475321	CA475321	AGENCOURT
530	28	0.7	1201	13	BX420026	BX420026	603	27	0.7	907	14	CB988790	CB988790	AGENCOURT
531	28	0.7	180	9	A1936867	wp70d06.x	604	27	0.7	944	14	CA477795	CA477795	AGENCOURT
532	27	0.7	183	9	A1497974	cm97g11.x	605	27	0.7	1026	13	BUS05117	BUS05117	AGENCOURT
533	27	0.7	198	9	A1499045	cm02d05.x	606	27	0.7	1067	13	BQ934612	BQ934612	AGENCOURT
534	27	0.7	207	10	AM139025	UI-H-B11-	607	27	0.7	1128	29	CNS06RDI	CNS06RDI	tr7 end of
535	27	0.7	240	10	BPE51823	UI-H-BM1-	608	27	0.7	1476	11	AK086146	AK086146	Mus_muscu
536	27	0.7	240	10	AM205815	UI-H-B11-	609	26	0.7	1477	13	BY000062	BY000062	BY000062
537	27	0.7	294	14	CB702202	AMGNNUC:C	610	26	0.7	160	10	BF193150	BF193150	244630 MA
538	27	0.7	361	14	CB968119	ERSTeF65	611	26	0.7	172	10	AM629635	AM629635	h167h08.Y
539	27	0.7	375	14	CB758371	ERSTeF620	612	26	0.7	174	14	CD342201	CD342201	ERSTeF49
540	27	0.7	392	14	CB774996	AMGNNUC:M	613	26	0.7	179	9	A1843475	A1843475	UI-M-AQ1-
541	27	0.7	400	10	BES83884	UX22h07.Y	614	26	0.7	185	10	AM214850	AM214850	BY000064
542	27	0.7	406	14	CD664952	ERSTeG50	615	26	0.7	187	10	BSE62132	BSE62132	BY000064
543	27	0.7	414	12	BG909688	TALr1107E	616	26	0.7	195	28	AQ848999	AQ848999	LMaJFV1_1
544	27	0.7	462	14	CB736553	ERSTeF54	617	26	0.7	200	10	AM919595	AM919595	ERSTeF50899
545	27	0.7	484	9	AV632518	AV632518	618	26	0.7	202	9	AV753500	AV753500	AV753500
546	27	0.7	485	12	B1895845	ERSTeF54	619	26	0.7	202	13	BY000064	BY000064	BY000064
547	27	0.7	487	12	BG929784	etERSTeF02	620	26	0.7	202	14	CD729710	CD729710	4037103 1
548	27	0.7	488	9	AA391431	LD09869.5	621	26	0.7	202	14	H33534	H33534	EST109643 R
549	27	0.7	495	13	B0645005	mgn017XD	622	26	0.7	204	28	A2397053	A2397053	1M0161B23
550	27	0.7	498	12	B1895846	ERSTeF035	623	26	0.7	210	13	BY358698	BY358698	BY358698
551	27	0.7	503	9	AV632519	AV632519	624	26	0.7	213	12	BG929698	BG929698	etERSTeF01
552	27	0.7	503	9	AV632519	AV632519	625	26	0.7	218	13	BY354960	BY354960	BY354960
553	27	0.7	511	14	CF103385	ERSTeG70	626	26	0.7	237	12	BM076910	BM076910	T-RE8910
554	27	0.7	520	12	CD346767	ERSTeG32	627	26	0.7	237	12	B1895396	B1895396	ERSTeG36
555	27	0.7	521	14	CD346767	ERSTeG97	628	26	0.7	257	12	B1895396	B1895396	B0362B09-
556	27	0.7	524	12	BM951289	UI-M-EH0-	629	26	0.7	268	14	BF058662	BF058662	RCO-HT088
557	27	0.7	524	14	CD912324	CD912324	630	26	0.7	270	10	BF088700	BF088700	RCO-HT088
558	27	0.7	526	9	AV703009	AV703009	631	26	0.7	270	10	BF088700	BF088700	ERSTeF46
559	27	0.7	540	10	BF073650	220587 MA	632	26	0.7	279	14	CD659108	CD659108	ERSTeF622
560	27	0.7	546	12	BM951300	UI-M-EH0-	633	26	0.7	279	14	CD666374	CD666374	ERSTeF622
561	27	0.7	556	14	CD346698	ERSTeG96	634	26	0.7	280	13	BY522026	BY522026	B1522026
562	27	0.7	556	12	BM305527	ERSTeG32	635	26	0.7	281	9	AA361962	AA361962	EST11301
563	27	0.7	566	14	CD347334	ERSTeG68	636	26	0.7	282	10	BBS62759	BBS62759	BBS62759
564	27	0.7	567	13	BQ599899	MT-P-B6-a	637	26	0.7	282	10	BBS60982	BBS60982	BBS60982
565	27	0.7	575	13	BX509225	DKFzP86M	638	26	0.7	282	14	CD666558	CD666558	ERSTeF626
566	27	0.7	579	14	CD912323	CD912323	639	26	0.7	286	12	BG276186	BG276186	UV01D01.Y
567	27	0.7	596	14	CF103512	ERSTeG72	640	26	0.7	289	10	BF040037	BF040037	BP250004B
568	27	0.7	599	10	AM940549	GHI4459.3	641	26	0.7	292	12	B1895497	B1895497	ERSTeG458
569	27	0.7	601	14	CD661453	ERSTeG47	642	26	0.7	293	10	BBS61999	BBS61999	BBS61999
570	27	0.7	613	12	B0215173	B0215173	643	26	0.7	295	9	AV167233	AV167233	AV167233
571	27	0.7	628	18	B2906589	CH240_29L	644	26	0.7	296	13	BY355017	BY355017	BY355017
572	27	0.7	632	24	CD579845	EST_PSF00	645	26	0.7	297	29	CG457530	CG457530	KRIAB_2D
573	27	0.7	641	28	A2627945	1M0469C20	646	26	0.7	304	14	CD665473	CD665473	ERSTeG44
574	27	0.7	659	10	BBE27807	uus4f01.Y	647	26	0.7	305	9	AA300819	AA300819	EST13767
575	27	0.7	699	14	CF8871938	tr:c029xe	648	26	0.7	310	14	CF545342	CF545342	1ae77H02
576	27	0.7	728	14	CB520243	UI-M-G10-	649	26	0.7	312	10	AM178929	AM178929	MRO-ST003
577	27	0.7	730	29	CB539637	cl1gr-g98-	650	26	0.7	312	12	B1020956	B1020956	112-MT017
578	27	0.7	741	14	CF877379	tr:c075xm	651	26	0.7	313	9	BY185424	BY185424	BY185424
579	27	0.7	745	14	278344	H8278344.Hu	652	26	0.7	317	12	BG929750	BG929750	bso1h04.Y
580	27	0.7	754	14	278344	H8278344.Hu	653	26	0.7	319	12	BG953065	BG953065	MR4-CY053
581	27	0.7	755	14	CB902165	tr:c029xe	654	26	0.7	324	14	CD660221	CD660221	ERSTeF56
582	27	0.7	755	14	CB902165	tr:c029xe	655	26	0.7	324	10	AM371805	AM371805	CM2-BT030
583	27	0.7	780	13	B0055071	UI-M-FC0-	656	26	0.7	325	13	B0411790	B0411790	60152487
584	27	0.7	789	13	BU0706387	UI-M-FC0-	657	26	0.7	326	13	B0411790	B0411790	OGW0590TH
585	27	0.7	794	29	CC476806	CH240_302	658	26	0.7	326	29	CG288718	CG288718	ERSTeG46
586	27	0.7	795	9	AV704315	AV704315	659	26	0.7	328	12	B1895457	B1895457	ERSTeG46
587	27	0.7	805	14	CB905720	tr:c075xm	660	26	0.7	328	14	CD600372	CD600372	RK123A3B0
588	27	0.7	808	28	BH083677	RPCI-24-3	661	26	0.7	330	12	B1895509	B1895509	ERSTeG63

662	26	0.7	331	13	BY220998	BY220998	735	26	0.7	370	13	BY174398	BY174398
663	26	0.7	332	13	BY778378	BY778378	736	26	0.7	372	9	AA899172	AA899172
664	26	0.7	332	29	CE800275	CE800275	737	26	0.7	372	10	BE286766	BE286766
665	26	0.7	333	14	T08930	EST06822.In	738	26	0.7	374	12	BI895484	BI895484
666	26	0.7	333	13	BY187135	BY187135	739	26	0.7	374	13	BY175970	BY175970
667	26	0.7	336	13	BY181564	BY181564	740	26	0.7	375	10	BE548841	BE548841
668	26	0.7	337	13	BY188050	BY188050	741	26	0.7	375	12	BI895759	BI895759
669	26	0.7	337	28	AZ852656	2M0155X15	742	26	0.7	375	13	BY005428	BY005428
670	26	0.7	338	28	AZ780299	2M0017H02	743	26	0.7	375	13	BY198412	BY198412
671	26	0.7	339	10	AM681888	CM3-CT034	744	26	0.7	376	13	BY205060	BY205060
672	26	0.7	340	13	BY098244	BY098244	745	26	0.7	378	12	BG561070	BG561070
673	26	0.7	340	13	BY186754	BY186754	746	26	0.7	378	12	BI895438	BI895438
674	26	0.7	341	13	BY136849	BY136849	747	26	0.7	378	13	BY028081	BY028081
675	26	0.7	342	13	BY109162	BY109162	748	26	0.7	380	13	BY133117	BY133117
676	26	0.7	342	13	BY176442	BY176442	749	26	0.7	380	14	CD345291	CD345291
677	26	0.7	343	9	A1944453	B601F01.Y	750	26	0.7	384	12	BG516259	BI895013
678	26	0.7	343	13	BY188076	BY188076	751	26	0.7	384	12	BI895013	BI895013
679	26	0.7	344	10	AM464785	BP230016B	752	26	0.7	386	14	CB806753	CB806753
680	26	0.7	344	13	BY190822	BY190822	753	26	0.7	388	13	BY174542	BY174542
681	26	0.7	345	13	BY181165	BY181165	754	26	0.7	388	13	BY174823	BY174823
682	26	0.7	345	13	BY184180	BY184180	755	26	0.7	389	12	BI895518	BI895518
683	26	0.7	346	13	BY186564	BY186564	756	26	0.7	389	9	AL709633	AL709633
684	26	0.7	346	13	BY192552	BY192552	757	26	0.7	398	13	BY018675	BY018675
685	26	0.7	346	13	BY349322	BY349322	758	26	0.7	399	14	CB706256	CB706256
686	26	0.7	347	13	BY208762	BY208762	759	26	0.7	401	14	CB548085	CB548085
687	26	0.7	348	13	BY186480	BY186480	760	26	0.7	401	14	U80749	U80749
688	26	0.7	348	13	BY186884	BY186884	761	26	0.7	405	9	AA065271	AA065271
689	26	0.7	348	13	BY191302	BY191302	762	26	0.7	405	9	AA065279	AA065279
690	26	0.7	349	13	BO169410	WHE3755-1	763	26	0.7	405	9	AA065308	AA065308
691	26	0.7	349	13	BY186927	BY186927	764	26	0.7	406	9	AA088367	AA088367
692	26	0.7	349	13	BY187211	BY187211	765	26	0.7	407	9	AI482508	AI482508
693	26	0.7	349	13	BY187368	BY187368	766	26	0.7	407	12	BG560846	BG560846
694	26	0.7	350	10	BP41599	BP250007.A	767	26	0.7	409	28	AZ297519	AZ297519
695	26	0.7	350	14	CF133709	WHE3362.D	768	26	0.7	410	10	BE920925	BE920925
696	26	0.7	351	13	BY180247	BY180247	769	26	0.7	410	13	BY180983	BY180983
697	26	0.7	352	10	BE839212	RC0-FN014	770	26	0.7	411	9	AY708830	AY708830
698	26	0.7	352	13	BY175643	BY175643	771	26	0.7	412	9	AI945592	AI945592
699	26	0.7	352	13	BY181335	BY181335	772	26	0.7	412	10	BE225249	BE225249
700	26	0.7	353	12	BG986317	CM1-HT114	773	26	0.7	412	9	AA575330	AA575330
701	26	0.7	353	13	BY180349	BY180349	774	26	0.7	412	12	BI895448	BI895448
702	26	0.7	353	13	BY199405	BY199405	775	26	0.7	415	12	BI895861	BI895861
703	26	0.7	353	13	BY200143	BY200143	776	26	0.7	415	28	AZ839702	AZ839702
704	26	0.7	354	13	BY024500	BY024500	777	26	0.7	415	29	CNS03JLV	CNS03JLV
705	26	0.7	354	13	BY177868	BY177868	778	26	0.7	416	9	AA549687	AA549687
706	26	0.7	355	13	BY177097	BY177097	779	26	0.7	416	14	CB767989	CB767989
707	26	0.7	355	13	BY205243	BY205243	780	26	0.7	417	12	BG516192	BG516192
708	26	0.7	356	9	AV708885	AV708885	781	26	0.7	417	13	BY189188	BY189188
709	26	0.7	356	13	BY177769	BY177769	782	26	0.7	418	9	AI551096	AI551096
710	26	0.7	357	9	AA065280	e01500c.T	783	26	0.7	419	10	BE988701	BE988701
711	26	0.7	357	13	AA417220	AA417220	784	26	0.7	419	13	BY201555	BY201555
712	26	0.7	358	13	BY177927	BY177927	785	26	0.7	419	14	CB968111	CB968111
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## ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION  
AGENCOURT 8346064 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6250774  
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ACCESSION  
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VERSION  
B0684810.1 GI:21810126  
KEYWORDS  
EST.  
SOURCE  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 907)  
NID-MGC http://mgc.nci.nih.gov/  
TITLE  
Unpublished (1999)  
JOURNAL  
Contact: Robert Strausberg, Ph.D.  
COMMENT  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DATA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/liml.at:  
http://image.liml.gov  
Plate: LIMC2394 row: f column: 23  
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Location/Qualifiers

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/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGACGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 19.9%; Score 786; DB 13; Length 907;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	241	CCCCCAACCTTACCAAAATTCATGAGCTTCAAGTCTTGGCGACCTCCCGCACCGC	300
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OY		3797	TCGACGGGGGTCTTCAATGCACAAGAGCTCAGAAGCTCAAGTTCCGTGTGAGCGGAATG	3855
Dd		661	TCGACGGGGGTCTTCAATGCACAAGAGCTCAGAAGCTCAAGTTCCGTGTGAGCGGAATG	720
OY		3857	ACAAGGTGTTTTTTGCTCAGTCCGCTCTGGGGGAGAGCAGCCAATTACTTAGATCATC	3914
Dd		721	ACAAGGTGTTTTTTGCTCAGTCCGCTCTGGGGGAGAGCAGCCAATTACTTAGATCATC	780
OY		3917	TGAACC	3922
Dd		781	TGAACC	786
RESULT 2		BUS42554	908 bp	mRNA linear EST 13-SEP-2002
LOCUS		AGENCOURT_10322513_NIH_MGC_40_Homo_sapiens	cdna clone IMAGE:65744339	
DEFINITION		5' mRNA sequence.		
ACCESSION		BUS42554		
VERSION		BUS42554.1	GI:22853037	
KEYWORDS		EST.		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL		NIH-MGC http://mgi.nci.nih.gov/.		
COMMENT		National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contract: Robert Strausberg, Ph.D. Email: cga@b-remail.nih.gov Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ruben Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LILCM2769 row: 1 column: 23 High quality sequence stop: 686.		
FEATURES		location/Qualifiers		
Source		1..908		
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		/mol_type="mRNA"		
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		/clone="IMAGE:65744339"		
		/tissue_type="carcinoma, cell line"		
		/lab_host="DH10B (phage-resistant)"		
		/clone_1ib="NIH_MGC_40"		
		/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Library constructed by Ling Hong in the laboratory of Gerald W. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."		
ORIGIN				
Query Match		19.7%	Score 779;	DB 13; Length 908;
Best Local Similarity		100.0%;	Pred. No. 0;	
Matches 779;		Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
OY		2679	CCTGTCACGCCACCACTCACCCACCGAAGAACGAAAGGCCAACCCACTTCGAA	2738
Dd		1	CCTGTCACGCCACCACTCACCCACCGAAGAACGAAAGGCCAACCCACTTCGAA	60
OY		2739	GGATGGAGTGGTGACTACCACTCTCGTGGAGCTGGTAAGAGCCCTGGCAAGAGCTGTT	2798
Dd		61	GGATGGAGTGGTGACTACCACTCTCGTGGAGCTGGTAAGAGCCCTGGCAAGAGCTGTT	120
OY		2799	CACGATGTTTGTGATCTTAGGATTTACCAAGCTTGAGAGCACTGGGGACAGATCCCAT	2858

Db	121	CACAGTGTGTGGATCTAAGGATCTACAGCCTGAGAGCGAGTGGGACAGACATCCCAT	180
Qy	2859	CACAGCCTTAAGTGGGTGGAGAGGGCACTCGGCTGCACCACTGCAGATACAGCTGAGGAA	2918
Db	181	CACAGCCTTAAGTGGGTGGAGAGGGCACTCGGCTGCACCACTGCAGATACAGCTGAGGAA	240
Qy	2919	GGGTTCGTGGTCAACGTGAATCCCAACCAACCCGGGGCCACAGTGAAGACCCCTGAGAT	2978
Db	241	GGGTTCGTGGTCAACGTGAATCCCAACCAACCCGGGGCCACAGTGAAGACCCCTGAGAT	300
Qy	2979	CCGGAAAGTACAAGAAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGCTCAA	3038
Db	301	CCGGAAAGTACAAGAAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGCTCAA	360
Qy	3039	CCTGCTGGTGGGCAACGAGAAACGGGCTGATGTTGCTGAGACCGAAAGTGGGCAAGGT	3098
Db	361	CCTGCTGGTGGGCAACGAGAAACGGGCTGATGTTGCTGAGACCGAAAGTGGGCAAGGT	420
Qy	3099	GTAAGACATCAATTTGGGGGGCGACGCTTCCAGACATGGAATGTCGTGAGGGGCTCAACT	3158
Db	421	GTAAGACATCAATTTGGGGGGCGCGCAAGCTTCCAGACATGGAATGTCGTGAGGGGCTCAACT	480
Qy	3159	GCTCATCAACATCTCAGGGAAAAAGAAACAACTCGGGTGTATTACCTGTCTTGCTCG	3218
Db	481	GCTCATCAACATCTCAGGGAAAAAGAAACAACTCGGGTGTATTACCTGTCTTGCTCG	540
Qy	3219	GAAACAGATTCTGCACAATGACCCAGAAAGTGAAGAAAGCAGGGCTTGACACACCTGGG	3278
Db	541	GAAACAGATTCTGCACAATGACCCAGAAAGTGAAGAAAGCAGGGCTTGACACACCTGGG	600
Qy	3279	GGAACATGAGGGGCTGCGGGGCACTACCGTGTGTGAATAAGAGGGGATTAGTTCTGTGT	3338
Db	601	GGAACATGAGGGGCTGCGGGGCACTACCGTGTGTGAATAAGAGGGGATTAGTTCTGTGT	660
Qy	3339	CATGCGCCCTCAAGAGCTCCGATGAGAGTATGACCTGGGGCCCAAAACCTTACCACAATT	3398
Db	661	CATGCGCCCTCAAGAGCTCCGATGAGAGTATGACCTGGGGCCCAAAACCTTACCACAATT	720
Qy	3399	CATGAGCCTTCAAGTCTTTTGCCGACCTCCGCCACCGGCTCTGTGTGACACTGACAG	3457
Db	721	CATGAGCCTTCAAGTCTTTTGCCGACCTCCGCCACCGGCTCTGTGTGACACTGACAG	779
RESULT 3			
LOCUS	BUB38349	969 bp	mRNA linear EST 16-OCT-2002
DEFINITION	AGENCOURT 8123283	Lupeki_dorsal_root_ganglion	Homo sapiens cDNA
ACCESSION	BUB38349		
VERSION	BUB38349.1	GI:24022744	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Bukacynska, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 969)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: csapbe-remail.nih.gov		
	Tissue Procurement: Dr. James R. Lupski		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.lnl.gov		
	Plate: LRAM3554 row: a column: 23		
	High quality sequence spot: 626.		
FEATURES	Location/Qualifiers		
source	1..969		
	/organism="Homo sapiens"		

/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6176926"  
/sex="male"  
/tissue\_type="dorsal root ganglia"  
/dev\_stage="adult, 36 yr"  
/lab\_host="DH10B"  
/clone\_lib="lupski dorsal root ganglion"  
/note="Vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
NotI Site\_2: SalI; cDNA made by oligo-dT priming.  
Directionally cloned using the following adaptors:  
5'-GACTAGTCTAGATCGCAGCGCGCCCTT(15)-3'. Size selected >  
1 kb for average insert length 1.7 kb. This is a primary  
library, non-amplified. Library constructed by Life  
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
College of Medicine) and is available through Life  
Technologies."

## ORIGIN

Query Match 19.2%; Score 757; DB 13; Length 969;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 757; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1553 AACCAAGCTGGGCGCCGAGAGTGAAGAGAAAGATGAACAAGCAGAGAACTTC 1612  
9 AACCAAGCTGGGCGCCGAGAGTGAAGAGAAAGATGAACAAGCAGAGAACTTC 68  
1613 CCTGGCCAGAGCAAGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1672  
69 CCTGGCCAGAGCAAGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 128  
1673 CAGGGGCCCCAG 1732  
129 CAGGGGCCCCAG 188  
1733 AGGGAACCGGCAAGTCTCTGCAAGACCAAGCCCAAGCTGCTGCTTCCAGCT 1792  
189 AGGGAACCGGCAAGTCTCTGCAAGACCAAGCCCAAGCTGCTGCTTCCAGCT 248  
1793 CCCATGACCCGCAAGCTCTGCAAGACCAAGCCCAAGCTGCTGCTTCCAGCT 1852  
249 CCCATGACCCGCAAGCTCTGCAAGACCAAGCCCAAGCTGCTGCTTCCAGCT 308  
1853 TCATCCGCGCAAGTCTGCAAGACCAAGCCCAAGCTGCTGCTTCCAGCT 1912  
309 TCATCCGCGCAAGTCTGCAAGACCAAGCCCAAGCTGCTGCTTCCAGCT 368  
1913 CCTGGGTCGCGCCAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1972  
369 CCTGGGTCGCGCCAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 428  
1973 CCACTGACCTTAAACACAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2032  
429 CCACTGACCTTAAACACAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 488  
2033 GACCTGAGAGCAAGTCCGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2092  
489 GACCTGAGAGCAAGTCCGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 548  
2093 CAAAGGCTTCAG 2152  
549 CAAAGGCTTCAG 608  
2153 ACCTGAG 2212  
609 ACCTGAG 668  
2213 GGCACCTCTCCGAG 2272  
669 GGCACCTCTCCGAG 728  
2273 ACAGCTCCCTGCTCTCCCTGAGAGATTAAGCCAA 2309

Db 729 ACAGCTCCCTGCTCTCCCTGAGAGATTAAGCCAA 765

RESULT 4  
AL551911 1201 bp mRNA linear EST 31-MAY-2003  
LOCUS  
DEFINITION  
AL551911 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
clone CS001060YH23 5-PRIME, mRNA sequence.  
AL551911  
ACCESSION  
AL551911.2 GI:31273727  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
1 (bases 1 to 1201)  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 15, 2001 this sequence version replaced gi:1289305.  
COMMENT  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 8486.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS001060CD1201P1cluster=8486.f. Contact :  
Feng Liang Email : fliang@life.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS001060CD120P1.  
location/Qualifiers

## FEATURES

1..1201  
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/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 18.6%; Score 735; DB 9; Length 1201;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

7 ATGGGCGAGCCAGCCCGCCGCGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 66  
258 ATGGGCGAGCCAGCCCGCCGCGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 317  
67 CCTGCTGGAGATTTTGAAGCTTGTGAGAGGTGTGTGCAATGAACTTACGAGGTATC 126  
318 CCTGCTGGAGATTTTGAAGCTTGTGAGAGGTGTGTGCAATGAACTTACGAGGTATC 377  
127 AAGGCTCGCATGTCAAGAGCGGAGAGCTGCTGCAATCAAGGTATGATGTACCGAG 186  
378 AAGGCTCGCATGTCAAGAGCGGAGAGCTGCTGCAATCAAGGTATGATGTACCGAG 437  
187 GACGAGAGAGAGAGAGATCAAGAGAGATCAAGTGTGAAAAGTACTCTCACCACGCC 246  
438 GACGAGAGAGAGAGAGATCAAGAGAGATCAAGTGTGAAAAGTACTCTCACCACGCC 497  
247 AACATCGCACTTACTTACGAGAGCTTCAATCAAGAGAGAGAGAGAGAGAGAGAGAG 306  
498 AACATCGCACTTACTTACGAGAGCTTCAATCAAGAGAGAGAGAGAGAGAGAGAGAG 557  
307 CTGTGCTGTGTAGTGAAGTCTGTGTGCTGTGTCAATGATGACTGAGTGAAGAGACCA 366

Db 558 CTGTGGCTGTGATGAGATTTCTGTGTGTGTGTTCTGATGACTGACCTGTAAAGACCA 617  
Qy 367 AAAGGCAACGCCCTTGAAAGAGACTGTATCCCTTATATCTGACAGGAGATCTCAGGGGT 426  
Db 618 AAAGGCAACGCCCTTGAAAGAGACTGTATCCCTTATATCTGACAGGAGATCTCAGGGGT 677  
Qy 427 CTGGCCCATCTCCATGCCCAAGGTGATTCATGAGACATCAAGGGGAGAAATGTGTG 486  
Db 678 CTGGCCCATCTCCATGCCCAAGGTGATTCATGAGACATCAAGGGGAGAAATGTGTG 737  
Qy 487 CTGACAGAGATGCTGAGGTCAAGCTAGTGAATTTTGGGTGAGTCTCAGCTGAGCCGC 546  
Db 738 CTGACAGAGATGCTGAGGTCAAGCTAGTGAATTTTGGGTGAGTCTCAGCTGAGCCGC 797  
Qy 547 ACCGTGGGAGACGGAACATTTTCAATTGGGACTCCCTTACTGAGTGGCTCCAGAGTCAATC 606  
Db 798 ACCGTGGGAGACGGAACATTTTCAATTGGGACTCCCTTACTGAGTGGCTCCAGAGTCAATC 857  
Qy 607 GCGCTGTATGAGAACCTGTATGCGACCTATGATTAACAGAGTGAATTTTGGTCTCTAGGA 666  
Db 858 GCGCTGTATGAGAACCTGTATGCGACCTATGATTAACAGAGTGAATTTTGGTCTCTAGGA 917  
Qy 667 ATCAACAGCATGAGATGAG 726  
Db 918 ATCAACAGCATGAGATGAG 977  
Qy 727 GCCCTCTTCTCTATT 741  
Db 978 GCCCTCTTCTCTATT 992

RESULT 5  
BUS42006 881 bp mRNA linear EST 13-SEP-2002  
LOCUS AGENCOURT 10252775 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:6573796  
DEFINITION 5', mRNA sequence.

ACCESSION BUS42006  
VERSION BUS42006.1 GI:22852489  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 881)  
NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.  
Email: rgs@dbp-remail.nih.gov

Tissue Procurement: DCTD/DBP

cDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILMN at:

http://image.llnl.gov

Plate: L1CM2768 row: b column: 04

High quality sequence stop: 680.

Location/Qualifiers

1. 881

/organism="Homo sapiens"

/mol\_type="mRNA"

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/clone="IMAGE:6573796"

/tissue\_type="carcinoma, cell line"

/lab\_host="RDH108 (phage-resistant)"

/clone\_lib="NIH\_MGC\_40"

/note="Organ: prostate; Vector: pOTB7, Site: 1: XhoI;

Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACAG(G). Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

Query Match 18.5%; Score 730; DB 13; Length 881;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 780; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## ORIGIN

Qy 2679 CTGTGTCCAGCCCGACCTCCTACCCAGGAGAAAGAGAAAGCCCAAGCCCTGGAA 2738  
Db 1 CTGTGTCCAGCCCGACCTCCTACCCAGGAGAAAGAGAAAGCCCAAGCCCTGGAA 60  
Qy 2739 GGATGGAGTGTGTACTACCAAGTCTGTGGGCTGTGTAAAGCCCTGGCAAGAGCTGT 2798  
Db 61 GGATGGAGTGTGTACTACCAAGTCTGTGGGCTGTGTAAAGCCCTGGCAAGAGCTGT 120  
Qy 2799 CACGATTTTGTGTGATCTAGGGATCTACCAAGCTGTAGAGGAGAGGAGAGAGATCCCAT 2858  
Db 121 CACGATTTTGTGTGATCTAGGGATCTACCAAGCTGTAGAGGAGAGGAGAGATCCCAT 180  
Qy 2859 CACAGCCCTTGT 2918  
Db 181 CACAGCCCTTGT 240  
Qy 2919 GGGTCTGT 2978  
Db 241 GGGTCTGT 300  
Qy 2979 CCGAGATTAAGAGAGAGATTTCACTCCGAGATCTCTGTGTGTGTGTGTGTGTGTGTGT 3038  
Db 301 CCGAGATTAAGAGAGAGATTTCACTCCGAGATCTCTGTGTGTGTGTGTGTGTGTGTGT 360  
Qy 3039 CTGT 3098  
Db 361 CTGT 420  
Qy 3099 GTATGACTATTTGGGGGGGAGGCTTCCAGAGATGATGTGTGTGTGTGTGTGTGTGTGT 3158  
Db 421 GTATGACTATTTGGGGGGGAGGCTTCCAGAGATGATGTGTGTGTGTGTGTGTGTGTGT 480  
Qy 3159 GCTTCATCAACATCTCAGGAGAAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3218  
Db 481 GCTTCATCAACATCTCAGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
Qy 3219 GAACAGATTTCTGT 3278  
Db 541 GAACAGATTTCTGT 600  
Qy 3279 GGAATGAGAGGGCTGT 3338  
Db 601 GGAATGAGAGGGCTGT 660  
Qy 3339 CATGCCCTCAAGAGCTCCGT 3398  
Db 661 CATGCCCTCAAGAGCTCCGT 720  
Qy 3399 CATGCCCTCAAGAGCTCTTTTGGCCGACTCCCAAGCCCTCTGTGTGTGTGTGTGTGT 3458  
Db 721 CATGCCCTCAAGAGCTTTTGGCCGACTCCCAAGCCCTCTGTGTGTGTGTGTGTGTGT 780  
Qy 3459 A 3459  
Db 781 A 781

RESULT 6  
CD557991 910 bp mRNA linear EST 11-JUN-2003  
LOCUS AGENCOURT 14423308 NIH\_MGC\_180 Homo sapiens cDNA clone

DEFINITION IMAGE:30387142 5', mRNA sequence.

ACCESSION CD557991  
VERSION CD557991.1 GI:31584059  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 910)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics / NIH  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: Dr. Michael Brownstein  
 cDNA Library Preparation: Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at: <http://image.llnl.gov>  
 Plate: NDAM456 row: 0 column: 23  
 High quality sequence stop: 637.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:30387142"  
 /lab\_host="DH10B-Ton A (T1 and T5 phage resistances)"  
 /clone\_1lb="NIH-MGC 180"  
 /note="Organ: Testis; Vector: pCMV-Sport6.1; Site 1: NciI; Site 2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.68 kb. Library was constructed by (Invitrogen). Note: This is a NIH-MGC library."  
 ORIGIN  
 Query Match 18.4%; Score 727; DB 14; Length 910;  
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 727; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 2952 CCGGGCCCAAGTGAAGCCCTGAGATCCGGAAGTACAGAAAGCATTCAGATCCGAGAT 3011  
 1 CCGGGCCCAAGTGAAGCCCTGAGATCCGGAAGTACAGAAAGCATTCAGATCCGAGAT 60  
 3012 CCTCTGTGAGCCCTTTGGGGGGTCAACTGCTGTGGGACGAGAAACGGGCTGATGTT 3071  
 61 CCTCTGTGAGCCCTTTGGGGGGTCAACTGCTGTGGGACGAGAAACGGGCTGATGTT 120  
 3072 GGTGACCGAAGTGGGACGAGGAGAGTGTATGACTATTTGGGCGGCGAGCTTCCAGCA 3131  
 121 GCTGACCGAAGTGGGACGAGGAGAGTGTATGACTATTTGGGCGGCGAGCTTCCAGCA 180  
 3132 GATGATGTGTGAGGGGGCTCAACTGCTCATCACTCTGACGAGAAAGAACT 3191  
 181 GATGATGTGTGAGGGGGCTCAACTGCTCATCACTCTGACGAGAAAGAACT 240  
 3192 GCGGGTGATTAATTCTGTCTGCTCCGGAACAAGATTCTGCAATGACCAAGAGTGA 3251  
 241 GCGGGTGATTAATTCTGTCTGCTCCGGAACAAGATTCTGCAATGACCAAGAGTGA 300  
 3252 GAAAGAACGGGCTGACCAACGCTGGGGGACATGAGGGCTCGGGCACTACCGTGTCT 3311  
 301 GAAAGAACGGGCTGACCAACGCTGGGGGACATGAGGGCTCGGGCACTACCGTGTCT 360  
 3312 GAAATACGAGCGGATTAATTCTGTCTGCTCCGGAACAAGATTCTGCAATGACCAAGAGTGA 3371  
 361 GAAATACGAGCGGATTAATTCTGTCTGCTCCGGAACAAGATTCTGCAATGACCAAGAGTGA 420  
 3372 CTGGGCCCCCAACCTTACCAAAATTCATGAGCTTCAAGTCTTTGCGGACCTCCCA 3431  
 421 CTGGGCCCCCAACCTTACCAAAATTCATGAGCTTCAAGTCTTTGCGGACCTCCCA 480

3432 CCGCCCTGCTGTGTCAGCTGACAGTGAAGAGGGGAGGGCTCAAGTCACTATG 3491  
 481 CCGCCCTGCTGTGTCAGCTGACAGTGAAGAGGGGAGGGCTCAAGTCACTATG 540  
 3492 CTCAGTGTGCTGCTTCCATGCTGTGATGTGACTTCGGGGAACGCTATGACTAT 3551  
 541 CTCAGTGTGCTGCTTCCATGCTGTGATGTGACTTCGGGGAACGCTATGACTAT 600  
 3552 CCTGTGACATTCAGAGCGGATCAAGCGCCATGCACTCTTCCGCCAACACCA 3611  
 601 CCTGTGACATTCAGAGCGGATCAAGCGCCATGCACTCTTCCGCCAACACCA 660  
 3612 CCGCATGAGATGTGCTGTCTCTACAGAGACGAGGCTGTACATCAACATGACG 3671  
 661 CCGCATGAGATGTGCTGTCTCTACAGAGACGAGGCTGTACATCAACATGACG 720  
 3672 CATCAT 3678  
 721 CATCAT 727  
 RESULT 7  
 LOCUS BC028888 1515 bp mRNA linear HTC 19-NOV-2003  
 DEFINITION Homo sapiens mishapen/NIK-related kinase, mRNA (cDNA clone IMAGE:4751958), with apparent retained intron.  
 ACCESSION BC028888  
 VERSION BC028888.1 GI:20809392  
 KEYWORDS HTC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 1515)  
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Diatchenko, L., Marins, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udell, T.B., Toshylyuk, S., Aramini, P., Prange, C., Raha, S.S., Loggellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smolins, D.E., Schermer, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 JOURNAL MEDLINE 22388257  
 PUBMED 12477932  
 2 (bases 1 to 1515)  
 Strausberg, R.  
 Direct Submission  
 Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: <http://mgs.nci.nih.gov>  
 Contact: MGC help desk  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: James Cleaver, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)  
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

REMARK  
 COMMENT







CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
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High quality sequence stop: 686.  
Location/Qualifiers

FEATURES  
source

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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.75 kb. Library constructed by Life  
Technologies."

## ORIGIN

Query Match 17.6%; Score 697; DB 12; Length 936;  
Best Local Similarity 100.0%; Pred. No. 6.2e-310; Indels 0; Gaps 0;  
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 CAGTGAAGACGACGAGAGAGAGCGAGCGGCGACAGAGGAGAGATACCCC 60  
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Db 61 TGGGGGCGGACGCGATGGGGATACAGACAGCGTCAGCAGTGGTCCAGAGTTCGA 120  
QY 2562 GGAATCAACGGGAGCCAGCCCGCATACGAGGGGCGGACATGGTGCAGCGCACCCC 2621  
Db 121 GGAATCAACGGGAGCCAGCCCGCATACGAGGGGCGGACATGGTGCAGCGCACCCC 180  
QY 2622 TGAAGAGAGCGGAACTGTCTGATCTGACAGCAATGGATACAACTTGCCTGACGT 2681  
Db 181 TGAAGAGAGCGGAACTGTCTGATCTGACAGCAATGGATACAACTTGCCTGACGT 240  
QY 2682 GGTCAAGCCGACCACTACCCACGAGAAACAGCAAGGCCAAGCCCACTTGAAGA 2741  
Db 241 GGTCAAGCCGACCACTACCCACGAGAAACAGCAAGGCCAAGCCCACTTGAAGA 300  
QY 2742 TGGGAGTGTGATCACTACAGTCTCGTGGCTGGTAAAGGCCCTTGGCAAGCTGTTAC 2801  
Db 301 TGGGAGTGTGATCACTACAGTCTCGTGGCTGGTAAAGGCCCTTGGCAAGCTGTTAC 360  
QY 2802 GATGTTTGTGATCTAGGATCTACCAAGCTGAGAGGAGTGGGACAGCATCCCATCAC 2861  
Db 361 GATGTTTGTGATCTAGGATCTACCAAGCTGAGAGGAGTGGGACAGCATCCCATCAC 420  
QY 2862 AGCCCTAGTGGTGAAGGAGGAGCTCGGCTGACCAAGTGAAGTGAAGGAGG 2921  
Db 421 AGCCCTAGTGGTGAAGGAGGAGCTCGGCTGACCAAGTGAAGTGAAGGAGG 480  
QY 2922 TTTCTGTGTCAACGTGAATCCCAACCAAGCCGGGCGCAAGTGAAGCCCTGAGATCCG 2981  
Db 481 TTTCTGTGTCAACGTGAATCCCAACCAAGCCGGGCGCAAGTGAAGCCCTGAGATCCG 540  
QY 2982 GAAATCAAGAGAGATCACTCCAGAGATCTCTGTGACAGCCCTTGGGGGATCAACT 3041  
Db 541 GAAATCAAGAGAGATCACTCCAGAGATCTCTGTGACAGCCCTTGGGGGATCAACT 600  
QY 3042 GCTGGTGGGACGAGAAAGCGGCTGATGTTGTGAGCCGAAGTGGGCGAGGCGAAGTGA 3101  
Db 601 GCTGGTGGGACGAGAAAGCGGCTGATGTTGTGAGCCGAAGTGGGCGAGGCGAAGTGA 660  
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Db 661 TGAATCAATTTGGGGGAGCGCTTCAGAGATGAGT 697

RESULT 11  
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LOCUS AGENCOURT 8353101 NIH\_MGC\_113 Homo sapiens cDNA IMAGE:6278193  
DEFINITION 5', mRNA sequence.

ACCESSION BQ706178  
VERSION BQ706178.1 GI:21845077  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 951)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strauberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)

Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>

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High quality sequence stop: 710.  
Location/Qualifiers

FEATURES  
source

1..951

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/clone\_id="NIH\_MGC\_113"

/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:  
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GGCAGCGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,  
Berkeley) using Zap-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a

NIH\_MGC Library."

ORIGIN

Query Match 17.5%; Score 693; DB 13; Length 951;  
Best Local Similarity 100.0%; Pred. No. 4.4e-308; Indels 0; Gaps 0;

Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 24 CATGTGTGTCACAGAGTCGAGAGATCACCGGAGCCAGCCCATACGAGGGCGGAC 83

QY 2601 CATGTGTGTCACAGAGCCCTGTAAGAGAGCGGAACCTGTGATGCTGACAGCAATGG 2660  
Db 84 CATGTGTGTCACAGAGCCCTGTAAGAGAGCGGAACCTGTGATGCTGACAGCAATGG 143

QY 2661 GATGATGTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2720  
Db 144 GATGATGTCAG 203

QY 2721 CCAAGGCCAAGCCCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2780  
Db 204 CCAAGGCCAAGCCCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263

QY 2781 CCTGTGAG 2840  
Db 264 CCTGTGAG 323

QY 323 CCTGTGAG 323



Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asempson@ludwig.org.br  
 This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL.  
 (http://www.ludwig.org.br/scripte/gethtml2.pl?l1=MR3&l2=MR3-HN0063-040101-002-h01&l3=2001-01-04&l4=1)  
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 High quality sequence stop: 714.  
 Location/Qualifiers  
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 /note="Organ: head normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 16.0%; Score 633; DB 12; Length 727;  
 Best Local Similarity 100.0%; Pred. No. 2e-280;  
 Matches 633; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 AAATACGAGCGGATTAATCTCTGTCATCCGCTTCAGAGCTCCGTGAGAGTGTATGCC 60

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61 TGGGCCCCCAACCTACCAAAATTCATGAGCTCTTGGCGAGCTCCCGGAC 120

3433 CGCCCTCTGCTGTGTCAGCTGACAGTAGAGAGGGGAGCGGCTCAAGTCACTATGAGC 3492

121 CGCCCTCTGCTGTGTCAGCTGACAGTAGAGAGGGGAGCGGCTCAAGTCACTATGAGC 180

3493 TCCTGCTGCTGCTTCATGCTGTGATGTCGACTGGGGAACAGTATGACATCTACATC 3552

181 TCCTGCTGCTGCTTCATGCTGTGATGTCGACTGGGGAACAGTATGACATCTACATC 240

3553 CCTGTGCACTCCAGAGCAGATCAAGCCGATGCTATCTTCCCAACACCGAC 3612

241 CCTGTGCACTCCAGAGCAGATCAAGCCGATGCTATCTTCCCAACACCGAC 300

3613 GGCATGAGATGCTGCTGTGTCAGAGAGAGGGGTCTACGTCACACGATACGGGCGC 3672

301 GGCATGAGATGCTGCTGTGTCAGAGAGAGGGGTCTACGTCACACGATACGGGCGC 360

3673 ATCATTAAGATGTGTGCTGTCAGAGTGGGGAGATGCTTCTGTGGCTTACATCTGC 3732

361 ATCATTAAGATGTGTGCTGTCAGAGTGGGGAGATGCTTCTGTGGCTTACATCTGC 420

3733 TCACACGATTAATGAGGCTGGGGGTGAAGAACATGATCCGCTCTGGAAGCGGGC 3792

421 TCACACGATTAATGAGGCTGGGGGTGAAGAACATGATCCGCTCTGGAAGCGGGC 480

3793 CACCTCGACGGGGCTTTCATGACAAAGAGCTCAGAGGCTCAAGTTCTGTGTAGCGG 3852

481 CACCTCGACGGGGCTTTCATGACAAAGAGCTCAGAGGCTCAAGTTCTGTGTAGCGG 540

3853 AATGACAAAGGTGTTTGGCTCACTCGGCTCTGGGGGAGAGGCAAGTTACTTCTATG 3912

541 AATGACAAAGGTGTTTGGCTCACTCGGCTCTGGGGGAGAGGCAAGTTACTTCTATG 600

3913 ACTCGAACGTAACGATCATGAACTGTGTA 3945

Db 601 ACTCGAACGTAACGATCATGAACTGTGTA 633

## RESULT 14

BM800664

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

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Average insert size 2.1 kb.

15.7%; Score 621; DB 12; Length 1037;

Best Local Similarity 99.9%; Pred. No. 7.7e-275;

Matches 671; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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140 ATGGGCAACCCAGGCCCCCGGCGAGCTGGAGACATTCGACTGCGCCCTGGGAC 199

67 CCTGCTGGGATCTTGAAGCTTGTGAGAGTGTGCGCAATGAACTTACGAGGTATC 126

200 CCTGCTGGGATCTTGAAGCTTGTGAGAGTGTGCGCAATGAACTTACGAGGTATC 259

127 AAGGTCGGCATGTCAAGACGGGCGAGCTGCTCCATCAAGTTCATGATGTCAAGAG 186

260 AAGGTCGGCATGTCAAGACGGGCGAGCTGCTCCATCAAGTTCATGATGTCAAGAG 319

187 GACGAGAGAGAGATCAACAGAGATCAACATGCTGAAAGAAAGTACTCTCACACCGC 246

320 GACGAGAGAGAGATCAACAGAGATCAACATGCTGAAAGAAAGTACTCTCACACCGC 379

247 AACATCGCACTTACTACGAGCTTTCATCAAGAGAGCCCGCGGAAAGATGACCGAG 306

380 AACATCGCACTTACTACGAGCTTTCATCAAGAGAGCCCGCGGAAAGATGACCGAG 439

307 CTCTGGCTGGTATGAGTGTGTGTGCTGCTGCTTCACTGACTGATCTGTAAAGACCA 366

440 CTCTGGCTGGTATGAGTGTGTGTGCTGCTGCTTCACTGACTGATCTGTAAAGACCA 499

367 AAAGGCAACGCCCTGAAGAGAGACTGTATCGCCATATCTGCAAGAGATCTCAGGGGT 426

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Db      |||
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Db      |||
560  CTGGGCCCATCTTCATATGCCCAACAAGGTGATCCATCGAGACATGCAAGGGGAGAAATGTCTG 619
QY      |||
487  CTGACAGAGAAATGCTGAGGTCAAGCTAGTGTATTTTGGGGTGTAGTCTCAGCTGACCGC 546
Db      |||
620  CTGACAGAGAAATGCTGAGGTCAAGCTAGTGTATTTTGGGGTGTAGTCTCAGCTGACCGC 679
QY      |||
547  ACCGTGGGAGACGGAACACTTTTCATTGGGACTCCCTTACTGATGAGTGGCTCAGAGGTCTATC 606
Db      |||
680  ACCGTGGGAGACGGAACACTTTTCATTGGGACTCCCTTACTGATGAGTGGCTCAGAGGTCTATC 739
QY      |||
607  GCGTGTGATGAGAACCCCTGATATGCCCATCTTATGATTTACAGAGAGTATTTTGTCTTAGA 666
Db      |||
740  GCGTGTGATGAGAACCCCTGATATGCCCATCTTATGATTTACAGAGAGTATTTTGTCTTAGA 799
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Db      |||
800  ATCAGAGCCATC 811

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LOCUS        603178186p1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5242509 5',
DEFINITION   mRNA sequence.
ACCESSION    BI916276
VERSION      BI916276.1 GI:16180239
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE    NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE        Unpublished (1999)
JOURNAL      Contact: Robert Strausberg, Ph.D.
COMMENT       Email: cgsabers-remail.nih.gov
              Tissue Procurement: Life Technologies, Inc.
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
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Location/Qualifiers
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Site 2: EcoRV (destroyed); RNA source anonymous pool of 3
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and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

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ORIGIN
Query Match      15.6%; Score 616; DB 12; Length 629;
Best Local Similarity 100.0%; Pred. No. 1.4e-272;

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14  GGCAAGGTGATGAGCTCATTTGGGCGGCGAGCTTCCAGACAGATGATGTCTGAGGGG 73
QY      |||
3151  CTCAAACCTGCTCATCACCATTCTCAGGGGAAAGAAACAACCTGGGGGTATTTACTGTGCC 3210
Db      |||
74  CTCAAACCTGCTCATCACCATTCTCAGGGGAAAGAAACAACCTGGGGGTATTTACTGTGCC 133
QY      |||
3211  TGGCTCCGGAAACAAGATTCTGCAATGACCCAGAGTGGAGAAAGAGCAGGGCTGAGC 3270
Db      |||
134  TGGCTCCGGAAACAAGATTCTGCAATGACCCAGAGTGGAGAAAGAGCAGGGCTGAGC 193
QY      |||
3271  ACCGTGGGAGACATGAGAGGCTGCGGGCACTACCGTGTGTGAAATACAGCGATTAAG 3330
Db      |||
194  ACCGTGGGAGACATGAGAGGCTGCGGGCACTACCGTGTGTGAAATACAGCGATTAAG 253
QY      |||
3331  TTCTGTGTCATCGCCCTCAAGAGCTCGGTGAGGTGATGCTTGGGCCCCCAACCTTAC 3390
Db      |||
254  TTCTGTGTCATCGCCCTCAAGAGCTCGGTGAGGTGATGCTTGGGCCCCCAACCTTAC 313
QY      |||
3391  CACAAATTCATGAGCTTCAAGTCTTTGCCGACCTCCGCCACCGCCCTGCTGTGAC 3450
Db      |||
314  CACAAATTCATGAGCTTCAAGTCTTTGCCGACCTCCGCCACCGCCCTGCTGTGAC 373
QY      |||
3451  CTGACAGTAGAGAGAGGGGACGCGCTCAAGGTCTATGCTCCAGTGTGCTTCCAT 3510
Db      |||
374  CTGACAGTAGAGAGAGGGGACGCGCTCAAGGTCTATGCTCCAGTGTGCTTCCAT 433
QY      |||
3511  GCTGTGATGTGACTGCGGGGAAAGCTATGACATCTACATCTCTGTGCATCTCCAGC 3570
Db      |||
434  GCTGTGATGTGACTGCGGGGAAAGCTATGACATCTACATCTCTGTGCATCTCCAGC 493
QY      |||
3571  CAGATCAGCCCCCATATGCTCTCTCCCAACACCGAGGATGAGATGTGCTG 3630
Db      |||
494  CAGATCAGCCCCCATATGCTCTCTCCCAACACCGAGGATGAGATGTGCTG 553
QY      |||
3631  TGCTACGAGAGCAGAGGGTGTCTACGTCAACAGTACGGGCGCATATTAAGATGTGCTG 3690
Db      |||
554  TGCTACGAGAGCAGAGGGTGTCTACGTCAACAGTACGGGCGCATATTAAGATGTGCTG 613
QY      |||
3691  CTGCAAGTGGGGGAGAG 3706
Db      |||
614  CTGCAAGTGGGGGAGAG 629

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Job time : 6345 secs

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